VOLUME XI

IN THE COURT OF QUEEN'S BENCH OF NEW BRUNSWICK

TRIAL DIVISION

JUDICIAL DISTRICT OF FREDERICTON

B E T W E E N:

HER MAJESTY THE QUEEN

- and -

ALLAN JOSEPH LEGERE

VOIR DIRE PROCEEDINGS held before Mr. Justice David Dickson at the Burton Courthouse, Burton, New Brunswick on the 14th and 15th days of May, A.D., 1991.

APPEARANCES:

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

Weldon J. Furlotte, Esq.,)
Michael Ryan, Esq.,) for the Defence.

Dolores Brewer,
Court Reporter.

Verna Peterson,
Court Reporter.

I N D E X

EXHIBITS

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COURT RECONVENES - 9:30 A.M.

CROSS EXAMINATION OF DR. FOURNEY CONTINUED BY MR. FURLOTTE:

Q. Doctor Fourney before we get on to the slides about the Canadian Indians maybe we will just go over the latest FBI report on your Environmental Insults Studies.

A. May I refer to my own copy?

Q. Sure. Do you have your own copy there?

A. Yes, I do.

THE COURT: This is what? VD --

Q. VD-93. First of all, in this report, Doctor Fourney, I notice that up at the top of the first page it's marked "In Press. J. For. Science." and

it's dated September, 1991.

A. That's correct.

Q. That hasn't been out for peer review as of yet, has it?

A. No. In fact that's incorrect. The fact that it's in press means that in a typical situation a journal is backlogged anywhere from six months to a year. The fact that it's in press for September means that it has gone through the official review process; it has been accepted; it has been peer-reviewed by members of the scientific community for publication.

Q. When you say the scientific community do you mean the forensic scientific community or the scientific community in general?

A. The general forensic science typically sends out their material to scientists in both communities. In the same manner that I would review articles from a non-forensic science community many scientists review articles for the forensic community.

Q. I would assume, Doctor, it really hasn't had sufficient time for people to assess it and either to criticize it or approve of it as of yet?

A. I would like to accept the fact that peer review is a fairly rigorous process and the very fact it was accepted for publication means that it has gone through that process.

Q. But the mere fact that it's accepted for publication doesn't mean that nobody is going to take objection to it.

A. As I indicated earlier, controversies exist in science and you are going to find people taking

exception to whatever you write.

Q. On page 2 of the report, the last paragraph on page 2, says:

> "Forensic evidence can be subjected to a variety of external influences prior to examination by crime laboratory personnel; therefore, an understanding of the effect of environmental insults or adventitious substances on DNA isolated from blood and other body fluid stains is (and I emphasize) necessary prior to implementing this technology in casework."

So would you agree with that that environmental studies are necessary prior to the implementation?

A. Yes, I would.

Q. I also notice on page --

THE COURT: Well actually it doesn't say that. It says "an understanding of the effect of environmental insults, etc. is necessary. It doesn't say that the studies are necessary. Aren't we distorting what it says around a little.

A. Yes, I see what you mean. I think what they are trying to suggest here is that we must have a general conceptual understanding of what could possibly happen to DNA under various insults. Whether or not you have done a specific experiment that would mock-up the exact situation in a crime scene is often difficult to predict ahead of the fact of actually seeing the information come in. What I am trying to say is that there is no way that, certainly in my experience, that a forensic scientist can predict all the variables that could be possible.

Q. I notice on page 3 of "Environmental Studies: Long Term Exposures to Sunlight" it states that after the stains were made it says in about the middle of

the paragraph, it says these stains were stored --

Maybe I'll go back a little further. It says:

> "One half of the stains were exposed to the diurnal cycle of sunlight and darkness. The other half were maintained at the same temperatures, but exclusively in the dark. Four blood stains from each set of stains were collected at intervals of two weeks for a period of ten weeks (5 samplings). These stains were stored at -80° C until a time at which all samples could be analyzed simultaneously."

Now, that would be a big difference in the forensic samples collected in his case work where here they are storing them immediately at -80° Celsuis to preserve them.

A. That's correct but you also have to understand the nature in which this particular experiment is conducted, also the nature of science. What you try to do is limit the possible variables that could occur. What they're specifically interested here is the actual exposure of these stains with respect to the same time frame between sunlight and darkness so in order to minimize any other variation that could be possible through sampling, extraction, etc., what they have done is they have only changed one variable and they have frozen the rest so that they could do the experiments simultaneously in order to derive a justified conclusion for the actual parameter that they are changing. If you wanted to ask the question about storage we would have to design an experiment simply for that.

Q. I understand, Doctor, that some of the case work from this particular case and the evidence, in particular the vaginal swabs 1-I and 1-J - they were collected

sometime in May of the year and they were stored in plastic bags at room temperature for up until the end of October when the tests were completed. That would be quite different circumstances than the results that these tests were taken, would it not?

MR. WALSH: My Lord, objection. I don't believe the record will show that, that in fact Mr. Furlotte says-- If that's a hypothetical, fine, but if it's what he is suggesting occurred in this case then the crown would suggest he's incorrect.

MR. FURLOTTE: Well, as I recall the evidence from the first voir dire on the admissibility of bodily substances I think the continuity shows bodily substances were collected and how they were stored.

MR. WALSH: Yes. In fact I believe that -- I can't remember the extent that we went into that particular aspect but I believe Mr. Furlotte is aware of the fact that these substances, the vaginal swabs, were stored in a refrigerator, if I'm not mistaken, at least through a certain period before they were taken to Ottawa. I'm just saying that if he wants to put it in the form of a hypothetical I have no objection --

THE COURT: Well let's treat it as a hypothetical question for the purpose of this --

MR. FURLOTTE: My Lord that's one of the reasons why I objected for the Crown not having to bring evidence to put forward the continuity of these exhibits because now I am unable to question or cross-examine on the storage of them.

THE COURT: Okay.

MR. FURLOTTE: Doctor, could those conditions have an adverse effect on the sampling of environmental insults?

A. In my professional opinion for the samples that I have seen come into the lab and the samples that I am aware of that other labs have processed, the major factor involved with storage of stains is actually the drying process. So if a sample is dry it tends to be retained for much longer period of time and if you're allowed to extract DNA that is very high molecular weight, and the bottom line in this entire questioning I would assume would be whether or not you would get high molecular weight DNA from your substance, and the net result of our findings at the R.C.M.P. Lab is that if you have high molecular weight DNA and you can show that it's human specific then there's an excellent probability that you will certainly get an RFLP banding which is reliable and valid.

Q. One of the concerns is to prevent bacterial contamination, that's why they want it dried right away?

A. I think bacteria may be present whether the stain is dry or not.

Q. But it's more apt if it's kept in a moist condition. Is it also not suggested that they store these in paper bags rather than closed-up plastic bags?

A. We actually store our stains in a plastic bag. They are dry and it's clipped to a sheet of paper and then it's put into a plastic bag in much the same way that the serological evidence has been stored in the past.

Q. Do you recommend that -- Or do you freeze your stain right away as is recommended in this report?

A. Yes. Anything coming into the R.C.M.P. Lab we would freeze the stains. If a sample, for instance, is a blood standard we would work from the blood standard directly but we would certainly make a stain from that for storage purposes and for later extractions.

Q. Again, on page 4, top of the page, first full sentence it says:

> "Samples of three bloodstains from each group were collected every 24 hours for a period of 12 days (12 samplings) during July, 1988. The stains were stored at (again) -80° C until analyzed."

So it appears that the conditions here are far from the conditions that are normally in case evidence and particularly in this case where so much time had went by from the time the samples were collected until the time they were analyzed.

A. Once again, it has been my experience, as I indicated earlier, if you can demonstrate the ability to extract high molecular weight DNA and it's human then you have an excellent probability.

Q. Have you ever personally done environmental insult studies?

A. Have I put stains on to material and extracted them?

Q. That would be one, yes, have you done that?

A. Yes, I have done that.

Q. Have you done environmental insult studies as to the effect that they have done them in this report?

A. I personally have not done this type of study, no.

Q. So you haven't done environmental studies on mixed stains, mixed body fluids?

A. It's a typical training program that we put all our people through. They would do a series of stains, generally they are a mixed stain, and they would have to get the expected results. It's part of our training program. Much of this work has been worked up in the Research and Development part of the R.C.M.P. Labs.

Q. I also notice on page 7 under the heading "Contamination Studies: Mixed Body Fluids" it states all stains were -- on page 7 at the top of the paragraph, middle of the paragraph, it starts:

> "All stains were air dried and stored at room temperature for 5 days prior to analysis."

Again, there would be a big difference between storing it at 5 days room temperature or six months?

A. Once again, the stain - the important feature is if it's dried.

Q. If it's dried.

A. That's correct.

Q. But there's no evidence that the body stains that were collected in these were - how they were dried, if they were dried, except that we - I believe on the first preliminary hearing they were kept in the locker in the Sackville Laboratory until they were shipped to Ottawa.

A. The specific nature of the samples I think you would have to ask either the officer involved with continuity or perhaps Doctor Bowen who received the actual samples.

Q. Page 8 under the heading "Results and Discussion" "Environmental" in that text it says in the middle of the top paragraph:

> "After 8 weeks of exposure to sunlight, DNA was degraded to such a degree that no RFLP banding patterns could be observed via autoradiography."

These samples - or the evidence in this case being stored for such a long period of time, it would attempt to degrade? If not totally, at least partially?

A. I am trying to relate that sentence to your question. The sentence is dealing with sunlight and you are asking me storage under a particular condition would it degrade?

Q. It appears from their study that --

A. Sunlight has an effect on the --

Q. Sunlight has an effect?

A. Correct.

Q. And if it's kept in complete darkness it will keep much longer?

A. Yes.

Q. But also time would be a factor aside from the sunlight and darkness?

A. I believe they have done that study with sampling over a series of weeks where they showed that the factor involved with degradation was in fact sunlight in that time.

Q. Also, at the bottom of page 8 where they run their sampling -- Let's see where I can start here. Find the first little sentence. I guess I have to go about the middle of the bottom paragraph on page 8 it says:

> "A comparison of estimated fragment sizes between the control stains and treated stains determined that no treated sample had DNA fragments which differed from the control greater than the 5% matching criteria established by the FBI Laboratory and in fact the maximum observed difference (positive or negative) between the control and treated samples by SLP for any fragment was 1.79% (D2S44) probe, 3.02% for the D17S79 probabe, 2.67% for the D1S7 probe, 4.12% for the D4S139 probe and 1.55% for the D10S28 probe."

So it would appear there, Doctor, that the environmental insults would have varying effects on different probes. Would that be due to strictly the fragment length in each of those probes or would that be due to something else?

A. Just by looking at this, for instance the D4S139, typically the fragment length that you would see there would be at the top end of the gel for instance.

Q. Let's take a particular --

A. But on the other hand D1S7 you can have bands up at the top or the bottom so it's actually a little difficult to make a conclusion along that line.

Q. Let's take the comparison D4S139 probe which is 4.12% and the D10S28 probe which is 1.55%. That's not quite but it's almost three times as great.

A. Yes.

Q. For the different probes.

A. There certainly seems to be a difference, yes.

Q. Now, on the bottom of page 12, last sentence it says:

> "In an examination of more than 100 cases involving sexual assault evidence, no DNA profiles produced from the non-sperm portion of the DNA extract taken from the evidence differed beyond established matching criteria from the known blood sample of the victim."

Now that's in the FBI's 100 cases involving sexual assault. I believe Mr. Legere's case was one of the

very few first ones that you have conducted, is that correct?

A. Yes.

Q. And in Mr. Legere's case in the R.C.M.P. system matching known samples from Mr. Legere you fell outside your matching window. So would this implicate that the R.C.M.P. system is much less efficient than the FBI's?

A. Once again, efficient relates to different aspects of the process.

Q. Well let's use the word 'reliable'.

A. Well first of all, we don't have that case load yet but what we have showed you in the slide, I believe, that was projected yesterday, that's 502 bin match comparisons and what we do with our typical samples now is that we add this to our actual data base for forensic comparisons so as we get more cases we will presumably have a larger comparison, that's certainly correct, but I feel justified in saying that to date with the information that was analyzed so far I think our 5.2% matching criteria certainly falls within the reliability of the evidence we are dealing with.

Q. My concern, Doctor, is that it appears that in this report they have analyzed through a hundred cases they went through and everything that they tried they were able to keep within the matching window, even subjecting them to environmental insults, you know, the stringest testing they could give them, they were able to keep them all within their matching window. And the R.C.M.P. just after a couple of cases - maybe Mr. Legere's was the second or third case in your lab, and you can't keep samples of DNA from Mr. Legere

which were not subjected to environmental insults within your matching window. Now does that make your system less reliable than the R.C.M.P. - or less reliable than the FBI?

A. I believe there is one standard that was outside the match criteria, is that correct?

Q. You are the one who reviewed the reports.

A. I think it was the D4S139 fragment which is at the top end of the gel. All the other fragments that we did look at certainly were within our match criteria.

Q. Some of them were borderline, were they?

A. Well, they are all within 5.2%.

Q. And if you added - which I know it's not the scientific procedure at least at this time - for the differences as shown here between when they were conducted - subjected to stringent environmental insults where there was a difference of 4.12% for the D4S139 probe, if you start adding those figures on top of the ones you received you could be well outside the window or less efficient or less reliable.

