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.

. . . . . .

Proceedings of October 16, 1991

Dolores Brewer,
Court Reporter.

COURT CONVENES. (Accused present.)

THE COURT: I might just at this moment deal before we bring in the jury with the application that was made by Mr. Furlotte to have Sergeant Poissonier made available as a witness, and my decision on that is this, that the Crown is obliged, having named him on a witness list, to produce him as a witness even though it may not choose to examine directly, and he is to be made available for cross-examination by counsel for the Accused. I am fully cognizant of the decision made by my colleague, Mr. Justice Stevenson, in R. V. Arsenault in which he expressed the view that witness lists attached to indictments are superfluous and really of no account and such has been the case since 1959 when a section was removed from the Criminal Code which required a list of witnesses to be included on the back of an indictment. I am inclined to agree with his views that the reason why that provision was in was before 1959 we had Grand Juries and Petit Juries. Petit Juries were the 12 person juries that we have today. In those days they were 12 men juries because females were not allowed, I guess, to serve on juries. But the Grand Juries were juries, I forget just what their numbers were, but they served the purpose of what the Provincial Court Judges or Magistrates do today in determining whether there's sufficient evidence to put an Accused on trial. The Grand Juries used to hear the witnesses listed on the back of the indictment. They would call them into a room, no lawyers or anybody else present, they interviewed

them. They didn't have to interview or hear all of the witnesses listed on the indictment. They could hear one out of twelve listed if they wanted to, or one out of two hundred and forty-three, and if they determined that an accused person should go on trial then they so ordered. They found what was known as a true bill, and they couldn't find no bill or order that an accused not be sent up for trial unless of course they heard all of the witnesses listed on the indictment, and that was the reason for the requirement at that time that the witnesses be included. Now, since the removal as far as I'm concerned it has always been the practice that the witnesses - the crown witnesses be listed on the indictment. There has been a bit of looseness in that practice recently because frequently when indictments are preferred at Motions Day, as we now call it, or have called it in recent years, the witnesses may not be listed but the Crown always gives an undertaking that they will provide the Defence with a list of the witnesses immediately and that list is attached to the indictment when the Accused is rearraigned at the actual trial.

In this case counsel will recall that on December 5th when the indictment was preferred I drew attention to the fact that the list of witnesses was not included and counsel at that time undertook to provide that immediately, and they did. Now, the sole question it's agreed - or it's common ground here that the name of Sergeant Poissonier was in the initial list. It was taken off, apparently, the

revised list subsequently. I fully recognize that the Crown can't be told what witnesses they are going to call or not going to call but I find that having named a witness that they are obliged to call that witness and make him available for cross-examination.

Now, I make this order that I am making but as far as the timing of his being called it's up to the Crown to decide when and presumably he will have to be wedged in between some of the DNA witnesses or at the end or at the end of the week or the beginning of next week or sometime, but that's up to the Crown, and presumably Crown Counsel can keep Defence Counsel advised as to what their intentions are so he can be prepared. Now, I make this order subject to this caveat, that I am not totally convinced that Sergeant Poissonier really would have very much to contribute in a cross-examination. The will-say statement that was provided, as indicated by Crown Counsel, suggested that he was being called initially only to prove the continuity of possession of the identity - the photo identity exhibit, and why it ever would have been necessary to prove the continuity of possession of that particular exhibit is not totally clear to me but I would say that the Crown certainly when they dropped him from that were acting wisely because I can't see the necessity - can't see from the Crown's point of view what the necessity would be. But I am not absolutely clear, and I don't want to get into it right now, of Mr. Furlotte's reason for wanting to cross-examine him. There was some suggestion that the cross-examination would pertain to why some of

these composite artist-prepared photographs weren't displayed to some witness or other. I'm not quite clear and I can't quite recall the exact reasoning on it. But if it has probative value of course he can be cross-examined, but if it has no probative value and it pertains only to the manner of the police investigation then the cross-examination wouldn't be admissible. So the only thing I can say is that before he's called I think we should have a voir dire at that session and I should hear more fully the - have a little better idea of the type of questions that you would be asking, Mr. Furlotte, on the cross-examination. For instance suppose the witness were to be asked did you, having heard the evidence from the artist that he prepared a sketch and from a witness that he gave the instructions on the artist what features to incorporate in this sketch, suppose Sergeant Poissonier - or defence suspected that he may have told the artist now you make that look as much as you can like a certain person, like the accused or some other person, and you wanted to ask him that question, did you tell the artist before that composite photo was drawn that it should be made. I mean I'm inventing a situation here. I don't suggest that this bears any resemblance to fact. But if that were the case then he could be cross-examined on that point. Or if he tried to influence the witness who had described the features that he told the artist to incorporate in the display that would be admissible on cross-examination, certainly, but to get down to whether or not the

officer showed the composite drawing to some particular witness or why he didn't or why he did, that's getting into the question of a police examination and it wouldn't be admissible. However, those are questions that can be gone into on a voir dire on that point.

MR. ALLMAN: If I could just respectfully suggest on that, I think what we should do is this. There's no point in us putting Sergeant Poissonier to ask him three or four questions about the composite. I think we should voir dire the whole of his evidence because what I propose to do now in light of His Lordship's ruling, I will put him on and I'll ask him what did you yourself do, what can you yourself tell us of your own knowledge, then you will know what he can say and see if we need him for that purpose. Mr. Furlotte can then ask him whatever questions he wants to ask him and you can see whether there's any admissible questions Mr. Furlotte wants to ask. If at the end of the day there are no admissible questions and we don't need him for the very limited Crown's purpose, then we wouldn't have to call him. I don't see any point in putting him on, asking him if he once handled a composite index, and then Mr. Furlotte not asking any questions if Your Lordship has ruled there aren't any questions of the ones that he wants to ask that are admissible. So why don't we just voir dire the whole of Sergeant Poissonier.

THE COURT: Well, that may be the best. I was trying to shorten - or thinking of shortening him up as much as possible. It may be that Mr. Furlotte, mind you, having given thought to this and having given thought

to what I have said he may feel look, there's nothing that I can accomplish. I am aware that the Crown did offer in an earlier discussion to make Poissonier available to Mr. Furlotte. I think --

MR. ALLMAN: For information, certainly.

THE COURT: Information as to what he might do. So I would ask you to look into this. It may very well be, Mr. Furlotte, that you will feel in the long run that there's nothing that you really can cross-examine Poissonier on, or that you would want to cross-examine him on. And if that's the case then tell the Crown and we can forget about the whole thing, or they can forget about calling him. But I will leave it up to counsel to discuss and work out the arrangements. If you feel, Mr. Furlotte, that there are subjects on which you want to cross-examine then perhaps we will follow the suggestion that Mr. Allman has just put up and have a full voir dire into it. Surely it wouldn't take more than an hour, and a ruling can be made at the end of that.

I'll deal with the other matter later today.

So could we have the jury in, please, now.

(Jury in. Jury called, all present.)

CROSS-EXAMINATION OF DR. WAYE CONTINUED:

Q. Doctor Waye before I go on today I think maybe we will just do one little - or a little part of re-viewing of your educational procedure for the purpose of the jury here. I believe you stated DNA is - that basically that's a universally-accepted theory that all cells in the body are the same?

A. That's a general statement, yes.

Q. General statement. And the DNA in each cell is the same because the cell is in essence the DNA?

A. The cell is not the DNA. The DNA is contained in the cell. The different cells are the same because all the cells in your body begin as the product of the sperm and the egg upon conception. That divides many, many, many times forming all the cells in your body. So the cells in your hand or in your hair roots or in your blood are actual clones of those two cells from your father and your mother.

Q. And from the time you're born until the time you die the sequence of your base pairs never changes?

A. No, that's not true. There's no absolutes in biology. From the time you're born until the time you die you mutate. So there are factors that can change the DNA in a cell. For example when people have tumors that's generally a change in the DNA molecule, say in a lung cell that gives rise to a lung tumor. So you have a change in the DNA in those lung cells that makes that one particular region on the DNA, let's say controls for growth factors or whatever that keeps the cell in line, it mutates, the cell goes out of line, and you have a mass of cells that has perhaps one base change relative to those other 30 billion. So they're not the same. There's one base pair changed in 30 billion - or in 3 billion. So if you want an absolute, no they're not the same but in all practical purposes they are the same.

Q. But for forensic purposes it would be inconsequential?
A. Very inconsequential.
Q. And basically the base sequence is different for every individual except identical twins?
A. Yes.
Q. Now, when you run your tests and you get your restricted fragment lengths basically we take your-- Now, these are supposedly your scissors here in the darkened area?
THE COURT: What number is that?
MR. FURLOTTE: This would be P-158(7). So in between this darkened area would be your restriction fragment length?
A. Yes, those sites would define a restriction fragment.
Q. And for each person the sequence in here would be very similar?
A. Could be very similar, yes.
Q. So your target DNA and your probe will in your process and here on P-158(6) --
A. Yes.
Q. So this would be your probes up here?
A. Yes.
Q. And it would be going through and it would be screening out and attaching to like a homing device on to this fragment length in here?
A. If that's the locus you're looking at, yes.
Q. Say if that's the locus we're looking at. It's just for example purposes. Now, that target DNA will attach to a sequence the same as here?
A. Similar.

Q. Or something similar to it.

A. Yes. What you'll have in different individuals is that you will have different lengths of DNA that are based on numbers that repeat. If this would be the smallest unit of repeat I might have twenty of these in tandem, you might have ten, so we will have different lengths of fragments. The sequence may be invariant; sometimes there may be a base difference here and the probe may correspond to one form or the other so it's not a hundred percent a hundred percent, but the probe certainly bears high homology or high likeness to its target. That's why it recognizes it.

Q. So when you get a match off your first probe, let's say you run a probe and you get a match between a known sample and an unknown sample, it could be the identical base pair sequence or it might be a little different?

A. Well almost certainly over the length of these repeats it will be a little different.

Q. But if it comes from the same person it should be the identical base pairs?

A. Well the probe would have to be derived from that person as well. The probe comes from one source; that's not the source of your target unless, of course, you work in Alex Jeffreys' lab where we're dealing with the one on chromosome one, it was isolated once from one individual, so the probe itself will correspond to that one individual it was isolated from and only that one individual it was isolated from.

Q. But basically the probe when it attaches to a fragment length of this DNA it may attach to something that is of the exact same sequence of the probe and it may attach to something which is a little longer in sequence or a little shorter in sequence.

A. That's the nature of the variation. You may have ten of those repeats, I may have 20 of those repeats, the probe will bind ten times to you, twenty times to me because we have different repeat lengths, numbers of repeat units.

Q. But what I am getting at is if we -- This is the result of a test, like of the autorad, the x-ray picture.

A. It's a schematic, yes.

Q. A schematic, which would be 158(10), and in lanes B and C they look very similar.

A. Yes.

Q. Right. So they could be identical in base sequences and length.

A. Yes.

Q. Or there may be a variation in sequence and in length even though they look identical on the end result now.

A. Yes.

Q. So your probe when it attaches to a fragment length could that fragment length be out by 10% of the length of the probe?

A. No.

Q. How much could it be out?

A. That would be - you're probably two or threefold off in the tolerances. I think we discussed that yesterday. 10% --

Q. 10% is not tenfold, is it?

A. One's a multiplication factor, the other's a proportion.

Q. Right. So if your probe had -- How many base pairs does your probe have?

A. Which probe?

Q. Any probe.

A. They all vary.

Q. They all vary. What's the average?

A. I would be guessing. Several thousand base pairs. Couple thousand. Two thousand.

Q. Two thousand each probe.

A. That's a guess. I don't have a calculator and I don't have that information with me.

Q. So the probe may be the exact same length as the fragment?

A. If it were it would be just luck. Remember different individuals give different fragment lengths. If your probe is this length and it happens to correspond to this person's length it by definition is not the same length as these people. So if you picked that example it would be luck because we know that people have different fragment lengths.

Q. Okay, but I'm more concerned about not so much the fragment lengths that are visibly different and total exclusions but the ones that are similar and which you would call a match.

A. I think I just explained to you that if the probe were isolated from this person it would be this length which isn't this length. I think that's the answer to your question and --

Q. No, I don't want to get into this question, I want to get into these two, and let's stay out of this lane here.

A. Okay. If we isolated the probe from this person from this band it wouldn't correspond to this band.

Q. Let's take this band, the top band, the top band in lane B and the top band in lane C.

A. Okay.

Q. Now, you call that match because they have travelled a similar distance - or you can't distinguish a difference in the distance that they travelled from the top of the gel.

A. Yes.

Q. So you call it the same length and you call it a match but it doesn't necessarily mean they are the same fragment length, does it?

A. No, because if we go back to your question, and you just said it so I do remember, you just said you called it a match and you called it the same length. I didn't call them the same length. I called them a match. I called them a visual match. You called them the same length. So I didn't say that.

Q. Oh, I don't remember calling them the same length.

A. You just said it.

Q. I'm just trying to say that you are determining them to be the same --

A. Same mobility.

Q. Same mobility. They travel the same distance?

A. Correct.

Q. But because they travel the same distance then you assume they are very similar in length?

A. Correct.

Q. Possibly the same length.

A. Correct.

Q. And if they came from the same individual they would have to be the same length?

A. They would be the same length, yes.

Q. They would be. Even right down to the base pair?

A. Correct.

Q. And right down to the sequence?

A. Correct.

Q. But there's no way we can tell that with your tests. Just that they travelled similar distance down from the top of the gel.

A. The test isn't designed to do that, no.

Q. Now, maybe, just again, to refresh the minds of the jurors, whenever you get the results of this test you have set up a binning system and say we're comparing B and C again, lanes B and lanes C, so for this particular probe that you've run you have a binning system which you have maybe I believe you said 27 bins that you will sort out the different fragment lengths and place them in?

A. Yes. The last data base I worked on was 27 bins.

Q. So we don't have the binning in evidence but maybe -- I have here the 'Rebin Population Distribution' which was on December 3rd, 1990 and for bin one they have all the fragment lengths which would measure from zero to eleven hundred and ninety-six base pairs. That would be appropriate or --

A. Let me see that, please.

Q. I think maybe if we go through this the jury might understand better how the binning system works if you describe the length of base pairs as to how --

A. Okay. Bin one is defined by fragments of zero length which don't exist so it's actually from one base pair to eleven hundred and ninety-six base pairs. That basically would be the fragments at the bottom of the gel. Bin two would be from eleven ninety-seven to thirteen fifty-two. Bin three - thirteen fifty-three to fifteen 0 seven. Bin four - fifteen 0 eight to sixteen thirty-seven. And you can go on and on and on until you hit bin twenty-six.

Q. So except for bin one which carries from one base pair up to eleven hundred and ninety-six which would cover anything in the range with eleven hundred and ninety-six pairs, thereafter they're roughly - anything with about a hundred and fifty base pair difference would fit into the same bin.

A. No, the bins themselves along the length of the gel are spaced roughly at uniform physical distances along the length of the gel. A physical distance on a gel does not linearly correspond to a number of base pairs, that is a half an inch here may correspond to five hundred base pairs in this range of the gel and most certainly will correspond to more up here because DNA fragments don't separate by the number of base pairs, they separate by their weight. So at the top a half an inch might be a thousand base pairs and at the bottom a half an inch would certainly be less than that. So it's not

a linear scale that you can transform that way.

Q. So basically when you set up to compare it and you set up your binning system which I believe you said is totally arbitrary, there was no scientific method or madness that went behind it --

A. That's not true, sir.

Q. That's not true.

A. Arbitrary -- It's not based on features. The numbers themselves are chosen with a very specific point in mind. They corresponded to fragments of known size and they corresponded to fragments that were evenly spaced. There was scientific madness that went into that decision. It was a decision that was labored over, again, by the technical working group, how to do it, and it was a rational decision. It wasn't hand-waving or an irrational decision.

Q. So is your binning the same as the FBI's or do you have --

A. It's very similar.

Q. Fragment lengths in different bins?

A. It differs, and again, I'm speaking from my experience when I was there, this was generated almost a year to the date after I left the R.C.M.P. so it's something that I didn't work on myself, but it's similar to the data bases I worked on and what you have is at the end - the bins at the very end are different in both systems. Everything in the middle is the same where the fragments actually lie that we study.

Q. So basically if there's 27 bins going down the length of the gel you would divide that into 27 slots like lines across?

A. Yes.

Q. And all the fragments lengths that would fall in that bin would be calculated as to the probability of how many falls into this particular slot between these two lines in relation to all the tests that were run of different individuals? Say like a thousand people and then maybe one hundred would fit into this line here.

A. You would divide it into corridors or bins and if you analyzed a thousand people and a hundred - you found a hundred bands there, so you're analyzing a thousand people, you have looked at two thousand bands and a hundred fell in there, it would be a hundred divided by two thousand. That would be the frequency of - an observed frequency of bands that fall within that size interval. That's all it is.

Q. Now, the method that you set up for doing the tests and for doing your calculations on the probabilities I would assume that that has went under some scrutiny by your scientific community.

A. There's a lot of different issues there and I can't think of any aspect of the test that hasn't been open to scrutiny. It's certainly all been published so unless people aren't reading it it's been open to scrutiny.

Q. But this would be proposed to be a great scientific discovery to be able to identify or --

A. I think the application of it certainly has a little flair to it that you can analyze small bits of biological fluid and use tests to confirm or deny identity. To scientists I don't think it was a very exciting application. I don't think people - scientists themselves were jumping up and down with excitement over the application.

Q. Not in the general field but any scientist in the forensic field would be jumping up and down?

A. I think they were excited about a new test that gave them more discriminating power.

Q. Right. And they would write up their findings and submit it to the scientific community for what we call peer review?

A. When they had work that they thought was at a point to be published it would be submitted for peer review, yes.

Q. And you submitted some work on this type of forensic procedures? You have submitted it for peer review yourself?

A. Yes, I have published papers in this area and they do go through peer review.

Q. And would you explain the process of peer review?

A. Generally you submit a manuscript to the editor. It varies with different journals. Sometimes it's totally at the editor's discretion who he will send the paper out to have peer-reviewed. Other times since there's so many different subspecialties they will actually ask you to suggest people to peer review it. Just suggestions. He doesn't have to obey your recommendations or follow your recommendations.

At that point it's generally two or three reviewers. He will send copies of your manuscript to them and they're given a few weeks to look over it and critique or criticize your paper. At that point they generally have three boxes at the bottom: you accept, reject or revise, and you list all your reasons for those decisions, and the editor will take your comments into consideration, the other reviewers' comments into consideration, and his own personal opinion of the paper into consideration and write back to the author and tell them that it was rejected, it should be revised in this manner, or was accepted without revision, or it's more suitable for another journal. They often say that. It's a good paper but it's not suitable for my journal, may I suggest you go to a more specialized journal or perhaps a more general journal.

Q. Okay. And once it's accepted for I suppose that's being accepted for publication, it doesn't necessarily mean that they accept everything that you state in there as being true and absolute?