A. There's not really any reason to believe that.

Q. Doctor, I am going to show you exhibit VD-78 which are the fragment sizings - computer sizings of probe D16S85 for autorad 890L1191-13 which I believe is a comparison of Mr. Legere's known samples in exhibit 335 and 83A, would that be correct?

A. It appears from this document that, yes, that's 335 at the top and 83A, yes.

Q. And I notice for this one for exhibit 335 - and that would be the blood stain from his nose -- It probably doesn't say there. I believe the crown prosecutor could substantiate that.

MR. WALSH: It's a blood stain on toilet paper, yes.

MR. FURLOTTE: On toilet paper taken from his nose. And I believe the percentage of differences between his other known standards is marked in the corner by Doctor Bowan.

A. Looks like 5.2.

Q. 5.2%. So that just meets your matching window.

A. Yes, if that is in fact 5.2% that's true, yes.

MR. WALSH: We had better clarify, Mr. Furlotte, as to whether or not those figures relate to within the gel comparison or the gel comparison because that autorad was used for that purpose.

MR. FURLOTTE: This would be a gel to gel comparison, would it not, with the known sample? When you reviewed these tests were those figures taken on comparison gel to gel and which other gel did they compare with?

A. I believe it would probably compare with initial -- Once again, I'm not sure of your exhibit numbers here but presumably one of the exhibits related to in the initial analysis. One of the autorads with the six series.

Q. So that would just barely meet your match window? Whether it's gel to gel or within a gel your match window is 5.2%, is that correct?

A. The analysis that we have done is we have taken all our case work samples whether --

Q. I'm just asking you what your match window is? Is it the same --

A. 5.2%, yes.

Q. -- within the gel and between gels?

A. Yes.

MR. FURLOTTE: Okay. (Pause.) Are all the sizings in?

MR. WALSH: If Mr. Furlotte is asking me, My Lord, if I have put all the sizings in, if he could indicate to me which one he wants we could perhaps try and assist in this regard.

MR. FURLOTTE: I believe it goes from 66 to and including 85 or 84. I just have 74 to 85 here.

MR. WALSH: So we're looking for 66 to 73.

MR. FURLOTTE: Okay, I have 66 to 85 here. (Pause.) I don't see the sizings there where the hairs -- the hair that was found on Father Smith and --

MR. WALSH: The sizings for that particular blot was not entered because there was no inclusions in that blot.

MR. FURLOTTE: Okay, could I have them entered then for the purpose of cross-examination?

MR. WALSH: Sure. Perhaps, My Lord, if we could take a five minute recess I could -- I believe Doctor Fourney has those sizings and if Mr. Furlotte wishes them to be entered we can do so but it would be easier if we did it with a five minute recess because we would be disruptive here by the time we get the sizings.

THE COURT: Oh well, take a five minute recess. I'll read along here and we'll carry on. We needn't leave the courtroom.

(Pause.)

MR. WALSH: My Lord I have the sizings. This would be for the blot number 89OL1191-14. The first one is with respect to D1S7.

THE COURT: I wonder if you could just read me that number again - the blot number.

MR. WALSH: The blot number is 890L1191-14, and it's with respect to probe D1S7, and it's headed "Calculated Fragment Lengths (log model)", two pages.

MR. FURLOTTE: I would move to have that entered.

MR. WALSH: These are copies of the original. Duplicate copies with Mr. Furlotte's consent.

THE COURT: This will be VD-98.

(Clerk marks 2 page document VD-98.)

MR. WALSH: The next document is "Calculated Fragment Lengths (log model)", same blot number, with respect to DNA probe D2S44.

THE COURT: VD-99.

(Clerk marks document VD-99.)

MR. WALSH: The next document, My Lord, is "Calculated Fragment Lengths", same blot number, with respect to DNA probe D4S139. Each of these documents is 2 pages.

THE COURT: VD-100.

(Clerk marks document VD-100.)

MR. WALSH: Next document, My Lord, same heading, same blot number, DNA probe D10S28, 2 pages.

THE COURT: VD-101.

(Clerk marks VD-101.)

MR. WALSH: Next, same heading, same blot number, DNA probe D16S85, two pages.

THE COURT: VD-102.

(Clerk marks VD-102.)

MR. WALSH: Next document same heading, same blot number, DNA probe D17S79, two pages.

THE COURT: VD-103.

(Clerk marks document VD-103.)

MR. WALSH: Next document same heading, same blot number, reference DNA probe D7Z2.

THE COURT: That will be VD-104.

(Clerk marks document VD-104.)

MR. WALSH; And the last document, My Lord, same heading, same blot number, reference DNA probe DYZ1.

THE COURT: That will be VD-105.

MR. FURLOTTE: Doctor, I am going to show you exhibit VD-102 which is the sizings for probe D16S85 and this would have been run in the third gel, lot #890L1191-14. I notice the computer sizings for this probe for exhibit 335 which is a blood stain from Mr. Legere's nose, okay, and the band of low molecular weight has sizings of 959 base pairs which calculated by Doctor Bowen is 5.5% away from the sizings he took in the first of Mr. Legere's hair samples, would that be correct?

A. I would have to -- From the values here in the side that appears to be correct.

Q. Right. And if we look down at the other hair sample that was run in the same gel as this one we have a base pair size of 997 base pairs for exhibit GT56B which I understand is a hair sample which was taken out of the Sackville Lab and from the same hair sample that was taken off Mr. Legere in 1986. Would that be correct crown prosecutor?

MR. WALSH: That's correct. I trust Mr. -- I'm prepared to agree to this at trial as well Mr. Furlotte.

MR. FURLOTTE: So this 5.5 fell outside the R.C.M.P. window, would that be correct?

A. The 5.5 is outside the 5.2% window, yes.

Q. And as we noted for the D1S7 we are within -- That band for D1S7 is -5.1% which we are just in the R.C.M.P. matching window.

A. Yes, that's lower than the 5.2.

Q. And yet for that same band or for that same gel and the same -- No, different band, I'm sorry.

Again, Doctor Fourney, it appears that the R.C.M.P. system cannot even identify the same individual and it's not reliable enough to identify the same individual. Is that correct?

A. That's based on what? I'm not sure I understand.

Q. Based on your test results.

A. You have one test with one band that's outside of our window so that would not be included. You have the other test that's within our window. It would be included. It's simply you would have to look at each specific test with regards to that probe.

Q. And this is run -- I'm trying to compare your tests and the reliability of your testing system with the testing system of the FBI just so you know what I am getting at, okay. But it appears that the FBI in running over a hundred cases hasn't even come close to what you have been able to accomplish in two tests, two or three tests, in your lab.

A. Those particular samples are outside of our matching criteria, yes.

Q. And they run theirs on samples which were - they subjected them to the worst tests of environmental insults and your samples were not even subjected to environmental insults which should have made your tests much easier to come within your matching window.

A. Well, I think that's a generalized statement. We would have to examine the nature of each sample and look at it. The fact that the hair standard, for instance, was looked at with respect to the blood stain and the one sample has fallen outside the window certainly doesn't invalidate the other probe results.

Q. But the same thing -- It appears to me, anyway, that what's going on here with these environmental insults studies the same thing shows up in your lab as what showed up in your lab with the effects of ethidium bromide - contamination with ethidium bromide where you show your lab is not able to handle those kinds of insults.

A. We certainly do not have the large number of samples as of yet in our case work but, once again, with the studies that we have done everything put together are matched - that is with all the forensic samples we have looked at to date in our comparison. The slides I think I showed the majority of those samples have all fallen within the 5.2% which is an empirical study that we have developed in our own lab using our own system and, yes, we are different from the 5% of the FBI. That's why we have developed our 5.2%.

Q. But you are more than different than just the 5.2%. There's a big difference in reliability of your testing. At least it appears that these statistics indicate that. Would you agree with that Doctor?

A. With respect to the environmental insults study?

Q. With respect if you're just conducting the analysis.

A. There are some differences, yes.

Q. Substantial differences.

A. Once again, I think I empirically established our window is 5.2 and that's certainly different than 5.0.

Q. Okay, Doctor, we may as well -- I think we have flogged that horse enough. Let's try our slides now on Canadian Indians. See what we can learn here.

A. How exactly should I present this?

Q. I'll leave it up to you.

MR. WALSH: Perhaps we could start by Mr. Furlotte asking the Doctor a question as to what he is trying to determine and the Doctor could address it.

MR. FURLOTTE: I want to determine Doctor as to you have done a - you have conducted or put together data bases for two different Indian groups in Canada, one in B.C. and one in Northern Ontario, and I would like to see how they differ and what their frequencies are and how substantially different they are.

A. Okay. Once again, if I may refer to my notes. I want to stress the fact that Doctor Carmody has not done any statistical comparisons on the Native Indians as of yet. He's primarily considered the Caucasians. These slides have been prepared primarily for a teaching aid for our scientists and for lectures that we often give so if you'll pardon the slight introduction.

Once again, we saw this slide yesterday and a copy of this has been entered into evidence. I want to stress the fact that in the Canadian population, for instance, the 95.7% figure represents the

Caucasian group as opposed to approximately 2.1%, the best calculated data from the 1986 report for the aboriginal populations in Canada.

THE COURT: May I just inquire here, some of these -- Have you got sheets of paper made for each of these slides?

A. Yes, I have sheets of paper for each of these slides. There is one change in one of these slides where there's a little bit of additional data from another laboratory.

THE COURT: How many are there altogether in this group? These all pertain to the native Indian studies?

A. Yes, in fact.

THE COURT: And how many are there altogether?

A. About 17. There is one study here for demonstration purposes of a Caucasian population just for comparison purposes.

THE COURT: Yes. Well, Mr. Furlotte, are you going to require that all these be put into evidence?

MR. FURLOTTE: Maybe after we're done showing the slides I could then look at the sheets --

THE COURT: This is really more of a fishing --

MR. FURLOTTE: -- and decide which ones I might like into evidence.

THE COURT: Isn't this more fishing than anything but --

MR. FURLOTTE: I wouldn't say more fishing but I do expect to catch something.

THE COURT: All right. Well, you decide whether you need these in. We don't want to clutter up the record with too much inconsequential matter.

MR. FURLOTTE: No, no, I agree.

A. The only slides I don't have copies of, there's two maps here, one of Canada showing approximate locations of Native Indian populations, and there's one for British Columbia, and that was simply to address the question that was put to me on Friday from the prosecutor with respect to demonstrating where the Native Indians have come from.

This is the breakdown from the Canadian Atlas, I think edition 5 - I'll just check my notes here - yes, National Atlas of Canada, the 5th edition, where what we see here of that small percentage aboriginals in Canada the large component is based on the Algonquin group which is 59.6%. These Native Indian groups have been arranged according to the linguistic dialects, and as you can see the greatest percentage throughout Canada is the Algonquin followed by the 8.4% here of the Athapaskan right across to the smaller percentages in some of the British Columbia Native Indians.

This map, which I apologize, is a full scale map and it's difficult to photograph. What we see is the largest section of Canada. Represented by the green is the Algonquin group, and our samples have actually come from Northern Ontario whereas the other samples that we have from British Columbia are from the Athapaskan and the Wakashan areas mapped out here. I think I have a blow-up. Yes. In this area here, the two different groups.

What we have done is we have sampled the population. This is basically showing you a difference in the population bin frequencies, the total bin

frequency for the Ontario Native Indians versus Ontario Caucasians for the locus D2S44. What is obviously apparent here is that on bin 8 there is a great percentage of the Native Indians representative in this bin up to - from the side it looks like about 43%, as compared to a smaller percentage just under 5 here in bin 8. So this is why I say you can visually see that there is a major change between the Ontario Caucasians and the Ontario Native Indians based on the D2S44 data.

Once again, this is a comparison using a histogram of the D2S44 allele frequencies. This time we are looking at the British Columbian Native Indian population versus the Ontario Native Indian population and even here we see a difference between the two groups of Native Indians.

This is the slide I mentioned that I do not have the exact copy - the Arizona Native Indians which represents preliminary data from another laboratory is on this slide. It's put on for teaching purposes. This shows our groups together where the British Columbia Native Indians are yellow followed by the Ontario Native Indians, the British Columbia Caucasians and, you can't see it very well but it's right there, and the last one here, the Arizona Native Indians. It's a difficult slide because there's too many comparisons on the slide. But the substantial differences are noted in the Native Indian populations.

D1S7, similarly, another locus where we have British Columbia Native Indians in the yellow and the Ontario Native Indians. Once again, we see some differences.

The British Columbia Native Indians versus the Ontario Native Indians for the locus D4S139. Bin 27 for instance seems to be a very noticeable difference. I stress that the statistics have not yet been done on these. On the other hand, this particular locus for D16S85 looks fairly uniform between the British Columbia Native Indians and the Ontario Native Indians.

One thing that should be recognized here is that in the British Columbia Native Indians we have a smaller sample set. I would have to refer to my notes but I believe it's roughly around 125 Native Indians whereas the sample size of the Ontario Native Indians, if my memory serves me correctly, is 232, I believe, samples, and we're expanding this on a routine basis. That's part of the reason for the slides being altered from time to time is because as our data bases grow we have to include the new data of course.

The D17S79 allele frequencies for British Columbia Native Indians versus Ontario Native Indians is represented here. These two samples I would suggest are different. This is the same locus for Canadian populations with, once again, the British Columbia Native Indians, Ontario Native Indians, the British Columbia Caucasians and the Ontario Caucasians.