A. No. It means it's gone through this peer review process and it's been deemed acceptable.

Q. Acceptable for publication?

A. Yes.

Q. Not accepted as being factual. They don't necessarily accept your opinions?

A. They have looked over the work and they agree - if they agree to publish they agree that it's scientifically sound and that as is it should be published.

Once it's published the purpose of publishing a work of science is to make it available for a broad audience, anyone who wants to read it, and the journals anyone can pick them up in a library and read them, and that, itself, is probably the broadest form of peer review, anyone can read your article and anyone can criticize it then.

Q. And anyone can criticize it. That's if they have the energy or the interest in doing so.

A. Yes. It's -- You know, there's not a wide audience for some of these journals. They're technical journals. They're journals that have a fairly focused audience.

Q. I believe you were the co-author of an article entitled "The Fixed Bin Analysis for Statistical Evaluation of Continuous Distribution of Allelic Data - From VNTR Loci for Use in Forensic Comparisons".

A. Yes.

Q. And how many drafts were necessary before that one would get through a peer review?

A. There was more than one. I wasn't the corresponding author of that paper. That was Doctor Budowle at the FBI. So handling the revisions and redrafting the paper to meet the referees' decisions, etc., that's his responsibility and that generally doesn't involve the co-authors if it doesn't change the paper substantially. So I would contribute to the initial paper. Subsequent drafts and revisions based on reviewers comments were Doctor Budowle's responsibility and he did do those because it did get

published, so you really would have to ask Bruce.

Q. Okay. Did that paper basically describe the methods which forensic labs are using for DNA for identification purposes?

A. Well, it was very focused on several aspects of typing, mainly this idea of defining alleles based on fixed bin systems, the title of the paper in fact, and all it was was trying to get this concept of the fixed bin analysis in a public forum. It had been presented many, many times at meetings over periods going back probably about two years before the paper had been published.

Q. Now, do you know whether or not there was any dissenting views on that paper or even just the general procedure that the FBI and the R.C.M.P. are using to draw calculations on the probability of making matches?

A. Well in the courtrooms, which I don't consider a real scientific forum of lawyers disagreeing with scientific views because they're not scientists.

Q. Let's just take outside the courtroom for now.

A. Outside the courtroom well there were the referees' opinions. I did see the referees' opinions of the paper. The paper did get published. I won't go into their exact comments. The paper was revised so not everything in the paper they agreed with. It's an abuse of the process for me to sit here and read their comments. The referees are anonymous; their views are anonymous.

Q. I just want to get a general view here, Doctor, but aside from the referees for the peer review after it

went into publication in the scientific journals or magazines, whatever, there were quite a few eminent scientists in your field who openly criticized your ability to make the claims that you make in your paper?

A. In a scientific way?

Q. In a scientific way.

A. In a proper scientific form, not in a newspaper or in a courtroom?

Q. Yes, in proper scientific form.

A. There was one editorial that I am aware of in a scientific journal.

Q. And who was that from?

A. Eric Lander. Doctor Eric Lander. And it wasn't really a criticism. It was - I think it was more an endorsement, many parts of that article.

Q. Was there not special panels set up to study your technique? Scientific panels set up to study your technique?

A. To study binning itself?

Q. Yes, to study your claims. Let's just put it broadly.

A. A panel to study our claims as expressed in that paper? Not that I am aware of, no.

Q. What about the Congress of United States Office of Technology Assessment? Are you aware of that study?

A. The O.T.A. Report, yes.

Q. O.T.A. Report.

A. That report was researched, authored and finished before that paper was ever published so it's not in response to that paper, sir.

Q. But it's in response to the claims that the R.C.M.P. are making, as the claims that Lifecode and Cellmark which are individual companies in the States who perform the same type of testing?

A. I seriously doubt that the U.S. Congress cares at all what goes on in Canada or in the R.C.M.P., but if you limit part of your question to what goes on in the United States like all technical matters the O.T.A. had a commission to look into DNA typing. They look into thousands of different issues.

Q. Yes, but you are -- All the technology that has went into the R.C.M.P. Lab in Ottawa has let's say been borrowed from the technology that went into the systems in the United States.

A. I don't think we borrowed technology from the States. We work with them in developing. I think you're shortchanging a lot of Canadian scientists, myself included, if you say we borrowed the technology from the United States.

Q. Any concerns in the Office of Technology Assessment Report would also apply to the system that is set up in the R.C.M.P. lab in Ottawa, would it not?

A. It could.

Q. It would, not could, is that right?

A. I think I just said it could.

Q. Is there great concerns in that report that it is not proper or that it is not valid that you can draw calculations as to the probabilities of making matches?

A. That's not stated in that report.

Q. That's not stated. Does it state in that report that it is of great scientific concern --

MR. WALSH: Well, My Lord, I'm going to object at this time. I would love to get into the O.T.A. Report. Perhaps Mr. Furlotte can read the direct quote from that report, put it to the witness, and then ask him questions about it, but I don't think we should play a guessing game of guess what's in the O.T.A. Report. Read the statement he wants and let the Doctor deal with it. I'll have an opportunity, I expect, on redirect to also get into the O.T.A. Report.

MR. FURLOTTE: First, Doctor, let's get into the O.T.A. Report and their finding about the basic test. Let's leave population genetics out and the area of calculating frequencies. But the basic test they found that -- on page 7 it states: "The Office of Technology Assessment finds that forensic uses of DNA tests are both reliable and valid when properly performed and analyzed by skilled personnel.". You are aware that they made that statement?

A. It probably says that, yes. It was an endorsement of the technology.

Q. And that's an endorsement of running your gels and making matches or making exclusions --

A. That's an endorsement of using this RFLP technology.

Q. So the first stage of your procedure at forensics, in running the testings themselves they found that to be reliable?

A. Yes.

Q. Do you know whether or not they validated the technique of calculating the probabilities of matches?

A. I don't think that was the purpose of their report. Their report - Congress to Validate Science - their report was to make recommendations to Congress. That's the purpose of their report. That's what the O.T.A. does, it makes recommendations to Congress. It wasn't there to validate anything. They certainly didn't invalidate.

Q. At page 66 of the O.T.A. report it says: "Debate over population frequencies and RFLP analysis takes several forms", and they state the pages in the report, pages 16, 17, 29, 57 and 69, and it goes on to state: "General agreement exists that any potential bias that could result from calculating population frequencies be conservative, i.e. in favour of the defendant. Nevertheless, questions are raised about whether existing population data bases are properly applied and whether they adequately support calculations of inclusions as currently practiced." That was one area of their concern?

A. I would like to focus on a lot of references to time there. We're dealing with a report that was researched and written several years ago and you're bringing it into 1991 which I don't think the report is meant to do. We're speaking of data bases that were in place several years ago. I know for a fact that the people who wrote it didn't have access to data bases that exist now because they didn't exist then. So you're taking something from the past, bringing it into the future.

Q. I have it printed here in July of 1990.

A. The report was finished - I was at a meeting December, '89 and the report was finished then.

Q. It was finished then. So you knew the concerns that's in this report back in 1989?

A. I don't think you stated any concerns there. You stated endorsements.

Q. After the O.T.A. Report was it recommended that the problems of population genetics and the calculation procedures used by the R.C.M.P. be studied by the National Academy of Science?

A. I think you'll have a hard time finding the word 'R.C.M.P.' in that report. That's a U.S. report. The O.T.A. didn't recommend anything about the R.C.M.P.

Q. Let's go with the system used by the FBI, Lifecodes Corporation and Cellmark Corporation in the United States, let's take those entities.

A. Okay.

Q. Okay. The R.C.M.P. basically follows the same procedure as Cellmark, Lifecode, and the FBI?

A. No.

Q. Pardon?

A. No.

Q. No. Not basically?

A. I wouldn't -- There's so many fundamental differences between Lifecodes and Cellmark and the R.C.M.P. that there's no way I could agree to that.

Q. Okay, tell me what they are.

A. Differences? They use a different --

Q. The fundamental differences. What are they?

A. They use a different restriction enzyme, they use different probes, they use different gels, different types of loci.

Q. Let's talk about population genetics. What differences do they have in that area?

A. Well, they apply many of those laws as we do so fundamentally they're very similar.

THE COURT: This discussion must really have very little meaning at all to the jury because they wouldn't have the slightest idea of what Lifecodes and Cellmark are. Mr. Furlotte don't you think you've got to lay some foundation here through this witness?

MR. FURLOTTE: Do you know what Lifecodes Corporation is?

A. Yes, it's a private corporation that does DNA testing, both for paternity testing and forensics.

Q. And for forensics?

A. Yes.

Q. So basically they do the same thing the R.C.M.P. lab does in Ottawa for forensics.

A. They approach similar questions with similar techniques.

Q. Similar techniques. Which are fundamentally different according to you.

A. No, you're asking about the testing procedures. They are fundamentally different.

Q. And what about Cellmark Corporation? Same thing as Lifecodes?

A. It is a separate distinct private company that, again, does paternity testing and forensic testing using DNA analysis.

Q. And the FBI lab in Washington?

A. The FBI lab in Washington again uses DNA for forensics. They're probably the closest in the systems.

Q. And are they fundamentally different from the R.C.M.P.'s?

A. Not in the methodology, no. Not fundamentally different, no.

Q. So they're basically the same, the FBI?

A. They're not fundamentally different. It's not the same organization. It's not exactly the same test.

Q. I'm not talking about the organization. I'm talking about the test procedures.

A. In my view --

Q. And the theories that you relied on.

A. -- the test procedures are more similar than they are different so of those four groupings the one that you'd pair up would be the R.C.M.P. and the FBI. They're the most similar.

Q. On page 66 of the O.T.A. Report it says: "Starting with the frequencies of the individual bands an assumption must be made that each represents statistically independent events." And it says here that an assumption must be made. Are you still making assumptions in regards to that today?

A. Could I read that, please?

Q. It says "Starting with the frequency of the individual bands an assumption must be made that each represents statistically independent events."

THE COURT: Do you want to see the whole page? Would you like to look at the book?

A. Yes, please. That's what it says, yes.

MR. FURLOTTE: Does that factor still hold true for today that assumptions must be made of independent events, or have you proven?

A. Have you proven that they're independent?

Q. Have these independent events been proven today or are we still drawing it on assumptions?

A. Well the assumption that you assume all the time is that these are Mendelian markers and that they follow the rules of Gregor Mendel who founded genetics. That's the assumptions that they're alluding to here.

Q. Right.

A. Markers on different chromosomes. It's a fundamental principle of genetics that they segregate independently. So, again, as a geneticist you make that assumption every day when you go to work. It's much like making the assumption that the sun will come up tomorrow. It's a basic premise.

Q. It's that strong an assumption, is it?

A. It certainly is.

Q. Assuming the sun will come up tomorrow is assuming a future event. The conclusions you're drawing in here you're assuming past events and present events.

A. I think it's fairly reasonable to assume that the sun is going to come up tomorrow, sir. I could be wrong.

Q. Let's stay in the same ballpark, Doctor.

A. You asked the question.

Q. Well how about a reasonable answer?

A. That was my opinion, the sun's going to come up tomorrow.

THE COURT: Well, we've established that as a likelihood at least. I'm going home for my raincoat.

MR. FURLOTTE: The assumption that the binning frequencies are statistically independent, is that a future event or is that based upon past experience or present experience?

A. That the binning frequencies are independent? So you're talking the frequency of this bin being independent of the frequency of this bin or -- I'm trying to understand the question.

Q. Let me go on then. The assumption -- Maybe you can explain what Hardy-Weinberg is. The Hardy-Weinberg formula. What's the terminology Hardy-Weinberg mean in population genetics?

A. It's a formula for predicting the frequency of genotypes - can be used to predict frequency of genotypes in a population.

Q. And what condition precedent must there be to assume Hardy-Weinberg?

A. Well, there's a number of conditions in that that are assumed for a system to be in Hardy-Weinberg equilibrium or to meet Hardy-Weinberg. It's a theoretical idea put forth about 80 years ago and with it there were several assumptions made which hold true for human populations.

Q. Is it not in dispute in the scientific community of population genetics that you cannot assume Hardy-Weinberg in DNA analysis?

A. Hardy-Weinberg equilibrium is something that you don't blindly assume, that you can and do test for.

Q. You can and do test for.

A. Correct.

Q. But it is in great dispute that not only can it not be assumed but that DNA analysis, your binning systems, you cannot put it in Hardy-Weinberg.

A. You cannot -- Well, something is or isn't.

Q. Right.

A. You don't put something in or take something out.

Q. And has the R.C.M.P. proved that one way or the other that it is or isn't in Hardy-Weinberg?

A. I'm not sure you are asking the right person that question. There's been literally hundreds of hours of studies gone into it and various different people, none of which I am, addressing that question. It's a very complex question. With these types of markers they're so variable that it's a difficult test to do. All a Hardy-Weinberg test is is that if I use the formula 2PQ, that the frequency of this is P, the frequency of this is Q, and I use 2PQ to determine how many people in a population have this two-banded pattern, to test that hypothesis what you do is you actually go to your data base and say how many people do have this pattern. Well if it's a common pattern you may find that 10% of the people in your data base have that pattern and the formula said eleven people would have it. Statistically those are very similar numbers. And for this particular test you say there's no problem with Hardy-Weinberg because the expected and the observed are similar. There's no gross deviations there between 10 and 11% in my opinion.

The problem with doing the tests for all of these patterns is that very often you are going to find patterns that are very rare. The formula will say this occurs one in a thousand. So if you only analyze a thousand people you may have seen it zero times, so you're comparing 1 to zero. Again, I don't think those are very different. But you may have seen it twice, so you're saying this occurs one in a thousand, your observations say two in a thousand. Now your frequencies in the population go from one in a thousand to one in five hundred. That sends up lightning rods with people.

Q. But let's get back to basics.

A. That is basics. I'm trying to teach.

Q. This event and this event, according to Hardy-Weinberg, before you can use the Hardy-Weinberg formula, each event has to be proven to be statistically independent, is that correct?

A. These are called alleles.

Q. Alleles, yes.

A. The concept is allelic. They are called allelic because one is on your maternal chromosome and one is on your paternal chromosome. Those are independent. Those are different chromosomes.

Q. But when you apply them to population genetics you go out and you get your survey, they must - before you can apply the formula, do the multiplication, they must be statistically independent with everybody else.

A. You know that these two bands are statistically independent before you do your survey.

Q. Within the individual, but when you apply them to your data base --

A. Your survey is of individuals.

Q. When you apply them to your data base they must be also statistically independent of each other, everybody else in the community whom you're testing, is that correct?

A. One of the things that you want to know with these things are if these things are not allelic. Every person that has this band -- Like if these bands are indeed not allelic and they're on the same chromosome every person that has this band will also have this band so they're not independent. That in fact is not the case. That's a statement of fact, sir.

Q. You are confusing the issue, Doctor.

A. No, I'm not.

Q. When you form your data base why must you go out and get randomly-selected individuals to form your data base?

A. Because that's good scientific practice. You're trying to establish a data base that reflects society.

Q. That reflects society, right. So it wouldn't be proper to go out and get a data base from one big family and apply it to the rest of the community, is that right?

A. No, that would not be appropriate, no.

Q. Why?

A. Because related individuals are more likely to share common patterns.

Q. Has a lot of band sharing. So therefore wouldn't it be a good reflection of what the bands might be in the community - in the general community?

A. You would understate the variability in the community.

Q. At page 67 of the O.T.A. Report it states: "One critical factor, these basic calculations are only valid when applied to populations in which the DNA fragments are statistically independent." Now, maybe you could explain to the jury what that means.

A. Again, what we're talking about -- There's no issue here; these are independent. They're on different chromosomes. They are allelic. We've been calling them alleles and they are in fact alleles. As a matter of fact a lot of the data bases are derived doing paternity studies in families and you can demonstrate that they are allelic. That one of the bands is coming from the mother, one is coming from the father. That's a given. I know you won't take it that way but it is. The real subject of independence here is when we go to two different markers and we actually want to look at markers on these two chromosomes. You want to know if the frequency I tag to this particular pattern is independent to the frequency on this. So it's another separate issue of independence, a perhaps more critical issue of independence, and that's something you can indeed test for, again, by looking at your data base. You can actually look at this and calculate a frequency if it's one in ten, look at this, if it's one in ten, and you make a prediction of one in a hundred. You can look at your data base and say

how often did I see this pattern? 1 in 10. How often did I see this pattern? 1 in 10. How many individuals share both of them? If it's 1 in 99 that doesn't differ from 1 in a 100. If these aren't independent it will be 1 in 10. You got people 1 in 10, 1 in 10, and it comes out 1 in 10 because they are linked. Those are things you can test by just looking.

Q. And is this also what we call linkage disequilibrium?

A. Yes.

Q. Has that ever been proven or is that another assumption?

A. Has that been proven? That these things are linked?

Q. Are linked or independent.

A. It's never been demonstrated --

Q. Has it ever been proven that they're independent?

A. It's never been demonstrated that they're not.

Q. Okay. So, again, you're going on an assumption.

A. No, I'm going on empirical data. Every time you look they're not. They're on different chromosomes again. There's no string holding these chromosomes together and making them segregate together. They don't. That's a fundamental principle of genetics.

Q. Are some scientists in the community of population genetics of the position that there is no proof that they are independent?

A. Where the controversy comes in, and it can be brought down to basics, where the controversy comes in is human population structures. If you're dealing with populations that aren't freely interbreeding, if you're dealing with populations that are mixtures of

inbred populations you can have deviations from this independence. That's the monster that's being raised now: is the Caucasian population actually a collection of many highly inbred populations that we have assembled together. They all look the same but genetically they're groups of very, very similar people and we've put them all together and now we're saying the population is very variable when in fact we've got all these inbred isolates and we've lumped them together because they're white. And that's a theoretical concern that's been raised. It's never been demonstrated; it's been raised.

Q. Have you ever demonstrated that it doesn't exist? Fact. Or are you assuming that the general population isn't a collection of all a bunch of little subpopulations?

A. Well, with every theory there comes a testable hypothesis. Now, if you say the Caucasian population is in fact groups of highly inbred people one of the things that follows from that is that if I go from region to region I should come up with very different distributions of alleles because I'm dealing with inbred people from this area and if I compare them to inbred people from this area these people should be much more similar to each other than to this other group of inbreeders and they should be very different from each other if the theory is right. Those sorts of things have been tested worldwide and it doesn't pan out.

Q. So you say that that's factual enough, that's proof enough to show that there isn't inbred in any subgroup populations in the general Caucasians?

A. No, I'm not saying that. I'm not saying that at all that there's no subpopulations. I think a person would have to be crazy to make a statement like that that there's no subpopulations. All the subpopulation is is a group that tends to breed within that group more than between groups and I think the biggest example in Canada would be French/English. It's much more likely for a person from Quebec to marry and have children with another French-speaking person than it is with an English person. It's not absolute but there is the general trend there. So that could broadly define two people that breed with each other preferentially as opposed to between which is exactly the definition of a subpopulation.