Now, what Doctor Carmody, I believe, has told the Court prior to my testimony is that there is no substantial significant differences in the Caucasian groups using all the tests that he has applied. Now, although we have not done the tests that he has conducted on the Caucasian groups for the Native Indians, I would suggest that there is some statistical

differences just from the visualization of these slides.

That's pretty well the gist of this topic.

MR. FURLOTTE: Does that complete all the probes?

A. There is one probe that is missing from here, D10S28, and we are just compiling that information now. I have not had a chance to make any slides of the complete data for that yet.

Q. Is that it Doctor, for the slides?

A. Yes. Do you have any questions concerning these slides?

Q. No, that's fine. I think if we just -- The only thing I would request be put into evidence would be these charts of the different probes. There's not that many anyway.

A. Perhaps it's best to do that now with respect to the slides so I can check them.

Q. Yes, okay.

THE COURT: We may as well give these all separate numbers. VD-106.

(Clerk marks reproduction of slide VD-106.)

MR. WALSH: Mr. Furlotte - does he want reproduction of everything that was on the screen?

MR. FURLOTTE: Yes.

MR. WALSH: I understand from Doctor Fourney - from discussions with Doctor Fourney last week, he is concerned and he has certainly no problem, My Lord, obviously filing these exhibits here, but he does have a concern with respect to some of this data. They haven't finished actually working on some of the data, and my understanding in the scientific community if

this data was to get out and be used by other people it causes a problem for them. The only thing is that we would ask an agreement from Mr. Furlotte that this data will only be used in relation to this particular case and not to be circulated or attempt to be circulated for any other purposes. That's the only concern.

MR. FURLOTTE: I can only speak for myself My Lord.

DR. FOURNEY: My major concern with this data is that our studies are tied to academic professors at universities whose livelihood and grants are often tied to unpublished information and, of course, they want to have the copyright on the first publication of this data. And the R.C.M.P. respects the right of privilege of copyright on new material where through collaboration, of course, these people have worked very hard with us and it would be unfair to them and to us actually, to have this preliminary data published out from under us so to speak prior to us getting a chance to actually write our own papers.

THE COURT: You will find yourself writing a letter to the scientific community like Doctor - what was his name, the other man?

DR. FOURNEY: Doctor Hartl.

THE COURT: Hartl, disclaiming responsibility for what he published two or three years ago.

DR. FOURNEY: This apparently has happened in U.S. courts with respect to the FBI.

THE COURT: I am wondering really -- I can appreciate the problem about it and the difficulty and this is scientific information. Are you going to cross-examine

at any length on this?

MR. FURLOTTE: No, I have -- I am not going to cross-examine at any --

THE COURT: Then why is it necessary?

MR. FURLOTTE: It is necessary for Doctor Shields to make comparisons. Doctor Shields asked me to obtain this information so he could draw comparisons between this and Caucasian data bases.

MR. WALSH: My Lord I would ask if that is going to be in fact the case I would ask for an order from this particular court prohibiting the publication of this data by Doctor Shields -- I would ask for an order prohibiting the publication of this data by Doctor Shields or by any other scientist associated with the defence in this particular case. I believe the court would have jurisdiction to actually - to make such an order to protect the scientific concerns here. We're not - I'm not asking for anything that would in any way violate any legal rights; I'm just simply asking for an order that would protect --

THE COURT: Well supposing I make an order of this nature and see if you have any difficulty with this Mr. Furlotte. That these sketches are being accepted in evidence solely for the purpose of this trial and the exhibits will not be released by the court for any purpose other than some purpose connected with the trial. If they are required in some subsequent appeal or something by one side or the other they must of course --

MR. FURLOTTE: I have no objections to that. I'm not interested in anything but this trial.

THE COURT: Does this satisfy you Mr. Walsh?

MR. WALSH: Yes, this satisfies the crown.

DR. FOURNEY: Yes, copyright acknowledgement of this work is well within what we would regard adequate for this.

THE COURT: Yes. Well would you put a red star or something, Mr. Pugh, as clerk, on these particular exhibits so that they will be marked - or identify them in some way with some big red mark in the corner or put 'restricted' or something on them.

DR. FOURNEY: We certainly thank the court. I would hate to have Doctor George Carmody upset with me.

THE COURT: Well, I can appreciate your problem from the scientific point of view. Now, we will go ahead and mark these and the special designation will apply to all of these exhibits that we are about to receive. The map of Canada is next - VD --

DR. FOURNEY: I can leave the slide of this. I do not have a -- It was just a photograph of a map.

MR. FURLOTTE: That wouldn't be all that necessary anyway.

THE COURT: Don't bother with that one then.

DR. FOURNEY: And similarly this one here is a blow-up from that map. This map is commercially available from Energy, Mines and Resources.

THE COURT: Well it in effect is a map of Canada showing the distribution of the Athapaskan tribes.

DR. FOURNEY: The Native Indian groups.

THE COURT: The Native Indian groups. The Athapaskans over most of Canada, exclusive of British Columbia, and the two groups in --

DR. FOURNEY: On this same map, this area here is blown up over here, and in actual fact that's what this slide is.

THE COURT: And those are the Athapaskans and the --

DR. FOURNEY: Wakashans. There are actually four groups of Native Indians in British Columbia on the mainland there.

MR. WALSH: Mr. Furlotte is not going to require reproductions of those two?

MR. FURLOTTE: No, I'm not.

DR. FOURNEY: This one here actually is part of a composite. I was hoping -- what I made here is the complete copy of all the data together on one map so I don't have the exact duplicate of this but this is simply done for demonstration of two groups before I showed all of them together, for instance this here. So what I have is that data, okay, on this partiuclar figure. I can make the other figure available.

MR. FURLOTTE: Okay.

DR. FOURNEY: That's the D2S44 data base.

THE COURT: Well all the D2S44 data is included in this one and you have a picture of this.

DR. FOURNEY: Yes, and I have -- The only difference, once again, is the Arizona group is on this, I see from the slide, and I have strictly left out Canadian Caucasian and Native Indian groups. Is this satisfactory?

MR. FURLOTTE: It should be.

THE COURT: D2S44 then - this will be VD-107.

(Clerk marks reproduction of slide VD-107.)

DR. FOURNEY: This is just the two of them together as you can visualize.

THE COURT: Okay. And we will make that VD-108.

(Clerk marks D2S44, allele frequencies, VD-108.)

DR. FOURNEY: This is D1S7 allele frequencies for the two Native Indian Ontario and British Columbia groups.

THE COURT: VD-109.

(Clerk marks D1S7 allele frequencies VD-109.)

THE COURT: This is a new one?

DR. FOURNEY: Yes. This is D4S139, allele frequencies, once again the two native Indian comparisons.

THE COURT: This will be VD-110.

(Clerk marks D4S139, allele Frequencies VD-110.)

DR. FOURNEY: This is D16S85 comparison between the Native Indian groups.

THE COURT: This will be VD-111.

(Clerk marks D16S85 comparison VD-111.)

DR. FOURNEY: D17S79, allele frequencies, comparison with British Columbia and Ontario Native Indian groups.

THE COURT: VD-112.

(Clerk marks D17S79, allege frequencies VD-112.)

DR. FOURNEY: And this is just a representative composite of - I believe I showed this slide - with the British Columbia Native Indians, Ontario Native Indians, as well as the British Columbia Caucasians and the Ontario Caucasian groups.

THE COURT: VD-113.

(Clerk marks D17S79 representative composite VD-113.)

DR. FOURNEY: And those are all the slides that I have shown.

THE COURT: I thought we might have a recess now but are there any questions you want to ask before we --

MR. FURLOTTE: I have no questions on these.

THE COURT: On these at all. Would it be possible Mr. Walsh or Mr. Furlotte to -- Mr. Walsh might do it perhaps, is get the photocopies made of these schematic drawings so that the crown would have a copy and the defence counsel would have a copy of them. You would like those?

MR. FURLOTTE: Do you have additional copies?

DR. FOURNEY: I just brought the one color copy but --

THE COURT: Well, they can make it black and white off these colors.

MR. RYAN: They are going to need to be in color My Lord.

MR. WALSH: My Lord perhaps the easiest thing is when Dr. Fourney goes back if he would indulge us and -- I think Dr. Fourney has access to a color copier and he could mail them down to us by Courier.

THE COURT: Will this give them to Mr. Furlotte in time for Doctor Shields to study or examine them.

MR. FURLOTTE: I will try to get them to him as quick as I can. I am expecting some other information. They are supposed to get some additional information to me, My Lord, and it looks like I won't get that either.

THE COURT: Okay, you can --

MR. WALSH: We will make every effort to get the information that Mr. Furlotte requires to him as quickly as possible so that he can provide it to Dr. Shields.

THE COURT: Well that's fair enough. In the meantime, these exhibits are available and perhaps black and white copies can be made and somebody can take a crayon and color them in.

MR. FURLOTTE: I'll do with black and white for now and I'll talk to Dr. Shields and see if he can work --

MR. WALSH: I'll make enquiries with the R.C.M.P. headquarters. They may have a color copier. If they do we can make some arrangements.

MR. FURLOTTE: We could make arrangments to take these out and get them copied.

THE COURT: Yes, sure. Well, it's just whatever arrangement you people can come to. We'll take a 15 minute break here now.

(RECESS.)

COURT RESUMES - ACCUSED PRESENT IN PRISONER'S DOCK.

CROSS-EXAMINATION OF DR. FOURNEY CONTINUED:

Q. Doctor Fourney we put into exhibit today, again, a rebinning of the R.C.M.P. data base where you stated five individuals had been taken out.

A. Yes, that's correct.

Q. And why were those five taken out again?

A. Because they were duplicates.

Q. And how did you know they were duplicates?

A. We have a program that the FBI has been working on called "Dysmatch" and it's designed to look at large data base rays and compare literally the bin frequencies -- or not, pardon me, the bin frequencies, the actual fragment sizes within a match window throughout the entire data base and it flagged those samples.

Q. So you were able to cross-reference every -- With your computer you were able to cross-reference --

A. Yes. It's a computer program derived by the Quantico FBI group.

Q. Therefore your computer can tell you how many people share this band size for any probe say. Say if that was probe D2S44, an individual, and these were determined band sizes, your computer would tell you how many people in your data base shared those exact band sizes?

A. Yes. You could put in a window and it will look for all those possible matches.

Q. And how many people in your data base share two probes?

A. Any two probes?

Q. Any two probes.

A. I don't think that -- We haven't really done that. I haven't made that kind of compilation.

Q. If you were able to find somebody in your data base, any two individuals who shared three probes, would that be possible?

A. That it would share three probes?

Q. That would share three probes.

A. It's generally been our experience that after two probes it becomes highly unlikely that they are going to share the third probe.

Q. But it's not highly unlikely that two people will share two probes? If it just becomes highly unlikely after then it's not highly unlikely before.

A. Right. I see what you are trying to say. The first probe, of course, you would expect some matches that could be coincidental. After the second probe it greatly decreases. After the third probe it is extremely doubtful and as you go through the probings of course it becomes very, very remote.

Q. Do you have any idea how many people would share two probes?

A. No. I would have to be assigned a number and then I would go through and actually do that calculation.

Q. Are you able to provide that to me?

A. Yes, we could. We could probably provide the -- Given the size fragments we could go through the data base.

Q. My position, Doctor, is that if two people in your data base share two probes and you calculate the frequencies of these two individuals sharing two probes it's likely to be fairly high.

A. It's actually fairly remote.

Q. Two probes is actually fairly remote?

A. Yes, and three is very, very remote for the Caucasian data base for example.

Q. So it would be very remote for two people to share two probes?

A. It's not a high frequency event, no.

Q. And what would you call remote?

A. I guess you would have to tie it to the actual numbers and the probabilities to get a direct impression on a qualitative statement like that.

Q. Well, I think maybe we could take, for example, sample 110 which has supposedly somebody, be it Mr. Legere, and here it is supposed to be Mr. Legere and an unknown subject supposed to share in two probes.

A. Yes.

Q. Right?

A. Yes.

Q. And I believe the frequency is what? 1 in 7400?

MR. WALSH: I believe you're correct.

Q. I believe the frequency for sharing these two probes is one in 7400. My position to you, Doctor Fourney, is that if somebody in your data base shares two probes you can't say the frequency would be 1 in 7400 but rather 1 -- the maximum could be 1 in the number of people in your data base which is 700 or so. Wouldn't that make common sense to you?

A. The probabilities are calculated on a large number.

Q. I know how to calculate it but I'm looking to throw your science out the window and use common sense here.

MR. WALSH: Objection!

MR. FURLOTTE: You tell me as to whether or not this makes common sense, okay.

A. Are you asking me, for instance -- Perhaps I'm just trying to understand your question.

Q. I'm not trying to trick you or anything.

A. No, no, but you are basically saying that we have simply looked at, for instance, you point out the exhibit 110 and we have screened our data base for those two.

Q. I suspect maybe matching -- You said for two people to match in two probes it would be remote and maybe the 1 in 7400 figure is a remote number, but at least that's the only example we have here in this particular case. Now what I am saying is through the Hardy-Weinberg formula and the product rule you come up with fantastic numbers that sharing two probes, as in this case, would be 1 in 7400, but your emperical data would tell you that if you went out amongst 700 people and you found two people to share these two

probes the probabilities is 1 in 700, not 1 in 7400. Your emperical data tells you that. Your experience would tell you that without having to rely on some double formulas which may or may not be appropriate.

A. Is this a question or a statement?

Q. This is a question. Don't you think it would be more reliable to rely on the actual data that you went out and collected than on some foggy formula?