Q. Okay, I'll go on and finish reading this paragraph. I'll start over again. "One critical factor, these basic calculations are only valid when applied to populations in which the DNA fragments are statistically independent" - which we just went through - "otherwise the value calculated might greatly underestimate the true occurrence of the pattern in the general population making a match seem rarer than it actually is." So that's the concern about having them statistically independent.

A. Yeah, I think I raised that concern that if I am multiplying two things and I expect it to be one in a hundred and it actually is one in ten I've done the accused a grave injustice and it's something we were all concerned about.

Q. Now, it goes on to state: "Essentially the population must be one where individuals randomly marry and reproduce so that distinct subgroups are absent. In such freely mixed populations there will be no correlation between the alleles on the maternal and paternal chromosomes, Hardy-Weinberg equilibrium, and no correlation between alleles at different loci, no linkage disequilibrium." Is that a fair statement? Do you agree with that?

A. No, I don't. I think that's a very absolute statement written by a nonscientist. I think you would have a hard time finding a population where people actually pick their mates and have children in a random fashion. I don't think that's in dispute with anyone.

Q. Was Doctor Eric Landers part of this report?

A. He didn't write that report. He was a consultant to that report.

Q. He was a consultant to it.

A. Along with many other people.

Q. But if he didn't agree with this don't you think he would have said so?

A. I think you'd have to ask him.

Q. It states on page 68, it says: "If the population is not freely mixed then correlation between alleles at two loci can exist even if they lie on different chromosomes. In fact alleles are not randomly distributed among individuals." Would you agree with that, that alleles are not randomly distributed among individuals? You explained the Quebec situation where the French people marry French people.

A. Well, alleles aren't random or you'd find situations moving towards an equilibrium where they all have more or less the same frequency and what we do find when you look at populations is that some are common, some are rare, so that they're not distributed in a random manner, the frequencies.

Q. It says "Certain alleles clearly concentrate within specific ethnic groups." Would you agree with that?

A. I have on occasion looked at ethnic groups wherein the Caucasians they differ from say Black Oriental individuals which is why we separate those into racial groups.

Q. Black Oriental or Indian?

A. Yes. Something may be more common in one racial group than another.

Q. Yes. When you calculate the bin frequencies for your different loci there are statistical significant differences between ethnic groups?

A. Yeah, that was an expectation of the system. That's exactly why they were separated into the different ethnic groups.

Q. Right. So if there was a Black person accused of a crime it wouldn't be proper to put his profile or to compare his profile with a Caucasian data base?

A. If all the people -- There's different philosophical ways to look at it. I'll give you my personal opinion. If you're dealing with a province that has--

Q. I want a scientific opinion here.

A. Then that's based on my scientific opinion too, but there's a little bit of logic that I think goes with it. If you had - and I'll use your example of a

Black man accused of a crime, if the crime were committed in an area where the frequency of Black individuals is say 1 in a thousand and the rest of the people are Caucasian, you can derive your numbers for a Black person. You should probably also derive them for a Caucasian as well because the other people-- If you're saying - if you're trying to derive the probability of someone in the general population who could have done this or could have matched that pattern fortuitously you probably should be looking at the population who lives in the area where the crime was committed. By just focusing on the Accused's race what you are doing is you're saying if it wasn't him what's the frequency of another Black man who did this which I think everyone would agree is a very racist type of assumption to make that a Black man did this.

Q. Right.

A. The answer to the question is you'd probably do both.

Q. But you will admit that it wouldn't be proper just to use the one data base?

A. You'd probably do both and you'd get the same answer - similar answers. Both populations are variable.

Q. You think you would get similar answers, do you?

A. Well, the answers -- Again, we'd have to define the word 'similar'. You could, for instance, define that it's one in a million in Caucasians and one in six million in Blacks. There's a five million difference there and people would say, you know, those are not very similar numbers. I sort of look

at it - we're looking at it common, not so common, or rare. One in a million and one in six million both say very rare to me. So those are similar numbers to me. It's much like being poor, moderately rich or being rich. If you win a million dollars or you win six million dollars in my mind you're very rich although there's a big - there's a lot of dollars in between there.

Q. That's the best comparison you can come with, one in six million and one in one million? How about possibilities of changing say from one in six million to one in two thousand, four thousand?

A. Doesn't happen.

Q. Can't happen?

A. Doesn't happen.

Q. Doesn't happen. You've never seen it happen?

A. I've seen people misuse statistics to do that. Again, if the technique is done properly and interpreted properly that's not going to happen.

Q. Isn't that the whole issue in this that there is a misuse of statistics - a possible misuse of statistics by the R.C.M.P. and the FBI and the other laboratories?

A. That's your accusation?

Q. Yes. Is that what is in dispute within the scientific community that there is a misuse of statistics?

A. No.

Q. By forensic labs.

A. No, not at all.

Q. Not at all. Okay, just before I go on, before you can use the Hardy-Weinberg formula to get your multiplication within a loci, and before you can use the product rule, what conditions precendent must exist? What facts must exist before you can use those mathematical formulas?

A. I think you just laid them out that what you're looking at are in fact alleles and that the different loci you're looking at are independent.

MR. FURLOTTE: My Lord I think it might be an appropriate time for a break.

THE COURT: Yes. Were you going to be very much longer with this witness?

MR. FURLOTTE: I expect I will be, yes.

THE COURT: But I mean are we talking today or tomorrow?

MR. FURLOTTE: I hope today.

THE COURT: This morning you indicated yesterday.

MR. FURLOTTE: I thought yesterday this morning but I may be going over.

THE COURT: All right. Well, we'll have a recess then.

(RECESS - 10:55 - 11:20 A.M.)

COURT RESUMES. (Accused present. Jury called, all present.)

MR. FURLOTTE: Doctor Waye you mentioned that you co-authored a paper along with Mr. Budowle of the FBI and I believe also Ron Fourney of the R.C.M.P. was a co-author of that paper?

A. Yes, Doctor Fourney was a co-author as well, yes.

Q. Now, I have a copy of the draft of November, 1990 and at page 21 under the heading "Hardy-Weinberg Equilibrium" the statement in your paper and the

other authors' paper, says: "The application of the conventional formulation of the Hardy-Weinberg rule requires discrete alleles and no measurement imprecision." The system that you use for DNA analysis I understand you do not have - or you are not using discrete alleles. It's a quasi-continuous allele system.

A. The fragments themselves are distributed in a more or less - or a quasi-continuous manner. The purpose of using the binning system is to get away from that continuous distribution and sort things into organized blocks or bins. In that manner you do have defined alleles. They're arbitrarily defined by the bins but you have brought it down into an allelic system that you can define alleles.

Q. So since they are arbitrarily defined you could not call them discrete alleles?

A. Well there's always -- An allele can be -- An allele is like a lot of characteristics. There's different levels that you can classify an allele. Depending on your criteria if you set out to classify an allele based on a binning system then that is an allele and that is a discrete allele. If your rationale or your approach to defining alleles is based on the internal sequence which is something that is now being done at a research level then you have changed the criteria for calling them alleles and you're defining discrete alleles on another level. But on this level they are discrete alleles.

Q. They're discrete alleles on your level that you're using them?

A. Yes. Something will be --

Q. I thought you said they were arbitrarily described or put into bins. The bins were arbitrarily formed.

A. No. The characteristics that define the alleles are arbitrary size patterns. They are fixed. The bins don't change from day to day. They have a set characteristic be it zero to eleven hundred ninety-six base pairs, but that is a characteristic that an allele will be classified under. Either it is that allele or it isn't that allele.

Q. Okay. But if I'm an allele in bin number 7 today and you run my profile tomorrow and I end up in bin number 6 I can't be very discrete.

A. No, you were - on one day you were a -- I can't recall your example.

Q. One day I'm a 6, next day I'm a 7.

A. And both of those are discrete characterizations. What you're talking about now is measurement imprecision.

Q. Okay. So you also state the application of the conventional formulation of the Hardy-Weinberg rule requires no measurement imprecision. So you do have measurement imprecision in your system.

A. What they're doing, sir, is restating the theoretical considerations that go into Hardy-Weinberg equilibrium. There is a number of theoretical considerations that go into it, none of which in real life are ever met. The fact that you have to have discrete alleles, no ambiguity in classifying those alleles, that the populations be freely interbreeding at random, that the populations be absent of people

migrating in or out of the population and that there be no selection on a certain genotype in the population. Those are very strict criteria and not even allowed to animal populations unless you have fruit flies in a jar can meet that sort of -- Fruit flies in a jar do meet that sort of population parameter. People don't.

Q. But my point is, Doctor, that in order to use the Hardy-Weinberg rule and formula you have to have all those restrictions.

A. No.

Q. Those restrictions must be in place before you can use the Hardy-Weinberg formula and the Product Rule to be able to multiply to come to your big numbers.

A. No, that's not true.

Q. That's not true?

A. Not at all.

Q. At page 24 of your paper you state: "The fact that the present methodology permits correct phenotyping instead of genotyping and the existence of the quasi-continuous data and measurement imprecision make the conventional approaches of the Hardy-Weinberg formulation inappropriate for addressing the genetic makeup of the sample population." What did you mean by that?

A. Could I see the draft, please? It's been a while since the paper was submitted and that draft was written.

Q. First paragraph here.

A. I think I have it in context now.

Q. Okay, what do you mean that the Hardy-Weinberg formulation is inappropriate for addressing the genetic makeup of the population?

A. He's not - or we are not discussing whether it's appropriate or not to use that formula. What we are discussing is expressed on the other page, whether the empirical test of homozygosity in the data base is the appropriate test for evaluating Hardy-Weinberg equilibrium. That's what's laid out in the page before this. What it goes on to say is that we are in fact phenotyping and not genotyping. We are scoring --

Q. Okay, maybe you could explain for the jury the difference between genotyping and phenotyping?

A. A phenotype is an outward appearance. That's the basic definition. And a genotype is the genetic basis for that outward appearance. Basically. In the context of what we're dealing with now, a phenotype would be what you see on the x-ray. I can give you alternate genotypes. I can say that these two bands - this is just a hypothetical - these two bands are on one chromosome and there was no band on the other chromosome. That's a genotype. A phenotype is what I see here. There could be two genotypes for that. You could have this band on one chromosome and this band on the other chromosome or you could have both on one or the other. So you have two alternate possibilities that will give you the same visual impression or the same phenotype.

Q. Okay, maybe we could go on. You state: "In fact these authors and others, (Jeffreys personal communication, and Brenner and Morris 1990) believe that, at present, it is not possible to assess whether or not a population sample is in Hardy-Weinberg equilibrium for the alleles at a particular VNTR locus analyzed by Southern blotting.".

A. And using this method, yes. You have to put it in context of what the discussion's about.

Q. So as far as for that test it's not possible to assess whether or not a population sample is in Hardy-Weinberg equilibrium?

A. Yes. I think they're making -- They're making the statement that if it fits it still may be out, and if it's out it still may be in. It's not the right test for evaluating this.

Q. So going back you're just going to go, again, on the assumption that you're in Hardy-Weinberg?

A. I think, again, you have to put this in the context of when it was written.

Q. Well we'll see how things develop later. You go on to state: "Although there could be some yet unknown restriction on randomness for these VNTR loci, it is true that for the vast majority of other inherited characteristics the alleles at each locus combine essentially at random.".

A. That's what it says, yes.

Q. You state: "Therefore, the main issue is whether or not there are dramatic differences in the population frequency distribution of particular VNTR loci for sample populations of a particular race and if there were significantly stratified

populations, what would be the implications (for forensic purposes).". Now, again, maybe before we go further you could say what you mean by the 'significant stratified populations'?

A. Again, if you were -- and a pertinent example is Caucasians. If we select a group of people because they are white or Caucasians and unknown to us they are actually two groups of - or the population is made of two or more groups of individuals that do not freely intermix, they will tend to marry and have children amongst the group or within the group more so than between the groups, then you have really assembled three or four different populations and you're treating it as one. Now, if there are frequency -- It really doesn't matter, if the frequencies of these alleles are the same in all the groups it really doesn't matter whether they freely intermix it's going to have - it will have effects on the population, they still don't intermix. It's not going to have effect on the numbers because the frequencies are the same. If there are differences, however, if you have something that's very common in one of the groups and very rare in the other groups, you are going to end up when you mix them saying it's half common, half rare, but you're going to be coining a frequency that really doesn't apply to either of the groups. One you're going to be overestimating, one you're going to be underestimating, and you're going to be doing this not knowing you're doing it because, again, you're defining your data base based on that they're Caucasians.

Q. So you go on and you say "The purpose of applying statistical weight to a match is to convey a guide-line for how common or rare an event is in the general population." Again, you're not going to be concerned with the stratified groups but you're only concerned with what it's going to be in the general population meaning the whole population.

A. I think we're very concerned about the stratified groups if in fact they have a forensic significance. As I said before, if there's two populations and they're stratified, they never intermix, but the frequencies are the same and these probes give highly variable patterns in each, it doesn't matter. You're mixing two things that although they don't intermix their patterns can be intermixed and it has no effect. So we're always concerned about these things but we're concerned about the end result.

Q. Right. And in order to find out what the end result would be you would have to assess them in their own stratified group, would you not, just like you do between ethnic groups?

A. Well, it's one approach. Again, you have to have a basis for going into that population and pulling them into the two groups that don't intermix. You have to define characteristic. We define the one group based on that they're Caucasian. What's the next criteria that you subdivide? Again, that's arbitrary. Do we subdivide it by street or by county? Do we subdivide it by religion? Do we subdivide it by language? I don't think that's the proper way to go because you have a lot of assumptions along the way

of how to separate the population out. You're making assumptions at the beginning of how the population is stratified before you know it's stratified. The better way to do it is to look at the whole population as a whole and say do I have evidence that this population is in fact stratified and that it does have an effect on the forensic application.

Q. And what would you do if you had evidence that it was stratified?

A. That it was --

Q. That the population was stratified and that it was not homogeneous.

A. If I did the empirical study -- Like I think what you're asking is if I did the empirical study and I found that the numbers I predict have absolutely no relation to the numbers that I observe in the data base that in fact is the definition that there's something wrong in there. And those tests are done.

Q. Okay. We're talking here - when you're talking about stratification we're talking about subgroups.

A. Correct.

Q. Okay.

A. And I'm at no argument with any expert that there are subgroups in the Caucasian population, again bringing the French and English or I think you could probably make assumptions that people in Ontario are probably more likely to marry people in Ontario than marry people in New Brunswick. It's not a general rule.

Q. So you admit then that there are subgroups within the general population of Canada which --

A. Well, certainly. I'd be a fool not to admit that. It's like logic.

Q. And also if you did a population data base on them you would find statistical significant differences in the binning?

A. Well those are precisely the studies that we have done, sir, and to answer that very question, first looking at different regions and then there's other ways of picking apart a population. A lot of those things have been looked at worldwide not just at the R.C.M.P. to answer those questions. They're obvious questions.

Q. Okay. but knowing a person would belong to a certain subgroup it wouldn't be proper to do a calculation on a general data base for all of Canada. You would want to find out the probabilities within its own subgroup.

A. I think if you had absolutely no idea the effects of that structuring it would probably be incorrect to do as you just said which is precisely why you do look at these factors and you ask questions what is the effect, if any, of any possible substructure or these differences. Having done that then you're not making an assumption, you're applying empirical data and empirical formula to answer your questions.

Q. But by applying him to the general data base say for all of Canada when there's a lot of different subgroups in it it would be most likely as highly prejudicial to float the numbers around that you would get out of a general data base.

A. I don't think so. I guess in theory you could in the extreme say that unless I actually sample that area, that particular county or whatever, I'm in error. In fact every time that you do do those types of studies and you compare region to region, language base to language base, within a racial group I'm talking, so you're setting out subgroups that intuitively you know exist, again people in one region are more likely to interbreed with people from that same region as are people of the same - in Canada French and English the example I alluded to earlier, like those aren't absolutes but they're fairly good starting points, when you do those comparative studies you don't find that we've been mixing - all the English are very similar, all the French are very similar, we're mixing two very similar things and we're saying everyone's variable. That's not the situation.

Q. Okay, but you know that there's a -- Is there a statistical significant difference between say the French Caucasians and English Caucasians?

A. The data that I have analyzed and, again, I'm not a statistician so when we say statistically significant I may point to the frequency of that allele in English Caucasians and say it's 6%, I may look in the French and say it's 5%, some statisticians may say that's significant, I'm not a statistician but I look at that and say 5 or 6, it's probably not that significant. And I'd be willing to give anyone the benefit of the doubt to take the more common value if that's how they wanted to do the figures.

Q. Okay, could you --
A. I have compared French and English data myself.
Q. Data itself.
A. Yes.
Q. From the Montreal data base, or Quebec, or --
A. The data was collected in Montreal, yes.
Q. Leo Lavergne, his data base?
A. Yes. The data was from Leo Lavergne, yes.
Q. And you have compared that with I assume the R.C.M.P. data base?
A. I compared it with data bases from all over North America.
Q. And you know how many people are in the R.C.M.P. data base?
A. Not exactly, right now.
Q. Roughly.
A. Again, I haven't worked with these data bases in quite some time so when I'm talking about R.C.M.P. data base and other people's data bases right now I'm walking back a couple of years when I actually worked with the data and generated the data and analyzed the data.
Q. Did you calculate that there was a statistical significant difference between the Montreal data base and the R.C.M.P. data base?
A. I compared the two. I didn't do exact statistical tests as you say.
Q. You didn't do any statistical tests?
A. What I did do was look at what I viewed as forensic significance. I'm always concerned as a scientist that I'm citing a frequency that may be five or six-

fold biasing against an accused individual. I don't want to do that. I have no cause in doing that. So when I look at these frequencies all I'm looking at is I want to compare each bin frequency and make sure that there aren't differences like 50% in the French and 1% in English. That would create havoc in applying these numbers. So what you do is you basically look at the data, the two patterns that you get. If they mirror each other - I don't care if it goes 5, 6, and then it goes 7, 8 in the next lane - those really aren't forensically significant differences.

Q. Are they any greater differences than 1 or 2% between the R.C.M.P. data base and the data base compiled in Montreal?

A. I can't recall exact figures. The numbers I said were 6 and 7 and I'm sure there's probably examples of 6 versus 9. Again, there's no examples of 6 versus 35 or 6 versus 50, or 10 versus 1, things like that. Not that I can recall and I did that analysis myself some time ago. I know that the data has recently been expanded, both those data bases, and I know that the data is being analyzed by people who do statistics for a living and I know that they will be testifying in this hearing so perhaps you're asking - I know you're asking the wrong person. There's somebody much more intimate, much more familiar with the data than I am.

Q. On page 29 of your paper you state: "Ultimately it would be desirable to define alleles discretely, to be correctly genotyping, not just phenotyping VNTR profiles, and to reduce measurement imprecision,

than it would be legitimate to apply the Hardy-Weinberg equilibrium.". What do you mean by that?

A. Again, could I see that and try to put it in context? Okay. Again, we have to back up a page to bring this into a discussion. These are statements on their own and you have to put them in some sort of context. What we're talking about here is how statistically you treat the situation not where you have two bands but where you have one band. As I mentioned yesterday, you can analyze people's DNA and with a lot of these probes about 10% of the time an individual won't have two bands, the individual will have one band. That's a phenotype. There's two possibilities for that. Most times if you have the parents available you would be able to demonstrate that the mother and the father share a band and that they both contributed the same size fragment to the child. So you see one band there and it actually represents two bands of the same size, one from mother, one from father. That's a phenotype and a genotypic interpretation of that phenotype. The other possibility is that when you did the test perhaps there was a band down here that you couldn't see. You didn't analyze enough DNA, you ran it off the bottom of the gel, but in fact this is a two-banded pattern that you're only detecting one of the bands.

Q. The R.C.M.P. it's not possible to run bands off the bottom of the gel, is it?

A. Not if the test is done properly, no. It is possible with small amounts of DNA that it's difficult to detect bands at the bottom of the gel though. And that gets into a whole issue of --

Q. But when you run your data base you run it all on sufficient blood samples. You weren't scratching for evidentiary samples from a crime scene. You were using blood samples taken from blood donors.

A. That's correct, yes.

Q. So you should have had lots of DNA?

A. Correct. The third possibility, other than running it off the bottom which if the test is done properly really shouldn't happen, you should be able to detect it, so what you're really dealing with is two bands that are so close in size that they appear as one to your eye under the test, so actually it looks like one band but perhaps if you ran the test again you might be able to see light between the two bands and it's actually a two-banded pattern. Now, statistically you treat those situations differently. There's a formula for calculating the incidence of a two-banded pattern and there's a formula - a different formula for calculating the frequency of a one-banded pattern. What's laid out in the page before what Mr. Furlotte read to us is that whole scenario, that there's alternate ways to figure this out. What it goes on to say is that we'll assume the worst happened and we will use a formula when we see a one-banded pattern that is the most conservative, and what that formula is is if you had a two-banded pattern you use if the frequency is P and the frequency is Q you use 2PQ. If you have a one-banded pattern you use P^2. P times P. What we have decided though, since we can't formally rule out that we have two bands that are close together, is that we'd

assume that there's another band there. Everytime we see this we'll say we'll assume that there's another band there, I can't detect it, and I'll give it a frequency of 100%. So I'm saying that every-time I see one band if that's in 10% of the population I'll assume there's another band and I'll give it a frequency of 100% which can't happen. No bands are in a frequency of a 100% or everyone would look the same, and you use 2P. So you generate - every-time you see a single band you generate very weak statistical strength from it because you've been overly conservative. You've hypothesized that there's another band you can't detect and you've given it an unreasonably high frequency. That's what's laid out in the page before. The paragraph that's high-lighted and that was read --

Q. Read it again.

A. It says "Ultimately" - and you could say in a perfect world but it says "Ultimately, it would be desirable to define alleles discretely.". So there's no alternate interpretations. If you see a single band you know it's two bands that are on top of each other, period.

Q. Are you now admitting that you do not have discrete alleles in your system? When I hit you back with that earlier you said yes it is a discrete allele system.

A. It is. Things fall into -- What you score is what you see. So when I score that, that is a discrete allele. Period. It will have a size and it will fall into a bin. That's a discrete allele.

Q. Is there a difference between an allele being discrete and you treating it as a discrete allele?

A. Well, there certainly --

Q. I interpret that as you admitting that you are not using discrete alleles. Read it again.

A. "Ultimately, it would be desirable to define alleles discretely," - and it goes on - "to be correctly genotyping, not just phenotyping VNTR, and to reduce measurement imprecision." That's a paragraph that says in a perfect world I'd like to know exactly how big that band is, I would like to be able to define all the bands, and I wouldn't want to have to - and then we would be able to apply the formulas as they exist, and whenever you see a single band you would in fact come up with a much stronger statistical statement than we softened here.

Q. Why would it be appropriate to reduce or let's say even remove measurement imprecision? To get you into Hardy-Weinberg?

A. It wouldn't get you into Hardy-Weinberg. If a system is out of Hardy-Weinberg it doesn't matter what the measurement imprecision is.

Q. I understood you to say on page 21 "The application of the conventional formulation of the Hardy-Weinberg rule requires discrete alleles and no measurement imprecision."

A. And I explained that that's one of the theoretical considerations to the Hardy-Weinberg equilibrium.

Q. Right. It has not just a theoretical basis. That has to be a factual base before you can use the Hardy-Weinberg formula.

A. No, sir, it does not.
Q. It does not.
A. Nor does no migration in or out of a population, no selection, all those things are theoretical considerations laid out in I think a theoretical form here.
Q. Is that your personal opinion or is that an opinion shared by the scientific community?
A. For over 80 years, sir. The Hardy-Weinberg formula has been used on animal and human populations for over 80 years and I assure you other than the fruit flies in a jar none of them meet those criteria.
Q. They have used it for multiplication for say in blood grouping? To calculate frequencies in blood grouping, right?
A. Certainly.
Q. Blood grouping you have discrete alleles?
A. Yes.
Q. Can't mistake an A for a B but you can mistake a fragment size for a bin 6 or a bin 7, is that right?
A. The fragment is a bin 6 or a bin 7.
Q. And one day it will fit in one and the next day it will fit in another depending on your measurement imprecision.
A. And it makes absolutely no difference.
Q. Not for forensic purposes.
A. Not for any purpose, paternity testing, genetics.
Q. Aren't some scientists concerned about that?
A. I don't think so. Not scientists that understand the principles.

Q. Now, maybe you could describe how you would distinguish a subgroup within a general population. What does it take to identify a subgroup?

A. I'm not sure you can use any of these - in fact I'm certain you can't use any of these statistical treatments to identify a particular subgroup. What you can do is you can identify the presence of one or more subgroups within a population. You can't look at -- It's like looking at different colored marbles. Once they're mixed up you can't look at the barrel and go in with one hand and sort them all out into their different colors. What you can do is you can do tests to find out if there are different colors in there or they're all the same.

Q. But all the marbles in the general population in Canada are not all the same color, are they?

A. Well, I think I told you that if you were looking at Caucasians you would be a fool to make the assumption that there isn't regional stratification or linguistic or religious stratification of some sort in the population. Those are intuitive responses to the question.

Q. A few months ago did you assume that there was no stratification in the Caucasian population in Canada?

A. Not at all.

Q. Not at all?

A. No. It's something that we've - I've always recognized that the human populations, Caucasians or any other racial group, are not freely interbreeding across the country. I don't think that's a difficult

concept. What we have done is you've recognized it can happen and you've done experiments to find out what the effect of that is forensically on these statistics. Is it having an effect? Are we biasing against the Accused unduly because of that effect?

Q. Would it be proper to run a French person from Montreal, and I'm not talking about particularly his able to speak French but comes from French ancestry, a person in Montreal, would it be proper to run him through the general population data base that the R.C.M.P. have?

A. Based on what I know?

Q. And just use that. Based on what you know.

A. Based on what I know it would not be improper.

Q. It would not be improper.

A. Because I know the effect is negligible. I know what both those population data bases look like.

Q. Do you know how much of a difference you could come up with?

A. In the numbers?

Q. In numbers.

A. You would have to pick a genotype. What you can do is - and when I used to do case work and present it in court I would take data bases from around the world and I would take the Accused's pattern and I run the numbers through every data base I can find whether it's his race, religion or geographic origin or not. So I would compare, in the last case for example, the Accused to people from Indiana, from Floria, from Paris, France, from Montreal, virtually any data base I could get my hands on, and the

purpose of that exercise is to demonstrate and to convince myself that it really doesn't matter which data base I use I'm not going to come up changing my mind that this pattern's going from extremely rare to very common or even moderately common.

Q. Okay. If you're looking at a subgroup within the general population it's possible for that subgroup to have - it's more common for them to share the bands that are being assessed than the general population?

A. That is a theoretical concern and that's why you would do those studies. It is possible. Again, you are going to have to invoke some assumptions on your own that this is an actual - that there's forces working in the dynamics of this population such as inbreeding or restricted movement in or out of that population.

Q. We could compare that to the analogy saying something like well we have the general population and if you run say my profile through the general population in the R.C.M.P. data base for five probes you might come out with well there's only one chance in say a billion that somebody else might have that same profile.

A. The numbers would probably be less than that but --

Q. Probably less, but okay, five hundred million or it doesn't matter, used for an example, and as a sub-group if we took a family subgroup the numbers might be up to I believe you said they'd be something like one in a thousand.

A. Well you're asking different questions. You're asking very different questions.

Q. I just want to use two extremes here. Now, to get to a subgroup --

THE COURT: Well, give the witness a chance to answer that Mr. Furlotte. You said you're asking different questions.

A. You're asking very different questions. First you are pulling people in general in the unrelated population and then you're pulling people who sit down at the same dinner table and have the same parents, and we know at the beginning that if they have the same parents there is a limited number of choices for what the DNA patterns will look like.

MR. FURLOTTE: And there's a lot of band sharing within families.

A. If they have the same parents they'll look alike too.

Q. So you're going to get band sharing.

A. You certainly will.

Q. Right. Just like you do maybe within an inbred population.

A. Yes. If you have a population where it's the norm for brother and sister to marry and have children, first cousins, aunt, niece, that whole clan, if you will, where the family do much more than sit down at the dinner table, they in fact intermarry within the family, that's the definition of inbreeding, you will have more similarity in that inbred population than you will with an outbred population.

Q. I agree. Now, to go from the two extremes, the general population which takes everybody in Canada and maybe a small community which is not as inbred as a family unit but nevertheless they're not

randomly mixing because they're staying within their community, there's nobody from outside the community coming in to breed with them so therefore they're a small community and they are likely to share a lot of common bands also. Not as many as a family unit but more so than the general population.

A. Again, this is a -- If you are going to suggest something like that you really have to look at the forces that would create a situation where a particular - when I say population I'm talking about a region of people, not a household or whatever, a region, a town or community I guess is a good word for it, a community of individuals, there have to be some sort of forces set up where nobody wanted to leave that community but nobody wanted to come there either. And where it's the norm for people who are related by blood to marry each other and have children, that it's the norm, not the exception - the norm, now you've set up the situation where - and this happens generation after generation after generation, no one in, no one out, marry your sister, marry your uncle, etc., etc.

MR. LEGERE: Sounds like the Miramichi.

A. Those are the type of forces that would drive a population to looking more similar to each other genetically than an outbred population, that is where you select a mate and you have a family not based on those types of restrictions.

Q. So if you were going to compare that type of a population with the general population for Canada the figures, again, may be reduced from one in five

hundred million down to one in four or five thousand even. A possibility.

A. Actually, last week there were some data presented in Washington where over several hundred years there's a tribe of individuals in South America where these probes have been run through and everyone in that community descends from one king and I believe either three or four queens. He had several wives. And then it was the norm in that community by definition, since everyone is descended from those people, for brother, sister, aunt, uncle, it was an incestuous community over several hundreds of years, and you can use these probes and have absolutely no problem uniquely identifying each and every one in that community. That's the extreme.

Q. And with how many probes? How many probes would you run through that community? I assume the test was done.

A. I didn't do the testing myself. Doctor Kidd presented this work and, again, it's his data and I believe he'll be testifying in this trial so he's intimately familiar with that data, it is his data, so it would be more appropriate for him. I don't know how many probes he did and I'd be guessing right now. I'm summarizing the work.

Q. Do you know of any cases where two people shared the same probes?

A. Two people shared the same --

Q. Two people may have shared a couple of probes?

A. Oh, certainly. I have done cases myself where you run the first probe and there's two Accused and they have the exact same pattern. You do the population

stats on that and you find out that one in twenty people have that pattern. It's not unusual that two accused individuals, unrelated individuals, happen to have the same pattern. You go to the next probe and one of the persons is excluded, the other person has a different pattern and he matches the sample. So one is no longer a suspect and the other you keep doing your tests on.

Q. Okay, that's going through one probe. Two bands in one probe.

A. The second probe usually resolves that, and within a family - even within a family after the second probe you can resolve all those brother relationships. It becomes improbable that even brothers, unless they're identical twins --

Q. That becomes more improbable.

A. In all the families that I have studied and, again, in this type of setting it's always suggested that they're a very inbred family, I have never observed that sort of thing that I have to use a large number of probes, an excessive number of probes.

Q. But that's just in case specifics that you're talking about.

A. No, these probes actually -- The history of most of these probes is that they were discovered because they are highly variable and the first families that these probes were ever used on were inbred communities. They were used on large families from Utah, the Mormons.

Q. No, but you were talking about your personal experience here.

A. That is personal experience again, through my genetics background. There's a set of families that geneticists around the world use because we like to use the same pedigrees and these are large families of Mormons which are a very closed inbred population in Utah, and that's how these probes were initially characterized and they are highly variable in those extreme populations as well.

Q. You mentioned that now you are certain that there are subgroups within the Caucasian population in Canada.

A. Well, I defined what a subgroup was and, again, I said you'd be foolish not to recognize the fact that there are groups that would associate and interbreed preferentially with each other and not as a whole throughout the country. You would be a fool to assume that doesn't happen.

Q. Do you know how many there would be in Canada? Different subgroups.

A. Again, you define these things regionally, religion, language. I'm sure you could break it down even that it's more likely for lawyers to marry lawyers and doctors to marry doctors. You could break it down financially, rich people marry rich people more often than rich people marry poor people.

Q. I'm talking about subgroups with DNA genetically - genetic differences.

A. Within the Caucasian population?

Q. Within the Caucasians.

A. We have looked for them and we don't find them.

Q. But did you find them in Montreal? Any statistical significant difference in bin frequencies?

A. You're asking a different question. I can find statistical differences when I compare the first two hundred people we analyzed from Ottawa to the second two hundred people we analyzed in Ottawa. The first two hundred people may have been 5%; the second two hundred may be 8%. That's not significantly-- It may be statistically significant; it certainly isn't forensically significant.

Q. Maybe you could explain to the jury how you would distinguish between two different subgroups. What would it take statistical-wise to say that this is one distinct group, this is another distinct group? What would it take so that they would be two groups and nothing else?

A. And I could justify separating them?

Q. I want a statistical significant difference between the two groups? How much of a difference would be necessary?

A. It comes down to the fundamental question, and I'm not trying to confuse you or the jury or the Court. I'm trying to answer the question -- The question you have posed is difficult because you are saying I have the ability to separate.

Q. I don't want anything about no forensic meaningful difference. That's got nothing to do with statistics. Okay.

MR. WALSH: Objection. He's testifying.

MR. FURLOTTE: I want the statistical significant difference.

A. I'm trying to lay out the problem. You go to a blood bank, 500 people give blood, so you have a thousand alleles to look at. You're coming to me and saying I've separated these into two sub-populations. I'm telling you based on picking a Caucasian data base and randomly selecting people I don't have the ability to pull them apart and then tell you how much different they have to be to be significant.

Q. Okay, I don't want to know what you can't do; I want to know what you can do. Let's say you assess a group of people from Toronto and you assess a group of people from Moncton. What would it take for you to say well there are statistically significant differences between these two groups. I can't put them all and treat them all as one group. What would it take to show the difference?

A. You would have to have differences in these frequencies that would make a difference in your final calculation.

Q. And how much of a difference would you need to make the difference?

A. Well, I can give you examples in my mind that --

Q. That's what I want, Doctor.

A. Well, there's the tenfold frequency difference. I think that would set off bells.

Q. I don't want one big extreme. What is the narrowest margin it would take to make a difference?

A. You determine that empirically. You compare what types of numbers you generate from one data base versus another data base. I think what you're confusing the issue is is you want to know exactly how

many people you have to look at to find this pattern again and I use the statistics only to define whether it's common or rare or how rare or how common.

Q. Doctor, you testified in court before in relation to this case?

A. Yes.

Q. And we went through this before. I asked you the same question before and you know what I want, don't you?

A. I have no idea what you want most of the time.

Q. You have no idea. So you don't recall going through this hassle before, for a better word?

A. There were many hassles for a better word.

Q. Okay, let me just try again, Doctor.

THE COURT: And they lasted for weeks too.

MR. FURLOTTE: The last time you testified you wanted to qualify yourself as a population geneticist?

MR. WALSH: He didn't want to qualify himself --

MR. FURLOTTE: Or as an expert --

MR. WALSH: Excuse me, My Lord, I object!

MR. FURLOTTE: I'm sorry, as an expert in population genetics.

MR. WALSH: The crown asked that he be declared an expert in the human population genetics as it pertains to forensic DNA polymorphisms. A very restricted area as the Doctor has testified. This Doctor didn't come asking to be declared anything. The Crown asked this Court to do so.

THE COURT: Well, what is the point you are making Mr. Walsh?

MR. WALSH: Well, he's rephrasing it to the point that Doctor Waye is coming here making claims of expertise outside what he's actually been declared an expert in. He said that he came here being declared an expert in human population genetics, period. That was my understanding of the point he was making. He has clarified that, My Lord, I believe during the time that he was being examined by me.

MR. FURLOTTE: Doctor, I asked you at the other hearing, I said "And if you were going out and doing studies in population genetics and if you come across a subgroup you would be able to recognize that there was a subgroup and it was substantially different from the general population.". Do you recall what you answered?

MR. WALSH: My Lord, if he would just show him the transcript. I mean we're playing a guessing game here.

THE COURT: Yes, I think --

MR. FURLOTTE: We're playing a game, My Lord, and it's -- Your answer was "Yes, I know --

THE COURT: Well now give the witness a chance - he can read it himself.

A. My answer to that question is "Yes, I know how to define a subgroup.", and I think I have defined this over and over again this afternoon as well.

MR. FURLOTTE: And I don't -- Continue.

A. "And I know how to design experts" - that should be experiments I'm certain - "to ask the question whether it had any significance."

Q. Okay. Kindly tell the jury what experiments you would design to ask a question whether it had any significance.

A. I would compare -- As I just said a few minutes ago, I would compare the frequencies that I would get using each of those data bases, and then I would do the prudent thing, I would take it to a statistician, somebody who plays with numbers for a living, and let him have a look at whether one in six and one in seven is significant and what effect it will have globally --

Q. It depends on the size of your data base, does it not?

A. What depends? Obviously, if you analyze thousands of individuals your confidence that you have in those frequencies or the significance - or, excuse me, the confidence that you have in those frequencies would be greater than if you analyzed a small number of people.

Q. Is there a statistical significant difference between the data base for Blacks and the data base for Caucasians?

A. Again, I'm not a statistician but you can look at the patterns and you -- You can simply look at the patterns and tell that they are different. So they are different.

Q. Is there a statistical significant difference so that you could not treat them as one group?

A. You're asking me a lot of statistical questions. Yesterday in court I couldn't multiply 10 by 10 by 10 by 10 by 10 and get the right answer. I got

10,000 and it was really a 100,000 so you're -- I know for a fact there will be statisticians testifying here and I'm not a statistician so you are asking me to come up with formulas off the top of my head in an area that I'm not an expert.

Q. Well, I'll try again, Doctor. If there's 500 people in the data base in Toronto and 500 people in the data base in Moncton, and for any probe, take the D1S7, your binning system for the D1S7, if in bin 7 there was 50 people in the data base in Toronto and for the data base in Moncton there would be 40 people in bin 7, same bin, same probe, two different populations, would that be significant enough to say that there is a statistical significant difference so that these two populations would constitute separate populations rather than being able to conglomerate them as one?