A. What we would like to do is obviously take a population, a fraction of that and analyze it, and we would want to get the correct population with respect to reliability. For instance our Caucasian population we assume that it is a very representative sample across Canada and from that we can extrapolate and make conclusions based on the probabilities.

Q. But the Hardy-Weinberg formula and the product rule is used for - what I understand, and I may be wrong - but it is my understanding that you can use that mathematical formula on pure matters of chance. Is

A. that correct?

A. It's generally applied to data and you make your probabilities based on -- Your genotype frequencies for instance, is a derivation that you would get with Hardy-Weinberg, and if they are independently related - or that's an oxymoron - if they're independent you can actually multiply them together which is what we do.

Q. I think, if I understand correctly, a lot of the components to your using this DNA analysis and running up the high numbers is that you cannot use the product rule in circumstances like this because they are not matters of pure chance. Is that a correct assumption on my part?

A. You are assuming that if it's not a matter of chance then that they are somehow linked. I assume that that's what you are getting at. And I think Doctor Carmody, in the best of his analysis, then his calculations have certainly told us that we're legitimate in using the product rule.

Q. If you searched your data base and computer - how many people in your data base right now?

A. The Caucasian data base, without referring to my notes, it's somewhere in the area of around 900 individuals.

Q. 900 individuals. So if you searched that and you found two people, as I explained, who would match on two probes and if you use the product rule to find out the probability of that, you come out with in this case 1 in 7400, and you in fact went out amongst 900 people and found two people that matched, then you could say that the chances are a lot less than 1 in 7400 but are in fact, at least in our emperical data, 1 in 900. And I've already went through that. Now, what I would ask you, Doctor, is if you went through your data base and computer and you found out there was maybe 6 or 8 people out there who shared two bands, whether they be the same two bands or not, they would be still sharing two different bands with these high probability numbers which would, again, support the proposition that you cannot use the product rule in circumstances like this.

A. There is nothing in my understanding of the way our data base was collected, processed, the statistical compilations that were done, to suggest that we cannot use the product rule, and in fact when you

multiply across loci, as you conduct each test successively, you begin to build up an understanding that by the third probe, for instance, it's becoming very remote and as you go through to the 4th and 5th probe it becomes highly unlikely that someone will match purely by chance across all these loci. That's the prime reason why we do a consecutive series of tests.

Q. But Doctor as a scientist - and you are going on that model and that theory of the product rule - but if you are continually coming up - keep coming up with examples and circumstances which tends to prove your theory wrong, do you normally reject these circumstances and this emperical data coming in and close your eyes to it or should it cause you concern that you want to really study the issue first?

A. You never prove a theory; you can only disprove a theory.

Q. Right.

A. In actual fact we could have the exact reversal. We could have a situation where we never see this pattern within our data base. It would be considered extremely rare. And then you would have a situation where you are going to put undue weight on the fact that you have never seen that. So you could have the exact opposite situation. In actual fact by doing a sampling like we have done it presents a more conservative estimate in the general population of the random man, for instance, having a match with respect to those band patterns. I believe that's --

Q. How difficult, Doctor Fourney, would it be for you to provide me with the information as to how many people in your data base share two probes?

A. I would have to work on that calculation.

Q. You just can't ask the computer to give it to you?

A. No. It takes some work to do that. Just to generate these numbers with the size of the data base we have it takes quite a bit of work.

Q. Do you think you might be interested in doing it?

A. Would I be interested in doing that?

Q. Yes.

THE COURT: If you are you will have to do it over the lunch hour.

A. Well, I certainly couldn't do it here.

Q. No, I wouldn't expect you would be able to do it here but once you got back to your lab do you think that might be an interesting feature to want to check out?

A. I would prefer, in the interest of the court, if you wanted to save time, for instance, that you could give me -- it would be faster to actually do it with respect to a couple of -- if you had an interest in any particular bands we could certainly do that.

Q. That would be a lot less chance of catching something too, would it not? If I just ask for two particular bands there might not be anybody out there share those two particular bands, but there might be still many people in the data base who would share two other particualr bands.

A. Well we already know that the frequencies of the actual bands are different within each probe. I mean

there are some, as the histograms indicated, there are areas where there is a lot greater counts, if you want to call it counts, in that particular bin for instance. So, yes, the frequencies are slightly different for the different bins within each probe.

Q. Okay. Let's take for instance then if we pick these two particular probes that were shared here and the bins - the fragment sizes that were shared.

A. Which two?

Q. Well, we'll say D4 and the D10 --

A. May I refer to my notes?

Q. Well, we have already calculated it to be 1 in 7400. It has already been calculated. We don't have to do it over. Like I'm just saying, for instance, if you happened to pick those two probes and those two band sizes - fragment sizes, and you went to your data base and you found two people in there who shared those, the fact that it's contrary to your theory and the product rule that it, you know, greatly exceeds or underestimates it, would you consider that to be an anomaly and ignore it or would it deserve looking into?

A. No, I would say that I have quite confident reliability in our data base size to give me a proper answer because you certainly don't want to get into a situation that we look at too few individuals for instance to get that kind of calculation.

Q. Do you know whether or not, Doctor, that some scientists ignore anomalies on purpose so that they can continue to use their model?

MR. WALSH: The objection I had yesterday, My Lord, I would repeat today, that I would like -- From the Crown's point of view I think Mr. Furlotte owes the witness at least to refer to what scientist said that.

MR. FURLOTTE: I never said a scientist said that. I just asked him if he thought it was possible --

MR. WALSH: He said some scientists --

MR. FURLOTTE: -- that some scientists would do this - or do this.

MR. WALSH: I mean I can't -- These kind of mind games are difficult --

THE COURT: Yes, well I don't think you are being very precise in your question Mr. Furlotte. Can't you put it in some other way or put up a --

MR. FURLOTTE: Well, My Lord, I'm just going back from my own studies and I took a philosophy of science course and --

THE COURT: Well, you're not a witness, understand.

MR. FURLOTTE: I'm not a witness but I am proposing --

THE COURT: And also a little knowledge is a dangerous thing.

MR. FURLOTTE: Yes. Sometimes too much is dangerous also. Doctor Fourney since I put this proposition to you or this - maybe the doubt that some people have, to you in this form, does it concern you at all that something like this would deserve investigation in your data bank?

A. We certainly have the capability of screening our data bank to see what the chances of random matches are but we already know from experience with respect to the number of probes that we look at in a typical

test that as you increase your number of probings you are certainly going to have a more remote chance to someone accidentally matching those probings. So it does not concern me in that respect. I think the tests that we have certainly are valid.

Q. Doctor, if the chances of something occurring was 1 in a million out of a certain number of events, it was 1 in a million, but maybe daily when there's only a thousand events occurring of the possible million, and out of that thousand events that are occurring one is coming up, you know, almost every day, would that cause you concern?

A. It would be like suggesting that you had a coin and you are going to flip it ten times. You would expect to get heads and tails; five times for heads, five times for tails, but you may in fact get seven heads and three tails.

Q. Right. But if every day you ended up getting nine heads and one tail --

A. I would suggest you would have a loaded coin.

Q. And there would be something wrong with using that model?

A. There is nothing wrong with the model; there is something wrong with that coin.

Q. But we're not talking about coins when we're dealing with DNA analysis.

A. That's correct.

Q. So if you continued defying the odds then there must be something wrong with the DNA that you're analyzing.

A. Well, we don't know if that is in fact the case with respect to what you have just asked me.

THE COURT: We seem to actually be getting into a field of argument here, Mr. Furlotte, really. There is no suggestion, is there, that any two people in the data base have the matching - or have the same matches?

MR. FURLOTTE: I believe he said there was.

A. There is certainly across two probes you can have matches and as you get to the more probings that you have you get the chance of this occurring less and less. Our bins are so large that we are over-estimating. We are conservative. We are trying to give the benefit of the doubt at all times to be very, very conservative.

MR. FURLOTTE: Doctor, I believe you said on direct examination that certain fabrics have an effect similar to ethidium bromide and creates band shifting.

A. Yes. There has been several occasions where I have noticed band shifting that seems to be related to the--

Q. And what type of material--

A. The particular material that I noticed was florescent shoe laces.

Q. Florescent shoe laces. And I suppose that's one of the concerns why the ultraviolet lights are something that may have an effect on stains?

A. No, that has nothing to do with it actually. Florescent colors I should specify.

Q. And that would be due probably because of I suppose the chemical that's in that particular dye?

A. Presumably it could be --

Q. As ethidium bromide is a dye and it's the chemicals we're concerned with.

A. It could be one of the aspects, yes.

Q. So if I put the hypothetical to you that, you know, that heavy smoke or water or chemicals from fire-fighting equipment, different stuff in the soil, and heat, could possibly have the same effect as these dyes in certain fabrics.

A. There could be an effect, yes. But I would like to stress the point that if you extract the DNA and it's human specific and it's high molecular weight DNA then there's probably no effect.

Q. Well you said that certain fabrics -- you said that certain fabrics could have the same effect as ethidium bromide which would make it very difficult to interpret your autorads.

A. That could be so. What I am also saying is that the DNA, once you have actually extracted it and looked at it and it looks intact and it's human specific, then you know that you have a very likely chance of getting extremely good results. And that most of the problems associated with in fact environmental contamination have nothing to do with the band shifting aspect; it's primarily to do with the actual extraction and recoverability of the DNA itself. So as most of the cases that I have seen, certainly this report, reports that are referred to in the back of this manuscript, indicate that you will either get a positive result or you will get no result as a result of the environmental insults. So in other words if you get DNA that's intact, if it in fact is human specific, then you have an extremely good chance of getting an accurate and reliable result.

Q. But Doctor in your experiments with ethidium bromide you got DNA intact and the experiment was to show how much band shifting it would create.

A. That's one of the reasons why we don't use ethidium bromide.

Q. Right. And you said on direct examination that certain fabrics has the same effects as ethidium bromide. So I would assume that certain fabrics or certain dyes or certain chemicals or whatever could create band shifting to the same degree that the band shifting was created in your system when you done your testing on ethidium bromide. Is that reasonable to assume that?

A. There are probably many substances out there that we haven't looked at that could have an effect.

Q. Yes. Now, duplicates that you took out of your data bank when you had took these five test results out, they were removed because they were extremely similar or duplicates as you say?

A. They matched across five probes.

Q. They matched across five probes. And there was five such of those matches.

A. There are five duplicates, yes.

Q. And you are assuming that they must have been identical twins?

A. No.

Q. What are you assuming?

A. I'm assuming that they're duplicates.

Q. You're assuming that same person come in twice?

A. That has happened, yes.

Q. I thought all precautions were taken against something like that happening.

A. By the Red Cross?

Q. Because I understood the samples to be taken on the same date when the blood samples were given is because you don't give blood samples twice in the same day to make sure that --

A. Some of these samples have come in over different periods of time.

Q. From different areas.

A. The Ontario samples have all been direct to us from the Ottawa Branch of the Canadian Red Cross.

Q. But it was requested that they -- What would the odds be of that happening?

A. Of what specifically happening?

Q. By chance collecting samples, you know, from five people twice out of the small data base that you had.

A. When we actually talked to the Red Cross about this they suggested there are several possibilities for this, one of which were identifical twins and they assured us that there had been identical twins donating blood in the past. The other possibility is that when these samples are drawn from the bag they might have given us two tubes instead of one tube. Now we specifically ask them to only give us one tube. The other situation is we could have loaded those samples twice.

Q. Or I suppose there's another situation where maybe, just maybe, somebody out there can share five probes.

A. I would find that highly unlikely.

Q. Because of your use of the product rule?

A. No, because of my experience and the fact that we have done extensive investigations.

Q. Now, Doctor, when you reviewed the material and the test results with Doctor Bowen was there any discussion with him as to what you would declare a match and what you wouldn't declare a match?

A. Prior to actually reviewing them myself?

Q. Yes.

A. No. In fact I examined the autorads by myself initially just to review them and then I asked for the actual - the exhibits. I went through them, made an evaluation, then I conferred with Doctor Bowen. If I had questions concerning the nature of a particular exhibit, for instance, I would ask him that but my matches were my own conclusions based on my own experience.

Q. And before you conferred with Doctor Bowen did you write down or make notes what your conclusions were?

A. I believe I quickly looked at the autorads and then I went through them in a more detailed manner with his notes.

Q. With his notes.

A. And I have my own notes as well.

Q. And did you in making your own notes as well did you put down what your conclusions were, what you called a match, and why you called it a match before you conferred again with Doctor Bowen?

A. I believe I -- If I did not write them down I certainly had a firm condition in my own mind what I was going to call a match.

Q. Do you know whether you wrote them down or not?

A. I have made some notes on those cases.

Q. Do you have your notes here?

A. I have some of my notes here.

Q. Would you mind checking and seeing if you made any notes as to what your interpretation was?

A. Is there a specific autorad or group or -- There's a number of them.

Q. Well, I suppose each specific one and then your final interpretation.

A. Oh, my final interpretation is actually that I am in agreement with Doctor Bowen's conclusions.

Q. Yes, I have heard that on direct examination. But did you make any notes as to what your final interpretation was before you conferred with Doctor Bowen? See if you made any notes to that.

A. Basically I went through every single autorad and my conclusions were such that I agreed with all the matches, and the sizings were done properly. And I don't have a summary statement of my entire set of analyses here but each autorad was a match with respect to the decisions that Doctor Bowen had made independent of myself, and I would agree with the entire group of autorads in that case. But the matches that were presented I certainly am in agreement with.