A. So you've looked at 500 people, correct? I've got to get the example correct. 500 people, so a 1000 chromosomes you looked at, a thousand alleles, and you said you found 50 people.

Q. Well, 50 --

A. 50 alleles.

Q. 50 bands.

A. 50 out of a 1000, so that's, again, I'm not a statistician and I have a hard time with math in my head but that's probably 5%, 50 out of a 1000, 5%, and the other population is 4%. I have no idea whether that's statistically different. My opinion is it's probably not, 4 versus 5. That in itself would not constitute evidence for substructuring. Not in my opinion.

Q. But if Moncton say only had 25 people rather than 40 and you have a difference between 50 in one bin and 25 in the other.

A. Equal sample sizes of frequency of 5 versus 2½. Again, if I consistently -- You're looking at one allele or one bin. If you looked across -- You have a twofold difference there. If you looked across the 27 bins and at every one you found a two-fold up or down so it bounced up and down at every bin, with those types of proportions I probably would be alarmed and take that data to somebody like Doctor Carmody who will testify later on statistical significance and look at it. If, however, I looked at 26 of the bins and they're bang on and I have one bin where it fluctuates by twofold, if it went 5 to 2½% and in the next bin it flips the other way, there's all sorts of different reasons that that could happen. That certainly doesn't constitute or define a subgroup.

Q. Basically what I get from your testimony, Doctor, is you don't know how to define subgroups. You wouldn't know a subgroup if it hit you in the head.

MR. WALSH: Objection, My Lord. That's not a question.

THE COURT: I don't think that's a comment -- Is that a question? Say no.

A. No. I've never been hit in the head with a subgroup.

MR. FURLOTTE: So when you say there's a difference in the binning system between the R.C.M.P. data base and the data base in Montreal you know there's a difference but you don't know whether there's a significant difference and you wouldn't know how to calculate it.

A. It's not my job or my interest. That's why we have statisticians, to go over the data. Everyone has their expertise and it really is a team of people who have specialized talents or skills. One of those is statistics; another is population genetics; and all those parts come together as a team to analyze the data. My part of the job was generating the data.

Q. I believe you stated that you know there is a difference between Blacks and Caucasians when it comes to binning frequencies. They would be considered two different populations or subpopulations of the world.

A. Yes. They are two different racial groups. When you do analyze their patterns there are differences and there are differences in many of the bins.

Q. Now, it wouldn't be proper to use the Blacks and Whites and pool them all in one population?

A. There would be a lack of logic in doing that. You would be violating some of your starting premises that you wouldn't want to mix populations that you know at the beginning.

Q. Would it also be say an improper application of the Hardy-Weinberg formula or the Product Rule?

A. It could be.

Q. Again, could be, or would be?

A. It could be. In a lot of instances, again I'm looking at a bottom line, a lot of instances you could - and people have simulated these types of things, you can mix two populations that you know are distinct, mix them together, look at a person's genotype with their

own racial group statistics, the other racial group statistics, and the mix of the two and it makes no difference to the statistics. So in some instances it would have an effect and others it wouldn't, which is why I say could.

Q. Okay. I'll show you a copy of the transcript of testimony you gave before, page 301 of volume V. Maybe you could read that paragraph and tell me whether or not you stated it could or would.

A. Reading what I said, and again we were on this topic of mixed populations that you know don't belong being mixed, here's the start of the quote: "If I could give an example, if you took -- if you took black individuals, white individuals and treated them as one population. If the frequency of a given band was very rare in the blacks, very common in the whites and you treated them as one population, you'd derive frequencies that don't apply to either of those racial groups. So that would be an improper application of the Hardy-Weinberg formula and the product rule."

Q. And there we're talking about subgroups?

A. Yes. And then I went on to say "That's called sub-populations ...". And I think that's precisely the example that I gave earlier. Perhaps not in those exact words but -- And in that particular example the word [would] is proper. If you switched that around and you said -- No, the converse of that, and it's not funny, is that if you had black and white and the frequencies were the same in both and you mixed them together it wouldn't matter which one you used, you'd get the same answer. So in that

particular situation it wouldn't matter.

Q. Right. But in general the frequencies are not the same between Blacks and Whites otherwise we wouldn't have - we wouldn't be treating them as two different subgroups.

A. Oh, there's many bands that are similar. There's many alleles that are bang on in frequency but there are also the other situation which I described there where one's common in one group and one's rare in the other.

Q. But we only need a difference of one band, not --

MR. WALSH: My Lord, I would like to at this point raise an objection. Mr. Furlotte showed Doctor Waye the transcript. My understanding of the purpose of showing Doctor Waye the transcript, and the only way he's allowed to do that, is to show some contradiction between what Doctor Waye said in his testimony here and what he said in that transcript. Now, Mr. Furlotte's smiling in the courtroom is not evidence of any contradiction. I would like to know, since he's given that to Doctor Waye, where the contradiction is between that testimony and the testimony he's given in the courtroom.

MR. FURLOTTE: I asked him to --

THE COURT: Where is the contradiction?

MR. FURLOTTE: I asked him -- He said it could and I asked him if it was [would), and the contradiction today he was saying [could] and the other time he testified it [would].

THE COURT: Well he's talking about a different thing I think, isn't he?

MR. FURLOTTE: I wasn't talking about a different thing. He's bringing a different thing up now.

MR. WALSH: That's not correct at all. Now Doctor Waye said it [could] meaning that in some circumstances you could run a Black and the Caucasian through the data base and come out with the same numbers. In other circumstances you may not. What he says in the transcript is if the frequency of a given band was very rare in the Blacks and very common in the Whites and you treated that as one population, you would derive frequencies that don't apply to either of those racial groups. That's exactly what he said here in this courtroom.

THE COURT: Well, let me comment on this. The cross-examination of this witness seems to have deteriorated into a good deal of nit-picking, the value of which is perhaps questionable insofar as it concerns anyone, and it's time now for lunch. Couldn't you sort of pull your thoughts together over lunch Mr. Furlotte and perhaps --

MR. FURLOTTE: Well, My Lord, before I go and go for lunch I would like to state that whether it's improper or proper to use the Hardy-Weinberg formula and the Product Rule to get at big numbers I would hardly consider that nit-picking.

THE COURT: Could you pull your thoughts together over the lunch hour and perhaps try to wind up with this witness within what - 15 minutes, half an hour?

MR. FURLOTTE: Well, I still have some material to go through, depending on how long it takes me to get through it.

THE COURT: Well, can we sort of get down to basics. Well, I'm not going to tell you how to conduct your cross-examination.

MR. FURLOTTE: Thank you My Lord.

THE COURT: I'm just trying to save the Court's time and the jury's time. I'm trying to get down to something that's going to accomplish something and we perhaps aren't doing that. However, we will take the jury out now and have lunch until 2 o'clock.

(Jury excused for lunch.)

THE COURT: Mr. Walsh, you had something you wanted to --

MR. WALSH: My Lord during the cross-examination of Doctor Waye around noontime the Accused made a comment - a scurrilous comment about the Miramichi in relation to the fact that when Doctor Waye was describing inbreeding he made the comment to the effect "That sounds like the Miramichi.".

MR. LEGERE: Like an urban --

MR. WALSH: In itself and by itself that is a comment that was made to scandalize a community, in this courtroom. He has been warned and warned and warned and warned and he is just constantly disobeying the rules of this Court. That in itself, My Lord, should force you to remove him from the courtroom at least to the completion of the Crown's case.

MR. LEGERE: That's your interpretation.

MR. WALSH: But in addition to that --

MR. LEGERE: That's your interpretation. I went out with your cousin.

MR. WALSH: In addition to that, that comment is directly related to --

MR. LEGERE: I went out with your cousin and you're mad now.

1321

MR. WALSH: That comment is directly related to what --

MR. LEGERE: Cheryl Walsh. Go and ask her.

MR. WALSH: That comment is directly related --

MR. LEGERE: What a nerve.

MR. WALSH: -- to what Mr. Furlotte and the defence expert are going to attempt to try and show that perhaps there is some form of inbreeding in the Miramichi community.

MR. LEGERE: Well there is!

MR. WALSH: That was raised at the voir dire. He is making this particular comment --

MR. LEGERE: How can you compare a data base with Camp Gagetown to the Miramichi?

THE COURT: Would you take the Accused out, please, and turn on the video machine.

MR. LEGERE: How can you compare a data base from the Miramichi to the Camp Gagetown when you never had a data base. Goddamn people are all inbred down there. What are you talking about? They share so many bands it would look like a bunch of rubber bands.

(Accused removed from courtroom.)

THE COURT: Well, we don't have the video hooked up. That might take a few minutes. I think we'll adjourn now until 2 o'clock and we can continue this voir dire at that time.

(NOON RECESS - 12:40 - 2 P.M.)

COURT RESUMES. (Accused watching proceedings from cell.)

THE COURT: Well, we are assembled again for the afternoon sitting. Mr. Pugh is the video camera on and functioning?

MR. CLERK: Yes, My Lord.

THE COURT: Mr. Walsh, you had something to say?

1322 MR. WALSH: My Lord if I may just briefly. I just wanted to finish my comment but the video system was not hooked up at the time. I just wanted to point out that I raised the objection after the jury left. The comment was made about a half hour before that. I didn't want to raise it for two reasons while the jury was present. One was I didn't want to alert the jury to it nor did I want to interrupt Mr. Furlotte in his cross-examination so I waited until the end of this part of his cross-examination until the jury left, and I just wanted to make that point clear. The second point I wish to make, My Lord, is that during my address to you on that Mr. Legere made a number of comments and as far as the comments are concerned it has no bearing to me but he did mention a name during that particular time. I don't know any person of that name nor if there is such a person out there I'm not aware of anything he's saying. I only say that because the voir dire will subsequently be published I expect. I know the press will respect whoever that person is out there in terms of her privacy. I just want to make it clear that I am not aware of anything of that particular nature. It's something he said and I really don't know anything about that. I just make that point clear. And I reiterate the motion I made this morning. Thank you.

THE COURT: Yes. Well, there's no way to strike it off the record but I do say for the benefit of the media, of course, that they should have regard for what Mr. Walsh has just said insofar as the identity of any person that the accused may have mentioned in his remarks is concerned.

Well, we are all ready to go again. I may say for the record that I have made an order under 650 of the Criminal Code for the exclusion of the Accused

on the ground that the Accused has so conducted himself by interrupting the proceedings so that to continue the proceedings in his presence would not be feasible. It's not intended as a permanent order necessarily, but I feel I am in the position in view of the remarks that I have to do something about it. I'm not sure that I would have made an order when the matter was initially raised but the subsequent remarks made by the Accused made it impossible for me to ignore it. I don't attach a great deal of importance to what he may have said before the jury. I appreciate your remark or your comment on it, Mr. Walsh. I sometimes have a very hard time hearing out of my left ear and I didn't catch the remark, if you believe that. I will have to make some comment to the jury about it.

(Jury in courtroom 2:15 P.M. Jury called, all present.)

THE COURT: A word just to the jury before we continue with the cross-examination here. I have, unfortunately, found it necessary to make another order under section 650 for the exclusion of the Accused, at least temporarily, from the courtroom. After you retired a brief discussion ensued here over a comment which the Accused had made during the cross-examination of the witness which probably you heard. I do ask you - I don't know whether that remark that was made was intended as evidence or not but I ask you to ignore the remark that the Accused did make during the cross-examination concerning the Miramichi area. That and the brief discussion unfortunately led to a further outburst or comments at any rate from the Accused which perhaps weren't all that serious in their nature

but were of a nature that required me to take some action on it and so I have made the order that he be excluded for the time being.

I would ask you, again, don't attach too much importance to that. It's the evidence before the Court which will be the determining factor in this trial.

Now, Mr. Furlotte, you were going to continue your cross-examination.

*****

CROSS-EXAMINATION CONTINUED BY MR. FURLOTTE:

Q. Doctor Waye in scientific testing is reproducibility a necessary factor to determine whether tests are reliable or not?

A. Yes.

Q. Basically if tests are not reproducible, that you can't get the same results all the time or the results you're looking for, then basically they would not be reliable.

A. If I can't analyze or conduct a test and get the expected result in a reproducible manner then there's something to be said about the reliability of that test.

Q. Now, if a probe was to attach itself to a fragment which only had say 70 or 80 or 85% percent of the target data on it how would that show up in an autorad?

A. That level of homology it would be of less intensity than the probe binding to an equivalent amount of DNA of a 100% homology.

Q. So it would show up as light bands?

A. Yes.

Q. Now, I believe there's incidences where if you're interpreting an autorad and you see where the bands are visually identical they could be out by as much as 5% in fragment length?

A. That's possible, yes.

Q. And, again, it's possible to see fragment lengths which are visibly distinguishable, one has migrated further than the other and they could only be out by maybe 2%.

A. No. Not in my experience, no.

Q. They would have to be within 5%?

A. I didn't say that either.

Q. How much percentage-wise would they have to be out before you could visually see a difference?

A. Again, these come from extensive empirical studies where you look at - where you analyze DNA's over and over and over again or different DNA's with a monomorphic locus and you look at bands that are visual matches and you ask the computer how big they are and how far out they are. Most of the time, and you can lump the results into various categories, 95% of the time everything's within three percent, 70% of the time everything is within one percent. I'm just making up these numbers, but there is a progression. Some of the results will be very, very close, some will be a little further away, and at the extremes there will be the odd case where it goes as far as 5%, the example you gave. So I can't give you a pinpointed number.

Q. Could you explain for the jury how a matching window operates with the R.C.M.P.?

A. The match --

Q. The bands for a matching window to be within the matching window. Maybe you could give an explanation to the jury on that.

A. The matching window currently in place with the R.C.M.P. is based on the percentage of the size of a band and what you first do is make a visual call what you're looking at. Comparing sample B to sample C that's a visual match in my opinion. The computer then would tell me the size of those bans. The size of those bands may be exact, they may be 1% removed from each other, they may be several percent removed from each other. What the match window defines is the interval within which those bands should fall if they're a visual match. There's no surprises here. You know what that interval will be because you established the match criteria by looking at hundreds of visual matches and establishing how far or what tolerance the sizes will be. And you do the computer sizing. The computer sizing is not to my mind done to verify or confirm the match. It's done to put a size to this band so we can go back to the data base and ask it a question. You can't ask it a question how often do I see a band that looks like that. You have to ask a question how often do I see a band that's 4,620 base pairs. You have to ask it a question that it can answer. And that's what the sizing is for.

Q. Okay. You've explained sizings. Now, back to the match window. You say -- I believe you give it

as sizing to be within the match window the bands are usually within plus or minus 2.6%, is that right?

A. Correct.

Q. You would expect a band when you are measuring it to be within 2.6% of its original - or its known fragment length?

A. We don't know the length of these fragments.

Q. No, not in the polymorphic probes, but you take your monomorphic probes or your markers you know the fragment lengths.

A. Yes.

Q. And they should be within plus or minus 2.6% after you run your test?

A. Yes.

Q. So, as I understand your match window with unknown samples and in polymorphic where you don't know the actual fragment length that they too should be within 2.6% of their unknown fragment sizes I suppose.

A. Of the mean of them, the average of them. You have two fragment sizes that are different. If you took the center point of those and went 2.6% up and 2.6% down those sizes, if they are visual matches, they will fall within that interval.

Q. So your match window is 5.2%?

A. Correct.

Q. Now, in depicting whether or not you have a visual match on an autorad I suppose that would be subjective to a certain degree.

A. Yes. You'd look at it and you make a decision as I look at B and C and I decide that they're a visual

match. Of course somebody else might look at that and come up with a different idea.

Q. Somebody might see a slight variation and say that it would be inconclusive?

A. Yes. Everyone has different abilities to see, your eyesight, or judge these things. Everyone would make their own judgment.

Q. And this is when you use the computer sizing to verify your visual matches?

A. No, I just finished saying that you don't verify your visual matches with the computer. You coin a size for them with the computer.

Q. So the computer is just for placing them in bins?

A. No, for giving them a character that you can go back to the data base with, a size. As I mentioned yesterday, throughout the world throughout science all this sort of analysis is done strictly with your eyes. People don't have computers in research labs or clinical labs to do this sort of thing.

Q. Okay. So if you looked at that and your computer sizings told you they were 7% apart would you score it as a match even though it was a visual match to you?

A. Myself as a scientist?

Q. Yourself as a scientist.

A. I'd score it as a match.

Q. You'd score it as a match.

A. Yes.

Q. And even if the computer sizing says it's 10% apart would you score it as a match?

A. It wouldn't happen, but --

Q. As a scientist you would call that a match because your eyes tell you this?

A. My eyes are pretty good, yes, it's a match.

Q. So that's because your eyes can't distinguish any difference between them. It's not so much because your eyes tell you they're identical but because you can't see that they are different.

A. My eyes are a much better instrument than the computer. The computer's an aid.

Q. How does the computer know how to find them?

A. You want to know about the process of how the computer does this?

Q. Yes.

A. The computer system at the R.C.M.P., if you can give a computer a thought process this is pretty much what it does. You take the x-ray film, put it on a lighted box, a light source. There's a video camera mounted above that. You lock on the image. You center it on and you focus it, etc. You lock the image on to a video camera. There's a computer program that takes the video image and transfers it into something that the computer can understand so it computerizes that video image if you will. From that computerized image of your autorad it will identify lanes, draw tracks, and then it will scan down the track and wherever there's darkness or a change in density it will draw a peak as to where the density is and how dense it is. At the end of that process it will find the center of that peak and compare it back to the centers of these peaks and

give you a relative size estimate. That's essentially the process.

Q. And is the computer program to look for two dense areas or one dense area or all dense areas to a degree?

A. The computer will find all dense areas. For example this is a schematic and for example I had a smeared fingerprint there which happens. People do these tests and sometimes you get a smear or a blotch. It has nothing to do with the test. It's just a visual imperfection. The computer will go down, sees this thumb print or smear and, again, that has nothing to do with the DNA you analyze, it has to do with how you did the test, and it will pick it up at the most likely or the darkest band. Well you as the operator tell it to ignore that because it's either not in a lane or you know it's not a band. There's somewhat operator control at that level. And then you instruct it that there are two bands and it looks at the next two likely candidates.

Q. Or when there's very faint bands on the autorads you have to point them out for the computer and say there's one here, measure it.

A. Well, you are again in a situation where you have got something that isn't a band and you have a faint band here. There's aspects of the computer program to ignore this and go to this region. It will go to this region. If it still doesn't find anything you can't place it there. If you direct it to that region where there's a faint band, we can't see one here but there isn't one, but there were a faint one there and you directed the computer to look in there

and it still couldn't find a peak which happens sometimes, it will fail to find a band and you can't put one there, you would be overriding the program and that's not done with case work.

Q. So in that aspect you rely on the computer? The computer's eyesight is just as good as yours.

A. No, it's not. Very often times you can with the naked eye detect a band that in fact the computer can't see. The computer is only looking at a computerized image of the video camera reflected through a light box. You're looking at the original thing with an instrument. The human eye is much more sensitive than a four hundred dollar video camera.

Q. Is there a telescopic lense on the video camera that might improve it?

A. I'm not sure you would improve it to the level of the eye. The eye's a pretty good machine.

Q. I take it you don't wear glasses.

A. I do.

Q. Do you wear your glasses when you visually inspect the autorads?

A. I wear glasses because I do that. I have looked at so many of them.

Q. So you do need visual aids.

A. Again, I'm retired from doing this professionally so I guess if I were the scanner at the R.C.M.P. now I probably should wear glasses if I were doing it. I'm not.

Q. Again, basically when you're assessing autorads and interpreting autorads it might be easy to interpret to see if two bands in two different adjacent lanes have migrated the same distance but what about whenever you're assessing an autorad and you're assessing lanes at the opposite ends, say a foot or eighteen inches apart or however wide your test gel is? Does it make it a little more difficult to see if there's any distinguishing characteristics?

A. Well the autorads themselves never reach this size. This is just for a visual impact. The width of the gel is 20 centimeters. Test samples, in my case work experience anyway, will never be at the extreme ends because they're always flanked by markers so the markers would be at the extreme ends. There's controls inside of that and so a lot of the outside portion of the gel is eaten up in controls. So the furthest apart anything could be would be quite a bit closer than 20 centimeters so it would never be 18 inches or 2 feet or a foot. It would be more on the order of this sort of distance.

Q. But the further the lanes are apart it might be a little more difficult to see if there is a difference?

A. If they're the exact same mobility?

Q. Yes.

A. It would be more difficult the further they are apart.

Q. It would be something like two people standing in a room if maybe one is an inch taller than the other and if you stand them 20 feet apart you might think that they are the same height.

A. I think it would be more like trying to compare people at the same bench to see if they are the same height if they were standing up, not across the room.

Q. But if you put them back to back then you might be able to tell that one is a little taller than the other.

A. You might be able to, yes.

Q. In a circumstance like that would you also rely on your visual observation rather than say take out a measuring tape and measure them to see how tall they are?

A. If the question were are these people the same height or different heights I'm not certain that the measuring tape is needed to absolutely confirm that. You line them up; it really doesn't matter whether it's five foot ten versus five foot six or six foot four versus six foot two, they're different heights. Or if they're the same heights it really doesn't matter what height they are if you are asking the question are they the same height or different heights. Now if I wanted to go to the population and say how many people are that height then I have to know how tall they are.

Q. No, I'm just trying to compare, Doctor, and from your testimony I understand you to say that the use of the computer to measure the fragment mobility in the gel you kind of disregard that and rely totally on your visual sense because your eyesight is much better than computer measurements.

A. The computer is not going to contradict the story. I have looked at many, many, many comparisons and you know that if your eyes tell you they are a match the computer is going to do the exact same thing. So it's not a visual check. You know what the answer is going to be the second time around. You designed the program.

Q. Designed it.

A. It's all designed on empirical observation.

Q. You mentioned in relation to your match window your computer could measure say this was out by plus or minus 2.6%, so it could fall anywhere within a 5% radius, I suppose, of the computer sizing?

A. Well the band wouldn't move. The band wouldn't move 5%. The sizings would be different by 5.

Q. The sizings would be different by 5%.

A. Could be.

Q. Could be.

A. Using that criteria.

Q. Now, what about if you run that same gel again - or not that same gel but if you run the same DNA. The DNA that's in lane B you have got the one test, the one gel. Now, tomorrow you decide to start your test all over again using the same person's DNA and you run it in a different gel. Again, you would come within your matching window?

A. That would be my expectation, yes. That's how those values were obtained in the first place, from multiple gels.

Q. Now, let's say day number 1 when you run it you come out with a thousand base pairs. Okay? So day two

you would expect it to be within 5% of a thousand base pairs. So you would expect it to be 950 base pairs or 1050 base pairs. Would that be a fair assumption? It's not quite the 5.2%. We're going with 5%.

A. Well, I don't like doing math from the top of my head. It's embarrassing. The formal expectation based on the empirical data would be that it could go up or down as much as a window of 5%. I'm not going to do the math here.

Q. No. No. A window of 5%. Okay. I'll do the math for you. Okay, so day one we come out at a thousand base pairs, day two we could expect anywhere from nine hundred and fifty base pairs to ten hundred and fifty base pairs, if that's roughly 5%.

A. Well you just made a window of 10%. You went 5% up and 5% down so you made a 10% window by my math.

THE COURT: You lose. You failed on math. Better turn it back to the witness.

MR. FURLOTTE: So the 5% would bring you then from 975 to 1025?

A. 50 base pairs out of a thousand -- That would be in the range of 5%, yes.

Q. Now, in day two if you run it and you come at 975 base pairs which would be within the 2½% of the thousand, right, which is what you would expect, again would you put a match window of that 2½% to get back maybe to 950?

A. If the question were we're analyzing two unknown samples on two different days and asking if that band is the same the two results that you have would have to

fall within that window.

Q. Yes.

A. Beyond doing the math I -- I can do it, I'm capable of it, but I need aids.

Q. Okay, that's fair. But you should fall within that 5.2% window every time you run the test if you're running your tests right?

A. For a given range of fragments that's the expectation, yes.

Q. Did you explain to the jury yesterday what non-specific binding was? Do you recall?

A. I don't remember. I can explain it.

Q. Could you tell me what nonspecific binding is?

A. You add the probe and if the probe binds to the target that has the complementary sequence that's specific binding. If the probe binds in general to DNA or binds in general to the membrane that's non-specific binding. It's binding places where it really shouldn't. It's binding based on properties other than sequence complementarity.

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

A. Anywhere from nondescript smears in a lane to the entire membrane being black and you get all variations in between. Sometimes it swirls, smears, the membrane itself is cloudy and there is bands on that back-ground, or the lane itself is cloudy and there's bands on that background. You get all sorts of variations.

Q. So then it's a matter of interpretation as to what is specific binding and what is nonspecific binding on your interpretation of the autorad?

A. Yes. As the operator you would have to be able to recognize what a band is and what a thumb print is or what nonspecific binding is, or what a swirl is, things of that nature. You have to be able to recognize a band.

Q. Would you say, Doctor, that the forensic setting is much more demanding than the diagnostic and experimental utilization of this procedure?

A. No.

Q. So the fact that you're dealing with maybe contaminated samples or degraded samples that doesn't make the technique more difficult?

A. It's an aspect of the forensic application that makes it difficult. There's aspects of clinical and pure research genetics that makes those tests equally difficult. Different tests and there's different things that can make the tests hard to do.

Q. If your match window was too large do you run the risk of having false positives?

A. Not in my opinion because - and, again, I don't do this for a living anymore but if my eyes tell me something isn't a match and yet it falls within the match window I won't call it a match, so the match window really isn't a determining factor there.

Q. I believe I asked you a similar question the time you were in court before, volume VI, page 115, top of the page. Maybe you could read your answer.

A. This answer?

Q. Yes.

A. First I'll read the question. It doesn't seem to have anything to do with the question you just asked.

The question was: "And the only thing you attempted on environmental insult was how the DNA was affected by certain materials --"

Q. I believe you might be at different pages here. That's page 108 and this is page 115. I only photocopied the pages that I was going to question you on. Would you like the -- Let me get the original for you. This is the page.

A. Okay, the question was: "I see also in the Yee case, page 129, that Dr. D'Eustachio appeared to be concerned that choosing a match window that exceeds an acceptable level of risk, that there is the risk of false positives, having too big a match window? Is that possible?" And the answer was: "Well, it's raising the concern that if I allow for bands to be 20 percent apart and still call them a match, that I am running the risk of false positives. Certainly, if you have a huge match window the largest extreme would be let's consider the whole gel, our match criteria, everything from top to bottom, everyone is going to be a match. That's the extreme." That's the question; that's the answer. And, again, in context, we're talking about using the match criteria to overrule your eye and make the call and I'm just saying that if the match criteria is too big and you allow things that don't look like matches, as the example here 20% apart, and you let the computer tell you that they're a match when they're not you run the risk of a false positive. It's not reality. It's not the way it's done. It's not the way it was done then. It's not the way it's done now.

Q. I believe you said the matter of declaring visual matches that it's very subjective.

A. Well, you look at them. I didn't say it was very subjective. There is a degree of subjectivity to it. You use your eyes. Different people can use their eyes. I think it's the beauty of the system. Everyone can look at it and everyone can make a decision.

Q. Right. But all matches aren't as obvious as this example here in lanes B and C on P-158(10)?

A. Well, certainly, there's matches that are more difficult to call than this schematic. As a matter of fact most of them are. This is a very artificial situation. But there's also things I've ever called forensically are about as easy as that to call. My five year old could do it.

Q. How long does it take to train somebody to do all these tests?

A. To physically do the tests? I could show somebody how to do it in a weekend.

Q. A weekend.

A. That's how long it takes to run the test and assuming they paid attention and followed along we could probably analyze each other's DNA in a weekend.

Q. Then it's quite a simple procedure.

A. No, I didn't say that. If they followed along and paid attention we could get the test done in a weekend. They may not be able to do it again without me there but they would be able to give it a once over.

THE COURT: Well, another hour and the jury will just about qualify.

MR. FURLOTTE: Doctor Waye we wouldn't want the jury appealing to authority, would we? Just taking your blind word for your opinion?

A. Would I want them just to accept what I say on the basis of saying it? No.

Q. Without them being able to understand what you're talking about.

A. Oh, I would like people to understand but if they don't I don't think it's a reflection on the technology. It's probably a reflection on my ability to teach this.

Q. Do you have a definition for what you would call a [natural population]?

A. A natural population? Natural implies something that exists and you didn't put together.

Q. How about Canadians? Are we a natural population?

A. I would say so.

Q. Would you say that Hardy-Weinberg has a lot of requirements tagged to it, none of which fit a natural population?

A. It has a lot of theoretical concerns tagged to it, none of which reflect reality in any species or any populations in the absolute sense.

Q. In an absolute sense.

A. In an absolute sense. That's the way biology works.

Q. In a sense of reality then it's not proper to attach the Hardy-Weinberg principle to natural populations.

A. I wouldn't agree with that. I was beginning to say that I'm aware of no situations in science, biology or life that are black and white. Hardy-Weinberg sets out in the theoretical sense, in the absolute

sense, a list of criteria, and I went through them before about no migration, selection, absolute definition, no mistyping of alleles, etc., etc., etc. Those are all absolute situations none of which apply to reality in the absolute sense and in the global sense they do. There are populations where allele frequencies aren't affected dramatically over the course of time by those factors, but in the absolute sense that's a rule that's not adhered to by natural populations, all those conditions, in an absolute sense.

Q. The Hardy-Weinberg principle is a theoretical model?

A. It's just that - it's a principle. A theoretical model would be a good way to describe it. It's been described before as the Hardy-Weinberg rule and that's incorrect. It's not a rule or a law, it's a principle.

Q. But it doesn't fit any populations?

A. Nevertheless it works. It doesn't fit in the absolute sense but all these factors that you can deviate somewhat from, not the absolute sense, populations don't completely randomly mix but it's a fairly random process. So in the absolute sense you haven't met randomness but in the global sense you really are, unless you talk the extreme of selective forces causing people to inbreed if you will.

Q. Tell me if I'm wrong then. As I understand your statement you're saying that the Hardy-Weinberg principle is a theoretical model, it doesn't fit any populations but if we use it it will still work.

Does it work just because you get nice big numbers that you want or does it work because it's -- in reality it works?

A. As I said, the whole principle was laid out long before anyone ever thought of using DNA for forensics or DNA analysis, period. Actually, it was long before the DNA molecule was ever worked out, some 80 years ago. It wasn't worked up by practicing forensic scientists. They had no idea its impact in the court or its use in forensics so it's hard to rationalize that sort of view. It was worked up as a theoretical model and with all theoretical models you lay out the parameters for that model and there are several of them, none of which in the absolute sense fit natural populations. With biology and life itself there's nothing that's absolute.

Q. Now, you are not contradicting what you had testified earlier but maybe I'll show you - maybe you can give a fuller explanation for the benefit of the jury, but when I asked you a question before in another proceeding the question was: "But it would still require discrete alleles and no measurement imprecision before you could use the Hardy-Weinberg rule?"

A. That's that question, yes.

Q. And you said you can't think of a population that it would fit, humans included?

A. That all of those conditions are met?

Q. Yes.

A. No, I can't. I can't think of a closed population, nothing in, nothing out, no selection, absolutely

free random mating, no, those conditions met in an absolute sense, no.

Q. Right. And in theory all those situations are supposed to be present before you can use the Hardy-Weinberg formula?

A. That appears to be the way you view it, over time, and it hasn't changed, but it's wrong.

Q. Is that the way I view it?

A. Unless you're quoting someone else, that's what you just said, and it's not true.

Q. Your statement here - and you're talking about the paper that you're a co-author of --

THE COURT: You know, aren't we back where we were two hours ago and reviewing exactly the same thing and you're putting exactly the same questions to the witness and getting exactly the same answers. Two hours ago.

MR. FURLOTTE: I only have a few -- No, I'm not getting the exact same answers here. I'm not getting the exact same answers. And there's only about three pages left - four.

You state that if you followed the way those fellows wrote their paper, you were one of the co-authors, and outlayed their requirements at the beginning for an ideal situation "I can't think of a population that would fit it, humans included.".

A. I'm pretty certain I just said that too.

Q. And you were the co-author of that paper?

A. I was one of the authors of that paper.

Q. All the conditions precedent that you have stated in your paper and which on the theoretical model ought to be present before you can use the Hardy-Weinberg formula, none of them have proven by the forensic field in DNA testing, have they?

A. I've already said that that - that those conditions aren't met nor are they expected to be met, and now you're asking me if they've been proven?

Q. Yes.

A. Well the answer is a crisp, clear no. They're not expected to be met.

Q. Let me ask you another question, Doctor. Before any weight can be given to an expert's opinion in science the facts upon which the opinion is based must be found to exist?

MR. WALSH: Objection, My Lord, that's a legal question.

MR. FURLOTTE: No, My Lord, I think it's also a scientific one.

THE COURT: I'll permit the question.

A. What was the question?

MR. FURLOTTE: If I as a student of yours was coming and forming an opinion, giving you a supposedly scientific opinion, and I never proved any of the facts upon which I based that opinion on, what would you do with me? How would you mark my paper or my experiment?

A. That's a tough situation you put me in. If you came into my class with an idea and you had no experiments to back it up with and you made conclusions you wouldn't do well. That's not what's been done here.

Q. I'd get a nice big "F", wouldn't I, a failure?

A. You would get a talking to.

Q. And you would tell me to go out and do it right.

A. Well, I'd tell you to design an experiment.

Q. Based upon facts, not assumptions.

A. Yes. If you came to me and you said that the human population, pick a place, Hamilton for instance, is static because over the last 2000 years no one's come in, no one's come out, it's freely interbreeding, there's been no selection on individuals and alleles can be classified, blah-blah-blah, all these different things in Hardy-Weinberg, I'd say get out there and prove it. I'm not sure anyone's ever raised that issue that you're trying to prove the assumptions laid out in a theoretical model. I've said probably a dozen times in the last half hour that it's not expected and that it's not even something up for discussion.

MR. FURLOTTE: I have no further questions.

THE COURT: Re-examination Mr. Walsh?

MR. WALSH: Yes, My Lord.

REDIRECT EXAMINATION BY MR. WALSH:

Q. Doctor Waye, Mr. Furlotte yesterday asked you at the outset of your testimony in cross-examination if while at the R.C.M.P. Lab you were ever subjected to a proficiency test to more or less evaluate how you would run these RFLP techniques. Do you remember that?

A. Yes.

Q. Do you know a defence expert by the name of Doctor William Shields?

A. I certainly do.

Q. Has he ever reviewed any of the RFLP tests that you would have conducted for any case?

A. Yes, he did.

Q. And what, if any, opinion did he give of the work that you did?

MR. FURLOTTE: My Lord I think we're getting into case specific evidence here which I thought we were going to save for later on.

MR. WALSH: I have no case specific -- This is not talking about this case. I'm talking about a case that he may have conducted personally himself somewhere else and I'm asking if his work had been reviewed by a defence expert.

THE COURT: Well, I'd permit the question. By case specific evidence which is being put over as far as this witness, you're talking about this particular case?

MR. WALSH: Yes, anything that dealt with this particular case.

THE COURT: Well that's all right. Go ahead.

MR. WALSH: Did he in fact review your work for another case that you did yourself?

A. Yes. In the last case I did as a member of the R.C.M.P., a case in Ottawa, he was the defence expert and we met prior to going to trial. We met privately both him and myself with all the data, and went over the data together, my explaining the results to him and him asking me questions, just as two scientists would discuss any data, and at the end of that he formed his opinions.

Q. Did he give those opinions in a courtroom?

A. Yes. He told me right after that that he agreed with everything and he thought the quality of the work was the best he had seen, and that's exactly what he stated in court.

Q. The best he had ever seen?

A. Yes.

Q. Mr. Furlotte raised with you the --

MR. FURLOTTE: My Lord I believe the Crown is misleading the court here because I think we should go on and ask about the general population aspect of it also.

MR. WALSH: You asked about a proficiency test. I put the question in relation to a proficiency test. A proficiency test deals with how you run an RFLP technique, am I correct, Doctor?

A. Correct.

MR. WALSH: And that's what my question was.

THE COURT: Well, what - have you got another question now?

MR. WALSH: Yes, I have another question.

THE COURT: What is it?

MR. WALSH: Mr. Furlotte raised with you the whole question of a match window yesterday, and you testified that the R.C.M.P. have a 5.2% match window plus or minus 2.6%, is that correct?

A. Yes, that's currently the match window that's being used.

Q. Just to clarify, when you were testifying today you were referring to the fact that you rely on a visual match. In the clinical or research setting do they use computers or do they rely on a visual match?

A. No, I've never -- Outside of forensics I've never been in a lab or a facility that uses a computer to verify what the eye has already told you.

Q. Okay. With the R.C.M.P., however, and with their match criteria, if you did have a visual match and for some reason the computer said that the bands were outside the 5.2% what would they do?

A. I haven't looked at the last set of their interpretative protocols. That very well may be called inconclusive although your eye tells you it's a match. Again, I haven't done case work there since this match window was implemented.

Q. But if they in fact did that that would be in whose favour?

A. Well, you've thrown out a result that you know is a match so certainly it would be in favour of the accused.

Q. That would be an added feature to a forensic setting that wouldn't apply to a clinical or research setting?

A. Correct.

Q. If with the R.C.M.P. criteria, if you did not have a visual match but the computer told you that it was inside the match window, would that be called a match, without a visual match?

A. No, I would not call that a match nor do I think the R.C.M.P. would do that.

Q. My understanding is that the only time that they would call a match is if it visually matched and it's within the 5.2% match window, is that correct?