Q. Do you recall in your notes -- I see D16S85 is inconclusive. Distinguishes inclusive. Why did you find D16S85 inconclusive?

A. I think the -- I have here 'very light bands are diffused; potential screen problem'.

Q. What do you mean by potential screen problem?

A. If the autorad itself -- In the making of an autorad you are placing the x-ray film directly on top of the membrane. There's, of course, a piece of plastic in between to protect the membrane. And if the screen is not held tightly in place then the radioactivity that's released from the probe tends to diffuse off the phosphotungstate screen and what it makes is instead of a tight band or a tighter pattern it could make a more diffuse pattern. And in this particular case I don't know if that was the reason but certainly that was my conclusions that they're quite light and it is difficult to define the bands so in the best interest of this particular case my decision would be that the blot was inconclusive.

Q. And what date was that?

A. December 3rd, 1990 I believe. That's the date that I have in my notes here. There is one other aspect here too that I see. There is an indication in lane two, for instance, of a stripping problem from the previous blot.

Q. On lane two that's Mr. Murphy?

A. I'd have to recheck.

Q. Doctor Fourney do you know why the testing in this case was put on hold for almost a year from December of 1989 to November of 1990?

A. I believe there is probably a number of reasons involved, one of which was the fact that our program was growing and we had more people coming in and that our lab was going to be extensively renovated.

Q. And at the time these tests were taken you were still in the process of building your system? Getting new equipment in all the time?

A. I actually think that there was no testing done on this particular case during the actual period of renovation problems.

Q. No, but before the renovation problems I believe.

A. As part of the Research and Development Section I routinely get new equipment in to test but that's part of the evaluation long before it gets entered into operational work.

Q. And I believe you and Doctor Waye trained Doctor Bowen to make these tests in early 1989.

A. Doctor Bowen was a special case with respect to molecular genetics. He had already had previous background. He had been conducting research on his own on a special sabbatical leave from the R.C.M.P. case work in Edmonton to look at D.N.A. typing with respect to various protocols and when he came in it was obvious that his background was sufficient to start him into a fairly advanced training program. So I would like to consider Doctor Bowen's period with us at the beginning as more of an apprentice to become aware of the variations that we may have at our own lab that Doctor John Waye and myself were using and, of course, a scientist entering another lab has to be familiar with the area and where things are and the samples and the various pieces of equipment that we're using.

Q. I believe, as I understand it from your direct testimony when you were at the voir dire here a couple of weeks ago on the admissibility of substances, you described - and I put it to you and you can tell me if this is still correct or not - said:

> "Actually, Doctor Waye and myself were both involved with training Doctor Bowen in the DNA typing procedures as they existed then and we worked quite closely with him. I believe Doctor Bowen, his specialty being in hair analysis, was quite interested in pursuing some of the issues we had with respect to paramount conditions in hair and we did several little projects at the time to see what we could get from DNA."

A. That's correct, yes.

Q. "The lab was constantly in a flux situation where we were working with old facilities but getting all kinds of new equipment in."

A. That's right.

Q. "We were going to undergo extensive renovations in the early spring of 1990 and we were existing in somewhat cramped conditions at the beginning and I was just trying to think exactly when we got into our new lab which I believe was in June of 1990."

THE COURT: What is this you are reading now?

MR. FURLOTTE: This is from the transcript of the preliminary hearing on page 38 of volume III --

THE COURT: Of?

MR. FURLOTTE: Not preliminary hearing - I'm sorry, the voir dire on the admissibility of bodily substances.

THE COURT: Oh yes, well that's all evidence now.

MR. FURLOTTE: So I would say, Doctor, the situation at your lab wasn't really ideal for conducting very intense and precise DNA testing?

A. Actually, what we were more or less getting ready for was not so much the conditions at the time but the predicted conditions that we were going to require.

So the fact that Doctor Bowen joined our team this is simply an additional one member. What we are actually going to get in the beginning of the next year would be a great number of individuals and considering the space that we had at that time then there would be a concern, I would think, but certainly when Doctor Bowen conducted his case work I think he was doing it in conditions that wouldn't jeopardize any of his conclusions or the testing.

Q. Well it's easy for DNA samples for cross contamination in the best of circumstances. I understand when you are testing - or at least isn't it possible that just flipping the cap off of a container of DNA too quick or something the aerosol spray could contaminate other sections of - or other samples of DNA, is that right?

A. Not at the limits of sensitivity that we have.

Q. Not at the limits of sensitivity you have?

A. No.

Q. Also, when you were explaining for Mr. Walsh on direct examination on that hearing on page 26 you stated:

> "The actual fixation process of this tissue" --

What were you talking about here? Anyway, it says:

> "The actual fixation process of this tissue can cause problems with DNA typing in the fact that it could affect the DNA structure itself rendering it either completely unusable or will render it sufficiently degraded or different that it would not give you a particularly good control standard on which to judge the normal tissue you are comparing it with."

You go on on page 27 in a question Mr. Walsh asked you:

"Apart from degradation, what, if any, concerns would you have with respect to a tissue of that sort in the actual typing process itself? What, if anything, could happen?"

Your answer was:

"Well, it has been known for instance, in my own experience with working with breast cancer material as well as papers I have read and people I have discussed this with, the actual process of fixation I believe in this particular case was a formaldehyde or formalin-fixed process. It can actually cause DNA to be -- the substance that is used to fix can cause a change in the DNA so that when you finally extract the DNA, if it is not degraded, will have an altered mobility such that it will be shifted in a -- upwards in the gel for instance or it will have a variation in the pattern that you would end up with as composed to normal tissues that would not be treated in this manner."

And the question was:

"What could that actually do in a typing test? What could that end up doing?"

Your answer:

"It could -- you could end up actually not being able to match your samples."

And that, I assume, you are talking about the effect that cancer may have on the migration of DNA fragment lengths?

A. No. That specifically relates to the formalin-fixed process or the formaldehyde fixation of the tissue in that the actual fixation process that this material goes through can have an effect on the material - on the DNA.

Q. On the DNA?

A. Yes.

Q. And how would this effect be recognized?

A. Generally, it's just in the fact you would never get DNA. It's a degraded pattern. Poor extraction in other words.

Q. Poor extraction. So it is the same aspect in effect as degraded DNA, is it not?

A. The formalin/formaldehyde process could, like I said, end up with a DNA -- You just don't receive retrieved DNA or it could be badly degraded. Very low molecular weight DNA.

Q. Now, when you were discussing about the wart on page 28 of the transcript, you mentioned the wart, you say:

> "I advised at the time there was an R.C.M.P. inquiry I believe and there was a fax or a telephone conversation. They were wondering if in fact this tissue would be adequate as a control standard so that we can make all our further evaluations. I suggested at that time that several things could happen with that particular tissue. One, we may not get any DNA whatsoever. It could be very badly degraded. Two, the DNA that we actually extracted from the material could be altered in such a way that we couldn't make a pattern comparison; and three, it could be degraded and give fairly mixed results. It would be difficult to actually get positive results."

And I assume that that is with degraded materials and you would get mixed results.

A. The condition of that tissue, you know, the fixation process, the fact that it -- I can't recall if it was paraffin-embedded or not but the entire summary of what I was given would make me believe that we would have trouble using that particular material as a control substance.

Q. Now when you say it could be degraded and give fairly mixed results what do you mean by that?

A. You possibly could have a situation where you have such low molecular weight DNA that it ends up with a

smear at the bottom. You may have a degradation pattern extending from one or two bands all the way down. There's a number of degrees of degradation that this could go through such that it could be - as the sample becomes degraded changes occur with respect to its mobility. You get more bands essentially. The DNA is being --

Q. You get more bands but as it degraded it affects its - you say its mobility and the rate at which it migrates through the gel such as maybe the DNA being not as smooth or a little more rigid. It's not so wormy as to goes through the gel.

A. In general what happens, if I could explain this possibly so that you could understand, for instance if you had a particular band at that size, say 4000 base pairs as a hypothetical example, as it goes through degradation you would not expect to see higher bands; you would only expect to see lower bands because it has to start off with something that size in that particular probing. So you would see an extension of multiple bands from the 4000 base pair size for a large fragment all the way down in much the way that if you had a piece of string, for instance, that was three feet long and you cut it a couple of times with a pair of scissors and then you came back and you cut it a few more times. If you put all the patterns together it would extend from the initial size to the smaller sizes.

Q. And if you added up all these sizes you would end up with what you had to begin with.

A. We would hope that would be the case.

Q. Again, Doctor Fourney, to get back to why the reasons in this probe you found it inconclusive because there were very light bands, because there would be very light bands in the homing device to where the probe identified it, if there was degradation it would be very difficult to know, would it?

A. The fact that we actually saw bands indicates that what the DNA on that membrane that was hybridizing to the probe was sufficiently intact to actually render a pattern, consequently, you would assume that DNA that was on the membrane - there just wasn't enough of it. It wasn't a question of whether it was degraded or not. And I believe that particular membrane had been stripped and reprobed a number of times and although we endeavored to maintain a high degree of DNA on this membrane the actual stripping process as it's successively repeated you will lose a little bit of DNA each time.

Q. I believe where we saw in some of the autorads where there was good intense bands in some of the lanes we could see degradation - signs of degradation, and just if you are going to -- But it appeared that you needed intense bands to be able to identify whether or not degradation occurred but if you only got very light bands to begin with you are not going to see the degradation because the degradation is lighter than the bands themselves. Is that correct?

A. There could be a very light background of degradation there but you would still be able to see the initial pattern and, once again, degradation extends from the intact band downward so that even with degradation,

depending on the limits of it, if the initial band that was cut up is still there you know where that fragment is.

MR. FURLOTTE: I believe, My Lord, it might be a proper time to have our noon break and I'll --

THE COURT: Are we getting fairly close to the end?

MR. FURLOTTE: We're coming to the end of this witness and this would be a good time to break.

(NOON RECESS - 12:25 - 1:45 P.M.)

(RESUMED AT 1:45 p.m., MAY 14, 1991.)

(ACCUSED IN DOCK.)

THE COURT: Something I just wanted to mention briefly, Mr. Pugh, would you prepare a little notice tonight or sometime later to put on the outside of that door back there saying that it isn't necessary for anyone to bow when they come into the court room unless they're a barrister. I feel a little embarrassed by the acknowledgment to the Court. It's not anyone paying penitence to me because I don't demand it, but I know it's to the Court but it does seem to be overdone a little. I noticed even some members of the public sort of walking in and I see perhaps some of the R.C.M.P. or something doing this at the back and they turn around and bow and scrape back there and it's sort of reached the stage of grovelling, I think, and I don't like that, so if you'd put a little note up there and it will spread anyway, the word. I still want counsel to grovel, of course. The instruction I give is just binding on myself, it's not binding on any other judges who sit here in future or next week or whenever. They can make their own rules but I think sometimes it gets overdone a little. Now, you have some more questions, Mr. Furlotte, to ask?

CROSS-EXAMINATION OF DR. FOURNEY CONTINUES:

Q. Dr. Fourney, I believe you stated there's been no tests initiated yet on assessing a data base for, say, small different areas in the Caucasians throughout Canada, say like a little area in New

Brunswick and a little area in B.C.? That has not been initiated, has it?

A. No, the data bases that we have presently are the ones that you've been reviewing.

Q. At least not on the same analogy as you're doing for the Canadian Indians? There's no similar being conducted at this time?

A. At the present time the data bases we have for Caucasians are exactly what was presented to this Court.

Q. Is there any studies being done on French Canadians and English Canadians?

A. I believe some of those studies are being conducted by the Police Laboratoire de Scientifique in Montreal by Mr. Leo Lavergne.

Q. Between French and English?

A. Yes, he's basically looking at a population base in the Quebec area and he's got a data base now from Montreal and I believe he's looking at other regions within Quebec.

Q. Right, so he's going to establish a data base just for Montreal?

A. He's going to establish a data base that would be used for the Province of Quebec.

THE COURT: Is that an R.C.M.P. laboratory?

A. No, it's a separate forensic laboratory that we often collaborate with.

THE COURT: A private one or -

A. It's a provincial government laboratory.

Q. Have you been able to receive any information from that laboratory yet as to, say, any statistical differences between French and English?

A. We've reviewed a bit of his data, the initial data bases that he's trying to establish, and I believe Dr. Carmody has been contacted for future analysis of the studies and there may have been some preliminary results but I think it's at a fairly early stage at this time.

Q. Do you have any numbers, any figures on the data so far?

A. He's related some of his data to me in confidence primarily because he wants to establish a data base using similar procedures that we currently have at the R.C.M.P. mainly to standardize so that we can share data in the future. At this time his laboratory is not open for case work, as far as I know, they certainly haven't gone to court, and if any of the case work that he's doing now would probably be very initial stages and I don't think he's at this time going to release any finalized data base product. He's still building it.

Q. Is he establishing a data base for French Canadians and English Canadians in the Montreal area?

A. No, I think the main rationale behind Mr. Lavergne's study would be the fact that there is one region in Quebec that he's particularly interested in north of Quebec City as a sort of a basis to draw a conclusion whether or not there's going to be any differences, say, between this region and the already established data base in Montreal.