A. That's my understanding, yes.

Q. That's an added feature over and above the clinical or research setting?

A. Yes.

Q. You testified yesterday, I believe, that the FBI match window was 5% and the R.C.M.P.'s was 5.2%.

A. Yes.

Q. Would you expect such small variations from lab to lab?

A. It's not unusual at all. They're different people doing somewhat different procedures. Subtly different but it certainly is the norm that both in clinical and research environments that different labs have different criteria. I know in hematology labs, for instance, each lab lays out their parameters, for example a routine blood run, they lay out their levels of what they call a positive and it varies from lab to lab, from hospital to hospital. These are very standardized tests as well.

Q. Yesterday Mr. Furlotte asked you about your findings at the R.C.M.P. lab which you published with respect to ethidium bromide, the stain that you put in. In your opinion for the R.C.M.P. lab you put this stain on after the electrophoretic gel is run, is that correct?

A. Yes.

Q. That's what you have concluded. The FBI put the stain on before the electrophoretic gel starts, is that correct?

A. Yes.

Q. You were consulted by defence lawyers and defence experts in the United States over that paper that

you wrote, am I correct?

A. Correct, yes.

Q. What were they attempting to argue with respect to the FBI's system? That it should be done the way the R.C.M.P. do it?

A. Yes.

Q. Or vice versa?

A. They were attempting to discredit the test results from the FBI's lab because they used a procedure that in our hands gave less accurate results.

Q. And what were they attempting to argue? That the R.C.M.P.'s system was better or worse?

A. A superior system, yes.

Q. Mr. Furlotte read you some excerpts from the Office of Technology Assessment Report. You referred to it as the O.T.A. Report, do you remember that?

A. Yes.

Q. That is a branch of the Congress of the United States?

A. Yes. It's an organization that basically does fact-finding for Congress. When they pass legislation in a certain area these are the people that write reports upon which they can base their decisions.

Q. I am going to refer you to the bottom of page 7, an area where Mr. Furlotte read from. Would you read the conclusion of the O.T.A. beginning with this particular paragraph here, the two sentences after.

A. Okay, this passage is all under the heading: "Are DNA Tests Valid and Reliable". The passage goes,

and I quote: "Genetic and molecular principles underlying DNA identification are solid and can be applied to DNA isolated from forensic evidence. The Office of Technology Assessment finds that forensic uses of DNA tests are both reliable and valid when properly performed and analyzed by skilled personnel. Molecular and genetic techniques can accurately disclose DNA patterns that reflect differences among humans. Questions about the validity of DNA typing, either the knowledge base supporting the technologies that detect genetic differences or the underlying principles of applying the techniques per se, are red herrings that do the court and the public a disservice."

Q. Do you agree with that statement?

A. I certainly do.

Q. Correct me if I'm wrong, Doctor, what they're referring to - what they're accepting is the procedure that you have outlined in exhibit P-158(6) and P-158(9), is that correct? The DNA typing procedure?

A. Yes.

Q. And what's outlined here in terms of interpretation in relation to P-158(10)?

A. Yes.

Q. Mr. Furlotte was asking you a number of questions with respect yesterday with whether or not perhaps you should be using more probes and I believe it was suggested that perhaps maybe ten should be used as opposed to you mentioned some labs use 3, some 4, some 5, of course depending on how much DNA you have available. In your experience, apart from identical

twins, and without even putting a probability figure on any match, have you ever seen a four or five probe match between different individuals using these highly polymorphic probes?

A. The simple answer is no but in my experience it's not uncommon depending on the profile to find two people that will match with one probe, less common with two. I can't recall ever seeing anyone outside of siblings match at three. Four and five never.

Q. Have you ever seen siblings -- You're referring to brothers, sisters --

A. Correct.

Q. Brothers, brothers, sisters, sisters. Have you ever seen them match at four or five probes using these highly polymorphic probes?

A. Generally within a family if two individuals or two siblings match with one probe the second probing is sufficient to distinguish them. On occasion I've seen out of a large number of brothers two individuals match at a couple of probes. Generally the third one resolves that ambiguity. You need not analyze 5 or 6 or 10 probes to tell two brothers apart.

Q. I take it that would also apply even more with respect to people who were further removed from the person, for example cousins, half-brothers, uncles, nieces.

A. Yes. Siblings are the extreme. Once you leave the bounds of that immediate family people very quickly assume different patterns because they have different parents.

Q. Would you expect a four or five probe match between cousins and sisters?

A. No, I don't expect it between siblings and I certainly wouldn't expect it between further-removed relatives such as cousins, first, second, whatever.

Q. And that's without even putting a probability figure on it. You've never seen that on that many probes?

A. Well I haven't analyzed a lot of cousins in that it's intuitive. The thing that makes brothers and sisters share the same patterns is that they have the same parents. As you move further apart and talk about cousins and half-brothers, etc., you're adding in the variables that they don't share the same parents or they only share one parent. It's intuitive.

Q. You were defining or what were you -- You were using the term this morning [inbred populations]. What are you defining as an inbred population? What are you referring to?

A. Well in its extreme it's a population that the family mates within the family. Clinically, if we see it in the clinical genetics lab, it increases your chances of getting genetic diseases. Usually carriers of diseases it's rare in the population so when two carriers come together very often it's because they're related by blood, and that for thousands of years in virtually every society that's why that type of marriage has been discouraged, either formally in religions or on a village to village basis, but in virtually every society there's taboos about shared blood.

Q. What forces would have to be at work in any society, not just in a family but in any society or any part of a society, to have an inbred or highly inbred population?

A. In the context of this you're looking at inbreeding like what kind of forces will make a population proceed from highly variable to converge down to everyone genetically looks the same, and we can do that in the lab. There's all sorts of what we call inbred mouse lines. You can breed mice, strains of mice, in such a way that over a large number of generations you can make a mouse that's going to be very genetically close to its siblings, much more so than any two wild mice, and you do that by mating brother and sister, child back to mother, and doing all these crosses within a family over and over and over again. You're basically creating children with the same genes over and over and over again and diluting out the variability.

Q. So how would that apply in a human population for example? What kind of forces would you expect to get a highly inbred or an inbred population?

A. Over many generations it would have to be the custom for people to marry and have children within a family or share blood that way if you will. It would have to be the custom. Also, you would have to look at other factors like is there a large flux of people moving in and out of this population because obviously you'd be introducing a new variance to the gene pool. And if those people participated in the breeding process they contribute variability

and that would work against inbreeding.

Q. You would have to have interfamily marriages over a long period of time?

A. And you'd have to disrupt the flow of introducing new genetic variability into that relationship. You'd have to somehow confine the breeding, if you will, to favour breeding within a family as opposed to between unrelated families.

Q. And you would have to have no immigration into the area or migration out from the area?

A. Well, you would have to minimize those effects because those people participating in the breeding process would introduce new variability.

Q. You said this morning when Mr. Furlotte was questioning on this aspect that even in highly in-bred populations in the world they are genetically different. What were you referring to there? What kind of examples were you referring to?

A. Usually native or indigenous populations in the world, populations that are isolated. There's, scientifically, a wonderful example from the Polynesian Islands. It's particular islands that have only been colonized for some four thousand years. They had a small founding population and until recently the population has been confined to that founding population and all their ancestors. So you really are starting off with a colony of people and because they're on an island their relatives will all go back to a small founding population. Even in those instances the variability that you see with these probes is comparable to what

we see in a Caucasian population, and there's simple reasons for that. There's a factor that a lot of people don't consider is that over time the variability in a population isn't static. New alleles are created all the time so even in a small founding population over a period of time new alleles or new forms will be created through mutation.

Q. So even in highly inbred populations using this technique you can differentiate between people?

A. Absolutely no problem in the example I just gave.

Q. You mentioned this morning with respect to - with regard to subgroups under the Caucasian race and you said you would be foolish not to state that there are in fact subgroups within the Caucasian race. For example you mentioned language, geographical area, geographical location, religion, people may because of religion stay together, because of language, marry other people of the same language, things of that nature. Am I correct in that summary?

A. Yes, that would be my opinion.

Q. You mentioned that you looked at French Canadians and English Canadians to do what? Why did you look at those populations?

A. Because that's a nice starting point. You know since this country was founded there's been fairly stable populations both geographically of English and French in this country, and they have stayed that way for quite some time and it's because there has been a tendency for French-speaking people to marry French-speaking people and English-speaking people to marry English-speaking people. An overall

tendency. Again, nothing is absolute. But you know looking at that situation from the beginning that that defines to my mind two distinct - a basis for defining two distinct subpopulations within the Caucasian race.

Q. But when you looked at it what conclusions did you draw in terms of using a data base that is made up of French and English Canadians, Caucasians?

A. The bottom line is they're both variable and the frequencies in both populations are comparable. As a matter of fact when I compared the global military base population that was compiled in Ottawa, that would be Canadians from all - that would include French and English, when you compare that to exclusively French or to people from Vancouver which I would make the leap of faith that that would be predominantly English-speaking Caucasians, the population from Montreal was no - the frequencies were no more similar to the Armed Forces population which included French as it was to Vancouver's population, so there didn't seen to be a gradient of similarity going from all French to part French to predominantly English.

Q. Based on that is there any reason why a Canadian Caucasian data base should not have French and English Canadians within it for the forensic purposes for forensic calculations?

A. Can you repeat that? I lost you.

Q. Do you see any problem in having French and English Canadians, Caucasians, in the same data base in terms of calculating frequencies?

A. No.

Q. Do you see any problem with the R.C.M.P. Caucasian data base being used to apply to a New Brunswick case?

A. I can't think of any reasons, no.

Q. During cross-examination the term [statistically significant differences] and [forensic differences] came up.

A. Yes.

Q. And you used an example of 1 in 1 million and 1 in 9 million, am I correct?

A. I may have used that example, yes.

Q. Maybe I'm wrong in that. But perhaps to start anew, could you explain, please, just so we're clear on that what is meant by a statistically significant difference as opposed to a forensic difference?

A. Again, this is my opinion as I understand the statistics. I'm not a statistician. What you are looking at at these end numbers is the product of multiplying five numbers together. Now, at the end you may come up with 1 in 5 million in one population and 1 in 9 million in another population. Now, there's a number of different statistical tests that will tell you that there is a difference between 5 million and 9 million and that's fairly obvious. The forensic significance of that to my mind, both of those are very rare events and that's precisely what the test is designed to do, define whether it's common, moderately common, or it's rare, and both of those say rare in my opinion. And I even question whether they're statistically significantly different

because they're the product of small differences. Very often you can take things like 1 in 50 on the first probe versus 1 in 45, and the next one will be 1 in 63 versus 1 in 58. Very similar numbers. By the time you multiply all these out together you have taken little differences, you have multiplied all these little differences, and it's very likely that you can come up with a scenario comparing 1 in 5 million to 1 in 9 million because you're multiplying all the differences. But the thing that you should really be looking at for significance is I think frequencies at the beginning. Are they really that different and even if they are that different is it really that meaningful whether it's one in 63 or one in 53. And when you get to the end is it really that much more common if something's one in 5 million as opposed to 1 in 9 million. Does it bring it down I think forensically to a level where you say it's very likely if you use the 1 in 5 million that this came from someone else. That's what to me forensic significance means. Did we bring this down into the realm of reality where I have to think is this common now?

Q. That leads to the next question. Would a probability figure for a 1, 2, 3, 4, 5 probe match as given using the R.C.M.P. - given by the R.C.M.P. lab for forensic use such as to be done in this case, the figure that's given, what is attempting to be expressed by that figure?

A. To my mind whether the event is common or rare and you'd like to -- The size of that denominator is your ruler of how common or how rare.

Q. Mr. Furlotte raised the question of the fixed bin method, the fixed bin paper, and the fixed bin method the R.C.M.P. use that to determine band frequencies, and the FBI, is that correct?

A. Yes.

Q. What are you attempting to do with the fixed bin method? Who are you attempting to bias the results in favour of?

A. The results using that type of procedure are bias in favour of the Accused, and the scenario that the method was set up - that the method was designed for at the beginning, the scenario we are trying to avoid is the instance where in the population you have a fragment say at this level that's very, very rare, you also have a fragment at this level that's very, very common, what we wanted to avoid is a possibility of confusing a very common event with a very rare event. What we do is we add them together and we make both of them more common than they actually are. So it's designed to avoid these prejudicial numbers. That's what it was intended to do. Unfortunately, that becomes its criticism.

Q. What becomes its criticism?

A. Initially it was criticized because it was too conservative, then it's evolved to let's make it bigger and make it even more conservative.

Q. In favour of who? In whose favour would that be?

A. Again, the numbers will move towards being more common because you've included more events that you know are distinct but you include them anyway to avoid mistyping and misrepresenting the frequencies.

Q. A couple of times in your testimony you referred to Doctor Kidd, Doctor Ken Kidd.

A. Yes.

Q. And you said that he was the keynote speaker at this genetic conference that you were at in Washington last week and they had geneticists from all over the world, is that correct?

A. Yes.

Q. What is -- He was the keynote speaker. Could you tell us what a keynote speaker is?

A. Well, it's a symposium where there was a limited number of speakers and they were given a lot of time -- Generally at these types of meetings there are workshops or symposia where 15 or 20 speakers will give their talks and they have 7 or 8 minutes to get the message across and then the next speaker will give their talk. At the specialized symposium as Thursday morning was, it was limited to four invited speakers of which Ken Kidd was the first speaker and he basically ran that session.

Q. And who is Ken Kidd in the scientific community?

A. He's a professor at Yale University.

Q. And what reputation does he have?

A. Very, very high reputation in my field in human genetics.

Q. Is he to testify at this trial?

A. It's my understanding yes.

Q. The final question is just more for clarification than anything. During your testimony you mentioned fruit flies in a jar and to dispel any notion you were being flippant, the fruit fly is known as

drosophila, is that correct? Is that the genetic term for it?

A. Yes.

Q. What significance does drosophila have to the whole area of genetics and population genetics?

A. For a long period of time drosophila was the organism of genetics for various historical reasons and for breeding purposes. If you want to ask genetic questions -- Genetics is the study of inheritance and if you want to ask questions of inheritance a nice organism to pick is an organism that you can breed very fast and they have large numbers of offspring and they have characteristics that you can measure easily. What color are their eyes, how many wings do they have, and you can breed flies and monitor these characteristics over a period of days whereas if you tried to do that with people you would be waiting years, or animals you'd have large cages, but you can look at thousands of fruit flies in a closed environment like this and it's a very inexpensive way to ask very sophisticated genetic questions.

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

THE COURT: One question. In my case it's old age and gout but why is it that you don't like to give blood?

A. I faint.

THE COURT: You had our curiosity aroused. I think the jury would want me to ask you this.

MR. WALSH: I ask that he be stood aside My Lord.

THE COURT: Let's recess until 4 o'clock and then we'll go on for about half an hour.

(RECESS - 3:40 - 4:00 P.M.)

COURT RESUMES. (Accused viewing proceedings from cell.)

THE COURT: Mr. Walsh Doctor Bowen is your next witness?

MR. WALSH: Yes, My Lord.

THE COURT: You, yesterday, tendered those things there. You had agreed with Mr. Furlotte --

MR. WALSH: What's in the grey covers we have agreed on.

THE COURT: You are not going to reach those this afternoon?

MR. WALSH: No, we won't My Lord.

THE COURT: Well let's talk about them in the morning.

MR. WALSH: Fine, My Lord.

THE COURT: Well, let's have the jury in then. Is the video on? Would you check that Mr. Pugh, please.

(Jury in. Jury called, all present.)

THE COURT: Now, you have another witness Mr. Walsh?

MR. WALSH: Yes, My Lord, I recall Doctor John Bowen who testified previously in this trial.

THE COURT: You are still under oath Doctor Bowen.

DOCTOR JOHN BOWEN, previously sworn, testified as follows:

DIRECT EXAMINATION BY MR. WALSH:

Q. You were sworn, Doctor Bowen, the last time you testified, is that correct?

A. That is correct.

Q. And you're in charge of operations of the Molecular Genetic Section of the Central Forensic Laboratory in Ottawa for the R.C.M.P.?

A. That is correct.

MR. WALSH: My Lord with your permission I would like to be able to take Doctor Bowen through his C.V.

THE COURT: Okay.

MR. WALSH: You have a Bachelor of Sciences and Honours in Biochemistry from Carleton University in Ottawa, is that correct?

A. Yes.

Q. You have a Masters of Science in Biochemistry from Queen's University in Kingston, Ontario, is that correct?

A. Yes.

Q. You have a Doctorate in Biochemistry from the University of Alberta, in Edmonton, Alberta, is that correct?

A. That is correct.

Q. During your educational time you have won a number of awards and scholarships?

A. That is correct.

Q. And you did a dissertation in 1986 on "An Evaluation of DNA in Hair Roots", is that correct?

A. That is correct, yes.

Q. Where, when and why did you prepare this particular dissertation?

A. That particular dissertation was prepared during my inservice training as a hair and fiber specialist in the Edmonton Forensic Laboratory. It was part of my inservice training, a research project that everyone has to do. I chose the "Evaluation of DNA in Hair Roots" for my particular project.

Q. I'm going to ask you just to speak up a bit, Doctor. Doctor Bowen has an extremely low voice and it's a real effort for him to speak loudly.

THE COURT: We'll train him.

MR. WALSH: Would you describe your role at the R.C.M.P. in relation to DNA and DNA typing, Doctor?

A. Currently my role is to be In Charge of Operations for the Molecular Genetic Section. I supervise people handling case work. I actually do case work myself that has been submitted to the laboratory. I am also responsible for training new individuals and veteran staff in the DNA typing technology.

Q. Does this also include the restriction fragment length polymorphism technique that Doctor Waye testified about?

A. That is the particular technique that we are currently using in the R.C.M.P.

Q. Do you have experience in other kinds of DNA typing techniques?

A. Yes, I do. I have some experience with the polymerase chain reaction, a method of amplifying or making copies of DNA prior to analysis.

Q. Who have you worked with? Who do you work with or have you worked with at the R.C.M.P. laboratory with respect to DNA typing?

A. The particular individuals that I've worked with at the R.C.M.P. include Doctor John Waye who we have heard from, and Doctor Ron Fourney.

Q. You are a member of the Canadian Society of Forensic Science, is that correct?

A. That is correct.

Q. You are also the "Canadian representative in the Technical Working Group on DNA Analysis Methods", the acronym is TWGDAM, sponsored by the FBI Research Laboratory, is that correct?

A. I am one of three Canadian representatives.

Q. Would you explain what kinds of techniques -- Would you explain what you would do at these particular group --

A. The group meets approximately every 3 or 4 months. It's basically a meeting to evaluate certain issues that have arisen through case work, through the court, and also to give a forum for various people interested in implementing the technology or who are already using DNA typing in case work to research various areas of matching population genetics and various other issues, data basing.

Q. I am going to ask you to speak up again. Would you tell us, please, what members or what groups are associated with that particular organization?

A. TWGDAM is composed of two members from the R.C.M.P., a member from the Centre of Forensic Sciences in Toronto, about thirty members from various State labs in the United States and several members from the FBI research facility and their headquarters' operational lab.