Q. General data base?

A. That's right.

Q. So at least there are some laboratories out there that thinks it's feasible to conduct that study?

A. Well, certain most laboratories, including the one in Toronto, for instance, are encouraged to develop their own data base and which to use, and the idea behind the entire network in North America is to share our data, and hopefully we'll be sufficiently standardized across the different laboratories so that we can do that, so it's anticipated that we would have free access to Mr. Lavergne's data base once it's finalized, as he would have free access to ours.

Q. Do the preliminary findings show that there might be a difference between French and English Canadians?

A. I think that as it stands right now Mr. Lavergne was developing new techniques in which to transfer his DNA and part of his findings at the beginning seem to indicate that he was going to repeat part of his data base before he would make any justifiable conclusions.

Q. Now maybe I'll ask the question again, that didn't seem to answer my question. Does his preliminary findings show that there may be a difference between French and English Canadians?

A. I'm trying to recall whether George Carmody might have looked at any of that data. He's been contacted and I think George found that with comparison in two probes, for instance, that Mr. Lavergne's data was very similar to ours in one region of the histogram, for instance, but there were a few bins that differed from the R.C.M.P. Caucasian data base and the differences seem to be possibly attributed to a technical problem that Mr. Lavergne had within his laboratory such that Mr.

Lavergne is now repeating that data base and hopefully once it's repeated we'll be able to draw just and valid conclusions. At this stage, as I would suggest, that any data that we wished to compare with Mr. Lavergne would at best be very preliminary.

Q. But it's possible we could end up with a situation like the Canadian Indians?

A. Well, in reviewing the data from other labs, certainly in the Caucasian populations, we know that there are bin frequency differences but overall, I think forensically they'll have no significance.

MR. FURLOTTE: I have no further questions.

THE COURT: Thank you very much, Mr. Furlotte. Now, Mr. Walsh, are you ready to re-examine?

REDIRECT EXAMINATION BY MR. WALSH:

A. Dr. Fourney, with respect to the case specific evidence here in The Queen versus Allan Joseph Legere, and with respect to the blot 89-OL-1191-6 what if any band shifting did you observe?

A. The blot that I reviewed, or at least the series of blots, all the conclusions that Dr. Bowen made with regard to a match there was certainly no evidence of band shifting, and I agreed completely with the results and the conclusions that Dr. Bowen had. I think they were both just, valid and reliable.

Q. Doctor, what is the probability in your opinion of band shifting going undetected across loci in the R.C.M.P. RFLP system?

A. It's highly improbable.

Q. Doctor, what if any validity is there to the

suggestion that if you run samples through the R.C.M.P. system and obtain an inclusion that by running the same samples through another lab with a smaller match window there is a possibility of an exclusion because of the smaller window? What validity is there to such a suggestion?

A. I would think that any lab conducting the same study that we would have would come up with the same results. If their window was smaller visually they would certainly be a match, they may suggest that it could be inconclusive.

Q. What if any effect does the size of the match window of the R.C.M.P. have on your opinion as to the possibility of false positives across several loci?

A. Once you conducted this study over and over again the chances of false positive across multiple loci are so remote that it's not even worth considering.

Q. With respect to the case specific evidence Mr. Furlotte asked you a number of questions with respect. One in particular related to a band, I believe on the third blot, that was outside the match window, is that correct? Do you remember that?

A. I believe you're referring a D16S85 probing?

Q. Yes, that's in fact correct, on the third blot. There was one reference to one band being outside the match window, do you remember that?

A. Yes.

Q. Can you tell us, please, whether or not that is a match? Are we referring to outside the match window within the gel or outside the match window

from a gel to gel comparison?

A. That was certainly a gel to gel comparison, and the 5.2% window that we use would indicate that that 5.5 was outside our match window, and those results were done with respect - from a gel to gel comparison as opposed to inside a gel comparison. There are some slight differences within a gel comparison.

Q. Could you tell us, please, what your expectations would be with respect to the percentage of differentiation within the match window between the comparisons made within a gel and from gel to gel?

A. You would expect to see slightly more deviation, certainly, from gel to gel comparison than within a gel comparison.

Q. And could you tell us - you looked at the sizings with respect to the matches declared on the blot 89-OL-1191-6 referred to in the chart VD-88, this particular chart here?

A. Yes.

Q. You have looked at those sizings and you've looked at the matches?

A. Yes.

Q. And can you tell us, please, whether or not any of the sizings, the percentage within the match window, whether it was close to the match window or whether it was so-called a tight match?

A. May I refer to my notes?

MR. WALSH: With His Lordship's permission.

THE COURT: Yes. That's VD-88 you're referring to?

MR. WALSH: That's correct, My Lord.

A. Is it possible to have the sizing from Dr. Bowen's analyses?

THE COURT: 66.

MR. WALSH: All right, which probe would you like first, Doctor?

A. I'll go in the order in which they were done. I believe it was D2S44.

Q. O.K., I'll refer you to VD-67.

A. The Exhibit 56A and 69A is, I believe - I don't have a list of the actual exhibit.

Q. Just refer to the number is fine, you don't have to try to identify it.

A. O.K., on the board there the - and it's difficult for me to see from this angle. D2S44 there's inconclusive results down to 135?

Q. According to the chart that's correct.

A. So essentially you're not matching anything in this -

Q. Down -

A. Oh, I'm sorry, this is D2S44.

Q. That's correct.

A. So -

Q. We're talking about the match made - according to the chart the match made at D2S44 between 56A and 69A in item 135.

A. O.K., that's - I don't see 135 marked on here.

Q. Second page, perhaps.

A. O.K. Oh, O.K., the match between these two is within 1.4% and 0.7%, so it's well within our match window, they're very, very close.

Q. I see, and again, Doctor, would you look at D1 - perhaps I'll have to give you the sizing sheet.

MR. FURLOTTE: My Lord, this is all stuff that was brought

up on direct examination and Mr. Walsh asking him to compare his analysis with Dr. Bowen's, and we went through all this with Dr. Bowen and this is not something new that I've brought up on cross-examination.

THE COURT: You brought up the matter of the 5.5 deviation, I think, and -

MR. FURLOTTE: Yes, but what's that got -

THE COURT: Well, he's trying to eliminate that, I guess. Can you come to this in a shorter way, Mr. Walsh?

MR. WALSH: Well, the other thing, My Lord, is that he also - if that was the only thing, but then he also - Mr. Furlotte bandied around the high of 4% or something to that effect. He indicated in cross-examination that some of them were close to the match window, and what I'm attempting to clarify on redirect because it was certainly not clarified in the cross-examination is whether or not these - what the percentage of deviation was with respect to a lane to lane comparison within one gel, what the percentage of differentiation would be from gel to gel, and how -

THE COURT: I'll permit that, but I would ask you to do it as concisely as you can.

MR. WALSH: As expeditiously as possible, yes.

A. Just reviewing this it's easy to see now that this - I was missing the second page on the first one. The match here is extremely good. It's well within, I think the largest percentage off is 1.8.

Q. Doctor, without actually going into each particular sizing, you've reviewed the sizings in giving your opinion?

A. That's correct.

Q. Are you aware whether or not - can you remember whether or not the sizings in relation to the comparisons within the gels in the first blotting from lane to lane, whether they were - what was your opinion with respect to the tightness of the sizings?

A. They're extremely tight, close-fitting matches.

Q. And with respect to the comparison from the blot 89-OL-1191-13, I believe it was, the second blot containing the two known samples - 13, that's correct.

A. Yes.

Q. Do you remember, Doctor, how tight the sizings were or the comparison between that blot and the first blot?

A. Comparisons between the two blots approached the top end of our match window.

Q. And is that unexpected or an expected -

A. That's a typical expected result that one would predict when you're matching between blots. You would always get a very tight match well within our sizing window, in this particular case it was evident within a blot comparison.

Q. And, Doctor, again we have - Mr. Furlotte has raised it and we've discussed it with respect to one band on the third blot in relation to its comparison to the first blot that was outside its match window, is that correct?

A. Yes, it was 5.5.

Q. What if any effect does that band being outside the match window on the third blot have on your opinion

with respect to the matches declared on the first blot? What if any effect does it have on the validity?

A. Very little effect on this first blot.

Q. Does it in fact detract from your opinion?

A. None whatsoever.

Q. What if any effect in your opinion does the existence of one band being outside the match window on the third blot when compared to the first blot have on the validity - in your opinion, the validity of the R.C.M.P. RFLP system to produce reproduceable results?

A. I have very high respect for the reproduceability of our system and the fact that there is one probing on one blot between gel comparisons does little to detract from my opinion that we have a very reliable and valid result, and in fact, this particular blot, 89-OL-1191-6, all the probes very close and a match would be very easily visualized and the sizings certainly back that up.

Q. Finally, Doctor, Mr. Furlotte has raised the Canadian Native Indian data base. Is that completed at this time, Doctor?

A. No, absolutely not.

Q. And the size of the samples, certain of your samples, are they in your opinion adequate samples - some of the samples, are they considered in your opinion to be adequate at this time?

A. No, in fact, the Vancouver data base, we would certainly like to see more samples added to it. There are -

MR. FURLOTTE: My Lord, I don't believe he was declared an

expert as a population geneticist.

THE COURT: Well, gosh, Mr. Furlotte, you can't have your cake and eat it, too. You've asked these questions about this and I think the answers will be permitted. It falls within the next - it's difficult to draw the parameters of these various expertise.

MR. WALSH: I'm trying to stay within what Mr. Furlotte has touched on in cross-examination.

THE COURT: Yes, well, that's fair enough so far.

A. We would certainly want to see more samples added to the Vancouver data base. The fact that the samples we have, I think the total number is somewhere around 125, comprise two different groups of Native Indians, the Wakashan and the Athapaskan, we would like to increase our sample size on both those groups to make a valid comparison within the Native Indians in British Columbia and with respect to other Native Indians throughout Canada.

Q. And, Doctor, can you tell me, please, whether or not in your opinion the VNTR frequencies that you've seen with respect to the Canadian native samples that you've actually looked at at this point in time, whether or not that they reveal polymorphisms or whether they're polymorphic or non-polymorphic?

A. They're extremely polymorphic as any of the populations that have been studied, to my knowledge. Certainly anything that's come into the R.C.M.P. that we've looked at is very polymorphic. You do not see a single histogram band for instance, you will see a multiple pattern. These VNTR loci are evolving and they're highly polymorphic.

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

THE COURT: Thank you very much, Doctor. That's all for you. You're excused from this phase of the trial unless counsel want to keep you here. Now, you were -

MR. WALSH: Yes, I have Dr. Waye available, My Lord, for further cross-examination by Mr. Furlotte.

DR. JOHN WAYE resumes stand:

CROSS-EXAMINATION BY MR. FURLOTTE CONTINUES:

THE COURT: You're still under oath, Dr. Waye, so we needn't re-swear you and we'll turn Mr. Furlotte loose on you again.

MR. FURLOTTE: Dr. Waye, I may be asking you some questions over again because of the length of time that you've been on the stand for cross-examination. I can't remember all the evidence you gave on direct examination nor can I now remember all the questions I asked on cross-examination, so if I ask the same questions again, which I'll try not to, please be a little tolerant.

THE COURT: No, don't be tolerant, just say, you asked me that before.

MR. FURLOTTE: Well, that would be sufficient, too.

THE COURT: Well, if it's on the record now there's no - and I quite appreciate that it's difficult for us to remember but Dr. Waye will very possibly recall if he has dealt with something before. I don't want to get into -

MR. FURLOTTE: Yes, I have part of the transcript of my cross-examination of Dr. Waye but I don't have the transcript on his direct examination nor on the first day of my cross-examination of Dr. Waye.

THE COURT: I don't want to get into whole fields, though, you know, covering the whole -

MR. FURLOTTE: No, I don't want to do that either because I've gotten a lot of answers to my questions from other witnesses since Dr. Waye and I don't intend to go over the same ones.

THE COURT: Yes, and I sort of labour under the impression that perhaps you don't have too many questions to ask Dr. Waye. Am I right, Mr. Furlotte? Haven't you covered most of the fields?

MR. FURLOTTE: At this time in the game you're correct. I don't believe I have that many more to ask Dr. Waye but it will take me, again, some time to go through my material to assess them, so there will probably be long pauses in between questions.

THE COURT: All right.

MR. WALSH: My Lord, if I could make a suggestion that perhaps - to facilitate Mr. Furlotte and to perhaps facilitate the actual cross-examination may I suggest a break at this point in time? I know it's early but we might make better use of our time when we do come back in, give Mr. Furlotte a chance -

MR. FURLOTTE: I don't think that's going to facilitate it. It's going to take me as long a time to go through these if I'm doing it on a break or in court, and it will be just doubling it, I think.

THE COURT: Yes, but we don't have to sit and watch you.

MR. FURLOTTE: Comes with the territory, My Lord.

THE COURT: It's 20 past two now, let's take a half an hour and you devote - don't drink coffee, devote that half-hour to getting your - going through your notes, and you can cover quite a bit of ground in

a half an hour. Say at quarter to three, which is 25 minutes, and then we'll come back and I think it would speed up the thing, and it becomes a little tiresome sometimes to sit here while you have to go through your notes. I'm not being critical of you but I think this would be a better way of doing it, and then we'll start at quarter to three and then we'll go on till about - that is if you haven't finished in the meantime, we'll go on till about, say, quarter to five tonight - half-past four, something like that, and then finish off, if necessary.

This is your last witness, Mr. Walsh, before you call Dr. Kidd?

MR. WALSH: Yes, My Lord.

THE COURT: And he's not coming -

MR. WALSH: Mr. Allman reminded me to remind you, I knew about this, I have to - I have Dr. Waye on recall. After Mr. Furlotte finishes his cross-examination I have him recalled to talk about - testify with respect to the case specific evidence.

THE COURT: Oh, that is right, too, yes.

MR. WALSH: But I don't expect to be very long on that.

THE COURT: No. That is right, yes, so this examination is really on what has gone - well, it's on everything that's gone up until now.

MR. WALSH: Up until the case specific evidence, that's correct.

THE COURT: And then he's going to testify on the case specific and then there will be cross-examination?

MR. WALSH: That's correct, My Lord.

THE COURT: You may have some rebuttal, I suppose, perhaps, on this aspect of it as well?

MR. WALSH: I have some rebuttal from what's occurred to now but my experience to date has been that my rebuttal is not overly lengthy.

THE COURT: This doesn't alter our plan anyway. Let's take till quarter to three.

(RECESS - RESUMED AT 2:45 p.m.)

(ACCUSED IN DOCK.)

DR. WAYE RESUMES STAND:

THE COURT: The Clerk tells me that arrangements have been made, I believe, to have those exhibits that were introduced earlier this afternoon reproduced in Fredericton.

MR. WALSH: Yes, My Lord, and Constable Charlebois is prepared to take them in to Fredericton. They are VD-106 through to and including VD-113 inclusive. They are for purposes of colour reproduction. If Mr. Furlotte would consent to the Clerk transferring them to the constable.

MR. FURLOTTE: I would consent to that.

THE COURT: The Clerk isn't here in the court room right at the moment, he's out arranging to have typed on each one, "The information contained herein is intended for use only in the R. vs. Legere case and is not to be otherwise disseminated by order of the Court", and he signs it as Clerk and with today's date on it, so that will be typed on the corner of each one. Now we'll get ahead with our cross-examination here, Mr. Furlotte.

MR. FURLOTTE: Dr. Waye, I believe when we left off I was cross-examining you on certain statements in evidence that was given in the Yee trial so I believe I'll just continue on there. Dr. Gilliam testified in the Yee case, and at Page 33 of the case law it states that: "Dr. Gilliam considered the problem of developing a quantitative match criteria to be one that has not been dealt with by the medical genetics community, stating, "It's only come up in forensic laboratories"." Would that be a correct assessment?

A. If that's what he said. You're just quoting what he said.

Q. I'm quoting what he said; would you agree with that?

A. That it hasn't been dealt with by the medical community?

Q. By the medical genetics community.

A. Generally when the medical genetics community scores a blot or analyzes a Southern blot they do it with their eyes. Most of the labs I'm aware of don't even have computer assisted equipment to size bands, etc. They know what size the bands they're looking for and they do it with their eyes, so there's some truth to what he's saying.

Q. So basically what the forensic community is dealing with is something substantially different than what had been dealt with before in the medical community?

A. No, not necessarily. You're trying to do the same procedure. You don't have an adversarial review of your data as you do in the court room for court purposes, etc. The forensic community has gone beyond what is generally done in the research and

diagnostic labs and they have come up with ways to actually try to size these bands a little more precisely than just using your eyes.

Q. At the time of the testing results in this particular case there was no quantitative matching criteria even between forensic laboratories, was there, let alone in the medical community?

A. What time frame are we talking when these tests were done? These were done over a long period of time and I didn't do them so -

Q. In 1989.

A. And the question is what?

Q. There was no - at that time, even in 1989, there was no quantitative matching criteria between the forensic laboratories let alone which was agreed to by the medical community?

A. Standard across all those disciplines? No, there wasn't.

Q. Do you feel there should be?

A. No.

Q. Each lab should set it's own matching criteria?

A. I think most people are in agreement that labs do things a little differently and that matching criteria should be established to suit your procedure and how you do things.

Q. So I assume that the position of the forensic laboratories is that, look, we don't care if we have general agreement in the scientific community, we're going to do our things our way and that's it?

A. Well, I think that is quite far from the truth. In fact, the exact opposite is true. Before even acquiring radioactive licenses to work with DNA

forensic labs, the first thing they did was consult the best research and medical genetic labs for advice on how to set things up and how they would do it. You know, the FBI did that, I know the R.C.M.P. did that, and I'm not aware of any forensic labs that didn't use that type of resource system to go to the experts and say, how would you do this if you were going to approach this problem.

Q. O.K., also in the Yee case at Page 33 the trial judge found that Dr. Gilliam concluded, "that the proponents of the forensic application of DNA technology are in using a quasi-continuous allele system taking DNA electrophoresis methods about as far as they can go and stated that it was a very technically demanding problem". Would you agree that the forensic community has taken this method about as far as you can possibly go?

A. No.

Q. So there's still room within it for greater developments and findings?

A. Yes, there's research being done as we speak.

Q. There's also, I believe the trial judge found in the Yee case that - on Page 33 again, that: "The larger FBI match window would increase the likelihood that a match would be declared". Would you agree with that?

A. Could you repeat it? I can't seem to find it on the page that you're talking about. Is this 33 of the judge's ruling in Yee?

Q. Yes. I'm not reading from the case law itself.

A. On my Page 33 he's just repeating what experts have said for the defence.

Q. I'm sorry, it's on Page 34. It states, "On cross-examination Dr. Gilliam indicated that the larger FBI match window would increase the statistical likelihood that a match would be declared". Would you agree with that?

A. That's what Dr. Gilliam said. That's a quote of his, yes.

Q. Would you agree with his assessment?

A. No, because that's only part of defining a match.

Q. Also at the bottom of Page 34 it states that: "Dr. Gilliam concluded by asserting that he was sure that investigators could discover probes that identified discrete alleles and that a forensically useful DNA identification technology could be developed based on a discrete allele system and this would put the forensic scientist's laboratories back into the realms of established technology and it would eliminate, if this line of experimentation proves successful, a lot of problems, matching rules and binning systems that they now have to deal with". So would you agree that maybe a discrete allele system would be more appropriate than a continuous - a quasi-continuous allele system?

A. They've been using discrete allele systems for years in forensics and the exact same criticisms, I imagine, were hashed over last week with regard to statistics. Those same defences are used against them. I'm not sure that everyone would accept those systems as well. They just use a different line of attack to discredit them. It would be a step backwards, certainly. We use discrete allele systems in clinical work all the time defining

whether somebody has sickle cell disease or they don't have sickle cell disease. You're dealing with two or three choices there.

Q. But it would eliminate the problems that we now have with matching rules?

A. I don't believe there are problems with matching.

Q. You don't believe there are problems with matches, O.K. What about the binning systems, is there any problems with the binning systems?

A. Not in my opinion. There are many different types of binning systems. They all have their own peculiarities and they all have their own aspects, both plus or minus, but in general I think it's a very good system.

Q. But the binning system used by the R.C.M.P. and the FBI is something that basically has never been used in the past? It's a new technique?

A. Grouping alleles? No, grouping alleles is -

Q. Fixed, in a fixed bin?

A. That precise binning method was new. All the crossing the T's and dotting the I's in that particular manner was new. The actual concept of grouping alleles is not new.

Q. No, it isn't, but it was based with discrete alleles not indiscrete ones? Alleles that were positively identified. In your system alleles are not positively identified.

A. Yes, so what's the point? You have to design a system that you can group them into something called an allele, and that's the method we do.

Q. Well, basically what you did was develop a system which could, I suppose, explain or allow you to fit in the limitations of your technique because your

technique is quite limited?

A. The technique is not designed to give base pair resolution so you have to arbitrarily develop classifications for defining alleles. There's nothing new or novel about that in genetics.

Q. Also at the bottom of Page 35 the Yee case states: "Similarly, Dr. Caskey testifying for the prosecution likewise underscored the necessity for a probability estimate", and I believe the judge quotes from his testimony. Dr. Caskey says, "I think if you have a match over three specific probings that that's very informative match and one has to pay attention to it. Now, you have to look at it in detail and if you go back to your population data base and you find that occurrences each of the matches you got were incredibly common alleles, then you say, wait a minute, you know, three probe match is an interesting match but it certainly doesn't give us a high power number. Therefore it could occur by chance". Would you also agree that a three probe match could occur by chance and it's not a high powered number?

MR. WALSH: Excuse me, My Lord, that isn't - that doesn't resemble - the question Mr. Furlotte asks doesn't resemble, in my opinion, what is - apparently Dr. Caskey has said. Certainly Mr. Furlotte is entitled to ask that question but not as if it's Dr. Caskey's statement.

MR. FURLOTTE: Well, it appears tome it was Dr. Caskey's statement from the bottom of Page 35, it says: "Similarly, Dr. Caskey testifying for the prosecution likewise underscored the necessity for a probability

assessment", and there's a quote, and then there's a colon, a full colon, and then we have the quotation of the statement given by somebody who - I would assume it was Dr. Caskey that said -

MR. WALSH: Oh, my objection, My Lord, was not that Dr. Caskey did not make that statement. My objection was Mr. Furlotte's apparent interpretation of what that statement mean in putting it in the form of a question as if Dr. Caskey had that interpretation. If Mr. Furlotte wishes to -

THE COURT: Well, the statement he made was that a three probed match could occur by chance.

MR. FURLOTTE: Yes.

THE COURT: And then it went on with some other words which I didn't -

MR. FURLOTTE: Then he goes on.

THE COURT: Yes, and you're asking the witness if he agrees with that?

MR. FURLOTTE: Yes, if he agrees with that.

THE COURT: Yes. Well, that's fair.

A. It's quite a qualified statement. He said if you find the occurrence of each of the matches you got were incredibly common alleles, so take the extreme situation where your three probe matches on bands that are of the most common in the population. Well, you are dealing with an extreme case there where that would be more common in the population, that three probe match, than say three rare genotypes, and he's not trivializing the system, what he's saying is that we have to have some way of judging whether it's at the very common end of the scale or at the very rare end of the scale, and

this was why we used the genetics numbers rather than going into court and saying it's a three probe match, I think that's good enough.

Q. O.K., I understand the R.C.M.P., they have a way of establishing their data base as to how many two probe matches there are in their data base or even how many three probe matches there are in the R.C.M.P. data base. Are you aware of that?

A. That computer technology was not in place when I was there so I have never used those programs. I have done that analysis by hand.

Q. You've done that analysis by hand?

A. Not for this particular case but for cases that I have been involved in in the past, yes.

Q. By going through the whole R.C.M.P. data base?

A. Yes.

Q. And how many two probe matches did you find in the R.C.M.P. data base?

A. I wasn't interested in two probe matches through the whole data base itself. Again we have to look at the bottom line, how many two probe matches or one probe matches or three probe matches, etc., match the person involved in the case who I was linking to a piece of evidence, that's what I looked at. I looked at the suspect who was linked to the evidence, I looked at his genotypes. and I looked through the data base to see how many people - how many hundred people we had analyzed at that time, how many people fortuitously matched one, two, three, etc., probes.

Q. And what were your results?

A. My results?

Q. Were you able to find a high degree of frequency within your data base?

A. The last case I did which was a five probe match between evidence and accused I with two of those combinations of five loci found one person in the data base that matched at two of those combinations for two probes.

Q. That matched at two of those combinations.

A. And it was well within the predicted numbers. I would predict that I would be able to find one or two people, nothing for three, nothing for four, nothing for five.

Q. And you searched just those particular ones, frequencies?

A. That's what's relevant to that case, the defence being that everyone in Ottawa will look like this person.

Q. Now, I notice in the OTA report that - it's an exhibit in evidence here, on Page 4, Office of Technology Assessment Report, Exhibit VD-24, at Page 4 it says: "The DNA from sperm to sperm is different".

A. From individual sperm cells?

Q. Yes, from individual sperm cells?

A. Yes.

Q. Would that be correct?

A. Each sperm results from a myotic event where you inherit half the chromosomes, and they'll be different halves inherited in each of the sperm.

Q. And that's O.K., that's all I wanted to - is there any way that could affect the results of testing sperm DNA on a swab?

A. Not if you're using this technique, no. If you were analyzing single sperm cells what you'd be picking up is half the pattern. You'd only be picking up one of the alleles, if you were analyzing - if you had the capability to do RFLP analysis on a single sperm.

Q. So when - I'm trying to understand it - when the DNA of the sperm is different, each sperm cell, what is it, one sperm cell has a combination of the man's mother and one sperm cell has a combination of the man's father or -

A. No, in my cells, in my body cells as well as the cells in the testes that make sperm, I will have 46 chromosomes, half of which are inherited from my father, half of which are inherited from my mother. When I in turn go through gametogenesis or making sperm cells a single sperm cell will contain either my mother's or my father's chromosome 1, either my mother's or my father's chromosome 2, etc., etc., so you have a lot of combinations going down there. They don't partition mother-father through all the chromosomes, it's either/or, and then you go to the next chromosome that's 50/50 again, so you effectively have one-half to the 23rd different combinations.

Q. So when you run a DNA test on sperm and you end up with this type of a pattern each sperm cell would have how many fragments that would show up like this?

A. If I had the capability of analyzing a single sperm cell, and those fragments are allelic, that is one

is on paternal and one is on maternal chromosome, I'd detect one or the other.

Q. You'd only detect one or the other?

A. Correct, but you would not be able to do that experiment or get that result using this technique, we can't use RFLP to detect single chromosomes or single loci in a single cell. What you're looking at here is analyzing hundreds of thousands to millions of sperm, half of which contain the one allele and half of which contain the other allele, and you're looking at a composite which will be 50/50.