Q. You compare your techniques and you discuss ongoing problems, make suggestions, etc., etc.?

A. Certain guidelines have been prepared in quality assurance and various other areas, yes.

Q. You are also a member of the "Workshop for Statistical Standards on DNA Analysis" again sponsored by the FBI Research Laboratory, is that correct?

A. Yes, that is correct.

Q. Would you explain your involvement in that and what, if anything, you do there?

A. This particular group was formed by the FBI to address certain issues with respect to statistical and population genetic issues that have arisen through the use of RFLP technology. The group included members from the R.C.M.P., the FBI, one or two State labs, but in addition to what normally would be part of the TWGDAM group we had several private companies, Cellmark, Lifecodes, and several members from the academic field, particularly in statistics and population genetics, individuals like Doctor Ken Kidd, Doctor Stephen Daiger, and Doctor Bruce Weir, a statistician.

Q. And what kind of things do you discuss at that group?

A. At that group we discussed certain issues regarding the match window, how to state a match, what sort of criteria have to be in place for a match, and also how to handle the population genetics.

Q. How did you yourself begin doing RFLP typing and what experience do you have in that particular aspect?

A. Well, I guess my first introduction to the use of RFLP or Southern blotting was when I presented a seminar to the Department of Biochemistry at Edmonton, University of Alberta, in 1978. Since that time during my doctoral thesis I became familiar with and did several RFLP typings. Consequent to that, in 1988 I had a year's sabbatical so to speak from case work in which I was involved in RFLP typing and PCR typing of hair, and in 1989 I joined the group in Ottawa, as I said before,

Doctor John Waye and Doctor Ron Fourney, and began using the precise techniques that the R.C.M.P. uses for RFLP typing that has been developed for case work.

Q. And outside actual case work how many RFLP typing tests would you have done?

A. I would say several hundred.

Q. What kind of samples have you done these tests on both in forensics and outside forensics?

A. I have handled hair, blood, liquid blood, blood stains, semen, vaginal swabs, buccal swabs, saliva.

Q. What is a buccal swab?

A. A buccal swab is actually a scraping of the inside of the mouth, the cheek, the epithelial cells that form part of the inside of the cheek.

Q. And just to refresh everybody's memory what is an epithelial cell?

A. It's a skin cell.

Q. And do you have any experience with any other fluids or substances?

A. I have attempted urine, nasal mucus. I think that's pretty much it.

Q. You yourself, actually, or part of your duties now include training others in these particular techniques, is that correct?

A. That is correct.

Q. How many actual cases at the R.C.M.P. lab have you accepted or completed using the RFLP technique?

A. Personally or as a section?

Q. Personally.

A. I believe the number is 33 or 34. And I have completed approximately 28 of those.

Q. And this might be an embarrassing question for you Doctor but do you know of anyone who has done more RFLP forensic cases in Canada than yourself?

A. Not to date. There are a few that are quickly approaching my case work.

Q. You have testified as a Molecular Genetic Specialist in forensic RFLP typing in the Provincial Courts of Ontario and Saskatchewan, Supreme Court of Ontario, Supreme Court of British Columbia, and the Court of Queen's Bench in Manitoba, is that correct?

A. That is correct.

Q. You are also, I see from your C.V., you have acted as a Defence Consultant as a Molecular Genetics Specialist in the Court of Queen's Bench in Alberta?

A. That is correct.

Q. Would you explain that? Defence Consultant. What do you mean by that?

A. The first consultancy occurred over the telephone. It was a case involving an individual who had performed a test, a DNA test in this case involving polymerase chain reaction on a sexual assault.

Q. This is the PCR test?

A. That is the PCR test.

Q. As opposed to the RFLP test.

A. That is correct. I was consulted over the phone and asked to testify at the trial. I went out for the trial --

Q. By whom?

A. By the defence. I went out for the trial and just prior to the prosecution witness testifying I

managed to sit down with him in front of the Defence and the Prosecution and we reached an agreement on what could be reliably determined from the case at hand.

Q. And the agreement you reached, did the expert that you were asked to - whose results you were asked to look at, did he say more or less than he was originally intending to say?

A. He said considerably less than what he was intending to say.

Q. Are you at this point with the R.C.M.P. laboratory in a position to do PCR testing for forensic case work yet?

A. We are not in a position to do that. It is certainly an area that is under-researched and we are very hopeful that within the next few years we will be implementing PCR base technology.

Q. I see from your C.V. you have participated in a number of conference proceedings and/or preparation of abstracts for meetings, is that correct?

A. That is correct.

Q. I see one of these being the "RFLP Analysis of Single Human Hairs" at the 35th Annual Meeting of the Canadian Society of Forensic Science in Toronto, Ontario.

A. That is correct.

Q. Again, Doctor, I'll ask you to speak up. You also were involved in an abstract, "Forensic Analysis of Restriction Fragment Length Polymorphism: Theoretical and Practical Considerations for Design and Implementation", in the proceedings of the DNA

Typing Symposium at Madison, Wisconsin, is that correct?

A. Yes, it is.

Q. You were participating with Doctor Fourney and Doctor Waye?

A. Yes.

Q. Again, with Doctor Waye and Doctor Fourney you were involved in "Forensic Analysis of Restriction Fragment Length Polymorphisms" - these are abstracts, correct?

A. That is correct.

Q. Of "Allele Frequency Distributions for Caucasian and Native Indian Populations", the annual meeting of the "American Journal of Human Genetics"?

A. Yes.

Q. Again, you participated with a number of other scientists, including Doctor Fourney and Doctor Waye, in an abstract "Forensic Analysis of Restriction Fragment Length Polymorphisms Using A Fixed Bin Approach: Variations in Allele Frequencies for Canadian Caucasian and Native Indian Populations" for the 12th International Association for Forensic Sciences at Adelaide, Australia, is that correct?

A. That is correct.

Q. Again, you participated with Doctor Fourney and Doctor Waye, among other scientists, in an abstract, the "Sensitive and Specific Assessment of Human Genomic DNA Concentration in Forensic Specimens", again presented at the 12th International Association for Forensic Sciences in Adelaide, Australia, is that correct?

A. That is correct.

Q. And, as well, again, you participated with Doctor Fourney and other scientists in an abstract, the "Interrelationship Between Forensic DNA Analysis Research and Case Work in the Royal Canadian Mounted Police" for the American Chemical Society Forensic DNA Symposium in New York City?

A. That is correct.

Q. And, as well, you have participated in an abstract with Doctor Carmody and Doctor Fourney and other scientists in an abstract the "Statistical Comparisons of Six VNTR Loci in Three Canadian Aboriginal Populations" at the 8th International Congress of Human Genetics in Washington, D.C.?

A. That is correct.

Q. You have also been an invited lecturer in "DNA and Forensic Science", the 12th Annual Conference of the Canadian Identification Society in Edmonton, Alberta?

A. Yes.

Q. And an invited lecturer on "Case Experience at the R.C.M.P. Laboratories" at the DNA Mini-symposium, the 37th Annual Meeting of the Canadian Society of Forensic Science in Ottawa?

A. Yes.

Q. You have attended a number of conferences and workshops and I take it that those deal with DNA typing, particularly the RFLP technique?

A. That is correct.

Q. One of them is the "Workshop on DNA Polymorphisms", the 35th Annual Meeting of the Canadian Society of Forensic Science in Toronto?

A. Yes.

Q. The "International Symposium on the Forensic Aspects of DNA Analysis" at the Forensic Science Research and Training Center at the FBI Academy in Quantico, Virginia?

A. Yes.

Q. You participated in a workshop on DNA "Quality Assurance and Quality Control Programs", the American Academy of Forensic Sciences 42nd Annual Meeting in Cincinnati, Ohio?

A. Yes.

Q. And a "DNA Symposium", the 38th Annual Meeting of the Canadian Society of Forensic Science in Montreal, Quebec?

A. Yes.

Q. What general field of science do you belong, Doctor?

A. Biochemistry.

Q. What relation would biochemistry have to DNA and DNA typing?

A. Biochemistry is essentially the study of all molecules of life. DNA just happens to be one of the more critical molecules of life and thus it is one that is intensely studied by biochemists.

Q. Are you the scientist who actually performed the case work for the Queen Versus Allan Joseph Legere?

A. Yes, I did.

Q. And you used the RFLP procedure in this particular case?

A. Yes, I did.

Q. Of the cases you have accepted yourself, personally, for case work, and I realize there's others accepting

cases at the lab, you mentioned - I forget how many you mentioned.

A. Approximately 33.

Q. Where did this particular case fit in that particular number?

A. It was about number 8.

Q. What does the forensic application of RFLP DNA typing entail, briefly?

A. The technique entails basically what Doctor Waye has described previously. The charts I believe 158(6) and 158(9) describing the DNA typing technology, essentially extracting the DNA, digesting it, running the gels, doing the Southern blotting, and hybridizing that membrane with various probes. The analysis also includes interpreting the matches that are found within the autorads and applying very fundamental rules of statistics and population genetics one can determine a statistical significance for any matches found.

Q. And you do that using what principles?

A. The fundamental principles used are the Hardy-Weinberg equilibrium and the Product Rule.

Q. And you use the binning method as well?

A. The entire method is based on the fixed bin method, yes.

Q. Are these mathematical calculations - are they fundamental principles?

A. Yes.

Q. In any of the cases you have testified in in court with respect to DNA evidence did you testify as to evidence as to whether certain matches existed?

A. Yes, I did.

Q. And in some of these did you put a statistical significance of those matches?

A. Yes, I did.

Q. Again, using these fundamental mathematical principles?

A. That is correct.

Q. Do you have experience with the issues involving the forensic application of RFLP typing?

A. Yes, I do.

MR. WALSH: My Lord at this time I would motion that Doctor Bowen be declared an expert in the field of biochemistry and the forensic application of DNA typing.

THE COURT: Any questions at this point?

MR. FURLOTTE: I have no questions.

THE COURT: I would declare Doctor Bowen an expert then in the field of biochemistry and the forensic application of DNA typing.

MR. WALSH: Thank you My Lord. You have indicated when you were going through your qualifications, you described the fact that you generally follow the procedure that's set out in those schematics and testified to by Doctor Waye, is that correct?

A. That is correct.

Q. Apart from the technique for generating the auto-rads, actually producing an autorad to look at, could you describe what is involved in the interpretation of the autorad?

A. As Doctor Waye first described, the interpretation first involves visually scanning the autorad to see if there are any matches apparent.

Q. That's with the human eye?

A. That's with the human eye visually scanning these. And first of all one can look across the various lanes that one has produced from the gel, that one can see if there's any exclusions or inclusions that can be made visually. These visual matches are then confirmed using the computer. It's a scanning computer as Doctor Waye described that actually captures the image of the autorad and assigns through the referencing the markers or the rulers at each end of the gel - it assigns a size to each of the bands that one has matched. Now, the R.C.M.P. uses a match window of 5.2%. If the visually matched bands fall within this match window then the match is confirmed. Subsequent to confirming the match one then goes to the data base to determine the frequency one would expect to see this particular pattern in a given population. The frequency is determined using the fixed bin method where certain fragment sizes are binned according to a range of fragment sizes and by determining the frequency of each of the bins for each of the bands matched one can determine through the Hardy-Weinberg equilibrium equation, 2PQ, the frequency of a two band pattern. Once this has been done for a particular locus or region of interest one then strips the membrane and retests the membrane with another probe and the entire process is repeated.

Q. And if you have another match you would determine the frequencies for that particular probe as well?

A. That is correct.

Q. And you would continue on?

A. That is correct.

Q. How do you determine your final calculation for say for example --

A. The final calculation is determined using the product rule. The individual frequencies for each of the loci are multiplied against each other in order to determine the genotype frequency.

Q. Just so we're clear, you're referring to loci, you're talking about the frequency for each probe depending on the number of probes in which there's a match been called you would multiply the frequencies together using the product rule?.

A. That is correct.

Q. Is that an accepted method?

A. Yes, it is.

Q. You indicated that at the R.C.M.P. lab you both need a visual match, your eyes have to say they match, and the computer must put them within the 5.2% match window.

A. That is correct. That is correct.

Q. If, for example, Doctor, at the R.C.M.P. lab you had a visual match but for some reason your computer said that it was outside the 5.2% window what would you do?

A. We would call that inconclusive and not use the bin frequencies or that particular match in our calculations of the frequency.

Q. This is an added feature to the forensic lab, is it?

A. This is an added conservative feature, yes.

Q. And in whose favour?

A. It's in the favour of the Accused.

Q. If for some reason the bands didn't match visually but your computer said that they were within the 5.2% window what would your lab do? What would you do?

A. It would be deemed an exclusion and reported as such.

Q. Meaning the person is excluded as having contributed that sample?

A. That is correct.

Q. So they both must match visually and within the match window?

A. That is correct.

Q. Have you been involved in any groups in which agreement was reached as to how an autorad is to be interpreted in the fashion you have said?

A. Yes, that was part of the function of the workshop on statistical methods in DNA analysis.

Q. And there was agreement reached on that matter on interpreting it in that fashion?

A. Yes.

Q. What, if any, agreement did you reach as to the possible conclusions that can be drawn from the interpretation of an autorad?

A. Agreement was reached that essentially there's three conclusions. That first the sample could not have come from the same person is an exclusion, the band patterns do not match. The second possible response is that it is an inclusion, that the bands match and that it falls within your match window thus you can

call it inclusive and the samples could have come from the same person. Or there is the inconclusive call where for various reasons one can determine that perhaps half the pattern is there, there is certain problems with intensity of bands, whatever, that these could be called inconclusive and thus no statistical weight would be given to those results.

Q. If you were calling something inconclusive, say for example you couldn't see something, would that exclude the person?

A. If there is any reason to exclude then the sample would be excluded and the --

Q. But if it's only inconclusive?

A. If it's -- Inconclusive requires that anything found in that particular lane is consistent with having come from the same source. If there's anything that's inconsistent with having come from the same source then it would be called an exclusion.

Q. How many separate gels or membranes did you produce in this case using your test? What I am saying is how many of these gels did you actually run in this particular case?

A. I ran four analytical gels.

Q. Did you make any matches in relation to this particular case from any of those gels?

A. Yes, I did.

Q. Did you assign a statistical significance to any of those matches?

A. Yes, I did.

Q. What data base did you use to assign the statistical significance?

A. I used the R.C.M.P. Caucasian data base that was dated December 3rd, 1990.

Q. And they comprise individuals -- They comprise what?

A. It is comprised of individuals from the CFB Kingston, the Canadian Forces Base in Kingston, individuals from the Ottawa area and individuals from the Vancouver area.

Q. Obtained in what fashion?

A. The samples were obtained partially through the Red Cross and the Vancouver samples in particular was obtained through the Pathology Department of the University of British Columbia.

Q. How does the method of calculation that you used to attach the statistical significance to the matches that you called in this case compare to the method described by Doctor Waye, that is binning, Hardy-Weinberg equation and the Product Rule?

A. It is identical to the way described by Doctor Waye.

Q. You testified previously during your being declared an expert, you testified that you have run tests on various kinds of substances and you mentioned semen, hair and blood, liquid blood, dried blood, a number of those particular things. What kind of extraction methods would you use to obtain DNA from these materials, for example hair root, blood, semen?

A. There are certain differences in the technology used to extract DNA from these particular materials. Blood stains, hair roots, are extracted by the same method. Liquid blood is extracted by a different method again and then swabs, semen stains, are

extracted through the method of differential extraction.

Q. Okay. That was touched on I believe with Doctor Waye but would you please explain to the jury what a differential extraction is?

A. A differential extraction is essentially a method - an attempt to enrich the female fraction which is the vaginal cells from the - the vaginal epithelial cells on the swab from the sperm cells found in the semen. It is an attempt to enrich it, as I say, specifically it is an attempt because not often is it totally successful, but it takes advantage of the various differences in the cell types. Vaginal epithelial cells are very easily broken. They can be broken open under very mild conditions. By taking advantage of that one treats the sample to mild conditions, breaks open the vaginal epithelial cells which releases the DNA from these cells, and that can be removed from the sample. Under harsher conditions the sperm cells are then broken open and the DNA is released from them, and one can thus achieve some sort of separation of DNA from the female fraction and DNA from the male fraction.

THE COURT: I wonder would that be a convenient place to stop?

MR. WALSH: I have a couple more questions and then it would be a logical place to stop My Lord, if you would permit me.

THE COURT: That's quite all right.

MR. WALSH: From a simplistic point of view then what you are doing with a differential extraction, you are separating - you're attempting to separate the female DNA from the male DNA that would be contained within the sperm - or within the vaginal swab?

A. That is correct.

Q. And you say that sometimes it's not successful or sometimes there is --

A. Sometimes there's not a complete and total separation. One will often get carry-over of the female fraction into the male fraction thus we have actually gone away from using the term female fraction and male fraction, but for the purposes of this particular case that's how I designated those samples.

Q. And how would an incomplete separation - what effect would that have in terms of how you interpreted an autorad?

A. If it's an incomplete separation one ends up with a mixed pattern. One, for example, could end up with four bands rather than the expected two bands for a given individual.

Q. And do you have a way of determining that, the fact that it's an incomplete separation and that's to account for the four bands?

A. Yes. There is a way of comparing what is in the first female fraction and in the mixed sample or comparing the victim's type to the sample plus any suspect's type to that particular sample to sort out where each of the alleles come from.

Q. An incomplete differential extraction then is not an unusual thing in a forensic lab?

A. No, it is not.

Q. Is there anything else that's related to the methodology of the RFLP typing procedure that could create extra bands on an autorad?

A. Incomplete stripping can cause what appears to be extra bands on a given autorad. This is essentially something that can occur if the temperature isn't quite hot enough when you're removing the probe from the previous hybridization or for certain samples of DNA there's more DNA, more probe bound to it. If the probe is bound really tightly it is sometimes more difficult to remove some particular probes which are what we term more sensitive, and one can visualize some small amounts of these particular bands on a subsequent probing.

Q. You mean actually reprobing with the same probe?

A. No, this is subsequent probing with another probe one can see some of the bands remaining from the previous probe.

Q. How would you account for that? Is there a method you use to account for incomplete stripping?

A. One can simply determine that it is a stripping problem by overlaying the two autorads to say that yes the bands match up with the previous hybridization so one keeps track of the order of the probings and then one can determine that. Further to that, one can strip the probe and reprobe with the same probe again and thus alleviate the problem and remove all the extra bands.

Q. Again, is that something that happens in a forensic lab that is expected?

A. Yes, it does happen on occasion.

MR. WALSH: My Lord I would suggest this would be a logical place. Thank you.

THE COURT: Yes. Okay then, we will adjourn until tomorrow morning at 9:30, and you shouldn't discuss the matter with anyone until all your testimony is finished as you know, Doctor. So would the jury - we will see you in the morning at 9:30, please.

(Jury excused.)

THE COURT: We will recess now.

(ADJOURNED 4:40 P.M. TO OCTOBER 17, 1991 @ 9:30 A.M.)