Q. What would happen if, say, you had all the sperm cells - first of all, maybe we'll establish, when it says the sperm cells are different is it that half would have one pattern and half would have another pattern or would there be three different ways they could be different?

A. Like I said, there's many different combinations. Chromosome 1 it could be either maternal or paternal, so there's two combinations there. You go to chromosome 2 there's yet another two combinations, so it's one-half times one-half of those two chromosomes, and you continue on down, so it's one-half to the 23rd different combinations that you can have. All the sperm cells will contain 23 chromosomes but they could contain either mother's or father's at the particular pairing, so you have a lot of different combinations. You have the entire individual's genetic constitution represented in those sperm cells, in the collection of sperm cells, just that you have them partitioned.

Q. Would one sperm cell or the other be stronger that one may, say, die or degrade before the other one?

A. I'm not aware of any examples of selected strength or weakness of sperm depending on which chromosome they inherit. Certainly when it results in an individual selection can occur then. If you have an allele that is lethal, say, you only have one of the alleles represented in the offspring, but that's something that occurs biologically after conception, not in just making the gametes themselves.

Q. I'm just wondering if you were going to have - say one was stronger than the other and one degraded so you'd end up with all sperm cells identical rather than your combination, would that - how would that react when you run the known person who the sperm come from and then that other sperm? What kind of result could you expect?

A. Well, if you created the artificial and unprecedented situation where one VNTR allele is going to be somehow lethal to a sperm cell, you've created a very strange situation there and if it was lethal to that sperm cell and the sperm cell all of a sudden was programmed to degrade if it inherited that allele you wouldn't see it in that person's sperm. I can't imagine how that would happen.

Q. Maybe I will leave this with you, VD-24, the OTA Report, "Genetic Witness".

A. Thank you.

Q. At Page 18 of that report it states that: "More automated machines (straightened lanes) account for inconsistent gel composition, variation in electric field, or other conditions prior to the calculation of fragment sizes". Does your computer which does your sizing, does it also straighten out the lanes and account for inconsistant gel compositions and variation in electric field?

A. The programs that I was working with when I sized for my case work and for population and stuff, population data, if you had a grossly distorted lane I've seen the program used, demonstrated, that you can actually trace a lane that is crooked. I never had occasion to use that particular program myself, I was never dealing with lanes that were crooked. I think it is incorporated into a lot of computer programs that you can do that. There are types of gels that habitually run crooked lanes or run curved lanes and you have to build that type of software into the computer, so it does exist.

Q. You build that software into the computer?

A. Yes.

Q. So when you get a computer image of your autorad where you had to straighten the crooked lanes would you end up with a straight one?

A. No, no, it doesn't. It doesn't correct for it, it just allows you to analyze the lane as it exists.

Q. For your sizings purposes?

A. Yes, if the lane - and again this is just an example to illustrate. If the lane went in a

curve like this and there were bands at different points in the curve you'd need to tell the computer to look along a curve and not along a straight axis to see all those bands, and there are capabilities to tell the computer that the lane actually is distorted. Like I said, I never had occasion to use that part of the computer program.

Q. On Page 30 of the OTA Report it states that: "Fewer than half the laboratories, 48%, surveyed by OTA believed setting standards was an appropriate role for the FBI". Now, as the R.C.M.P. laboratory would you want the FBI setting your standards, or would it be acceptable to you?

A. I think that would have made my job redundant from the beginning if the R.C.M.P. had a policy to adopt the FBI standards. There'd be very little development work for myself and I wouldn't be here today.

Q. It also states at Page 30: "Others not connected to crime laboratories probably will object to FBI oversight as a situation of the fox guarding the hen-house". Would that be an adequate assessment for forensic laboratories if they set their own standards?

A. It's obviously somebody's view. I'm not sure that's my view. I'm fairly certain it isn't my view. Somebody has to set standards and committees have been set up that involve both forensic people, non-forensic people, non-scientists, both prosecution and defence, people involved in ethics. I think there's a fair mix of people giving opinions as to how things should be run.

Q. But there's a good chance that the general scientific community and not the general scientific community of the forensic field but the medical field and in general would not approve of the independent laboratories, forensic laboratories, setting their own standards?

A. It's been my experience that most people in the other fields show very little interest in this area to begin with. I'm not sure they'd relish the opportunity to be involved in the decisions. They're not interested in it from the beginning. I don't think they'd object to the forensic community being involved in setting standards for their own tests, they certainly do it for their own testing.

Q. Most of them are too involved in their own work to get involved in yours?

A. Well, no, geneticists define standards for doing their own tests. I certainly wouldn't consult an architect to design my genetic tests for screening genetic diseases.

Q. And the OTA Report again at Page 61 says: "False inclusions could occur by incorrectly placing DNA samples on a gel or by loss of bands due to sample degradation". Would you agree with that statement?

A. Yes, if the - well, the first part of that example is the classic case if I loaded the accused's blood sample twice instead of loading the accused's blood sample and the evidence sample, so I'm comparing him to him and I will always identify him as him. If that's - that certainly is a misuse of the technology and it will - if interpreted that way will lead to an incorrect conclusion, and we went through several

examples before that. If you had a two banded pattern where one band degraded, say a high molecular weight band, and you called that as you see it you'd falsely exclude, and I'm sure you can dream up situations where if you called it incorrectly as you see it you might falsely include at that particular locus. Again you're misusing and misinterpreting the technology.

Q. I notice at Page 69 of the OTA Report it says: "Even flipping the top of a tube containing DNA can create an aerosol with enough sample to contaminate a nearby tube or, I suppose again, a nearby lane".

A. Yes, this is all with respect to the polymerase chain reaction which is a technique that a machine literally makes millions to billions of copies of the DNA that you provide it. Obviously if you sneeze in the tube and provide it with your DNA you're going to make millions and trillions of copies of your DNA which you're subsequently going to analyze and try to associate with an evidence sample. In that particular case you'd be likely to falsely exclude because you'd be identifying your own pattern as the investigator, but that's a totally different technology than we've been talking about here.

Q. When you're loading your gel up at the top with the DNA in the different lanes how is it actually loaded?

A. You use what's called a micropipetter. It's basically - some of them don't look too much different from this, they have a tip at the end, a disposable

plastic tip that you use for each sample. You attach the tip and it usually has a trigger which will draw up solution into the tip and then you can expel the solution into the tube.

Q. It's like a syringe or -

A. Very much, it works on the same principle. You suck the material up and then expel it.

Q. What would happen if a drop of that fell into an adjacent lane?

A. You'd be analyzing it in the wrong lane. You again would be misusing the technology.

Q. And that would be called like cross-contamination or -

A. Of the lanes? You've loaded your sample in two lanes instead of one lane. Again the operator has made an error.

Q. As is stated in the OTA Report at Page 70, it says, "In forensic analysis the problem of cross-contamination could be particularly serious should a suspect sample accidentally contaminate a questioned sample containing degraded or no DNA".

A. Yes, that's pretty much the case of analyzing the blood sample twice, that type of scenario. Yes, that would be a problem if you were prone to misloading your lanes.

Q. At Page 82 of the OTA Report it says: "Setting standards for forensic application of DNA testing is the most controversial and unsettled issue, yet standards are the cornerstone of quality assurance". Would you agree with that?

A. Yes, what they're saying is true. It's hard to build

a quality assurance program if you don't have the guidelines within which that system is supposed to operate, so yes, you do have to set standards, follow those standards, and then devise systems to ensure that those standards were followed. I think the contentious point is which standards should everyone follow. Certainly every lab has their own standards.

Q. And it states again at Page 82: "Technical and operational standards for DNA typing and forensic case work are needed and needed soon". It continues to say, "Agreement on what standards are appropriate, who should decide, how implementation of standards is best achieved, and whether they should be mandatory has not been reached". You would agree that that is the case, Doctor?

A. Yes, there's no legislation governing how one does the test from A to Z, all the different steps. I think that's the purpose of this book is to advise lawmakers. They're just setting out the groundwork for this document is that there are standards in the various labs but they're not all the same, and do we need legislation to make them all the same, with respect to the United States.

Q. So would you agree that the general scientific community finds that standards are necessary and that none are in place?

A. If the general scientific community took that view openly I think they would be demonstrating quite a bit of hypocrisy. I can't think of two labs that if you went into them would do the Southern blot the same way, yet they'd be doing them for very

important end uses like determining whether to continue or abort a fetus, yet they do the same procedure. They have slightly different ways of doing it, slightly different standards, slightly different quality control. If they turned around and said the forensic society should all do things exactly the same I think they'd be hypocrites.

Q. Would you say that the OTA Report is a fair assessment of the opinion or of the general opinion in the scientific community?

A. From start to end, the OTA Report?

Q. Well, basically and in general.

A. I haven't read the report in several months and when I did read it I didn't comb over every word of it. Again I'd hate to speak for the entire scientific community myself. I think they went to great ends to ask as many people from as many different areas what they thought of how DNA was progressing at the time that this was drafted. This is not a current document by any means.

THE COURT: What is the date, as a matter of interest? Isn't it almost two years old now?

MR. WALSH: July, 1990, My Lord.

A. The report itself, though, I believe the principle author - yes, Robyn Nishimi was the project director and she presented this work in a more or less complete form at the end of 1989 and the report was available in pre-print shortly after that, so it basically represents findings that were obtained in 1988, 1989. The study was at its conclusion quite some time ago.

Q. You would agree, Doctor, that in 1989 that you set

your own standards for the R.C.M.P. lab and that they were not and would not have been accepted by the general scientific community?

A. No, I wouldn't agree with that.

Q. Do you agree that they were not accepted by the general scientific community?

A. No, in fact many of the criticisms that the strongest opponents to DNA used in forensic science, many of their criticisms or their solutions to what they viewed as problems were in fact things that we had already incorporated into our system.

Q. Well, I thought you testified that there were no generally accepted standards within the forensic community let alone the scientific community. I thought you said each forensic lab sets their own standards.

A. Well, at that point we're really talking 1989. I have to keep putting these in context of when we're talking. Each lab would basically amount to R.C.M.P., FBI, Lifecode, Cellmark, those were the only labs actively doing DNA typing, so it's not a large number of labs. They use pretty much the same technologies. Again there were some differences. They had somewhat different standards, and as I said, some of the criticisms of the other labs we had at that time were quite adequately addressed by our protocols and by our standards.

Q. By your protocol and by your standards, but I'm talking about standards that were accepted, or I should say that you admit were not accepted. They were not even put to the scientific community.

A. I have very little power over how Lifecodes or Cellmark or the FBI set up their standards. My responsibility is to make sure that we were addressing relevant concerns.

Q. And you set your standards according to your opinion as to what you felt was necessary?

A. Well, it was certainly not just my opinion. We went to great lengths again to attend meetings, participate in working groups, again, query the scientific community, anyone who was interested, of course.

Q. And the OTA Report says at Page 82 again:

"Technical standards are needed to specify proper gel controls, electrophoresis conditions, the extent that computer assisted matching should be permitted, population data to compute probabilities of matches and many other parameters".

THE COURT: What page was that?

MR. FURLOTTE: It's Page 82. Again, Doctor, do you feel that this is necessary?

A. And we did in fact have standards as these other labs did. I think the OTA Report, it's a catch phrase on almost every page here, is stating that standards need to be used for this procedure and that procedure and that standards need to be used. I don't see anywhere in the report, and I may be mistaken, that they say everyone in the world should have the exact same standards.

Q. But it should say that they have standards that are accepted by the general scientific community, should it not?

A. I don't think we'd ever -

Q. Accepted as being reliable.

A. Accepted as being reliable, I think that goes without saying that the procedure be reliable, and I think there's a wonderful quotation here about questioning the reliability of RFLP typing, something to the effect that it serves science and community a disservice to even question the reliability of this technique. That may not be an exact quote, if you give me a minute I might be able to find it, but I don't think the reliability of the technique was ever in question.

Q. You agree now that one of the standards that the R.C.M.P. lab should have is proficiency testing by its operators, or of its operators?

A. As a standard to ensure that things were being done right?

Q. Yes.

A. Yes, proficiency testing is a general part of a lab operation.

Q. But when you were in operation of the lab in 1989 you didn't have your proficiency testing, either open tests or blind tests?

A. For myself?

Q. For yourself and your operators.

A. I was the operator when I was doing it. No, I didn't proficiency test myself.

Q. What about when you weren't the operator? How many proficiency tests were conducted on Dr. Bowen?

A. I have no idea.

Q. Did you conduct any proficiency tests on Dr. Bowen?

A. Not to my recollection, it wasn't my job.

Q. I thought you were one of the kingpins in setting everything up for the R.C.M.P., standards?

A. It's mainly a chronological job description. I was one of the first people hired to set up. If that makes me the kingpin it's only because I was the first in line. There were several people employed in developing the system. It does them a discredit to say I'm the kingpin.

Q. Whose responsibility was it to set up standards for proficiency testing?

A. I'd have to look at the job descriptions of other people. It certainly wasn't my responsibility.

Q. In fact, Doctor, there was no standards set for proficiency testing while you were at the R.C.M.P. lab, was there?

A. Proficiency tests were being conducted. They weren't being designed, set up and scored and arranged by myself.

Q. Are you talking about proficiency testing when you were training Dr. Bowen to do these tests?

A. Again I didn't train Dr. Bowen.

Q. Do you know whether or not it took more than two days to train Dr. Bowen?

A. Dr. Bowen was there quite some time before doing case work. Again, Dr. Bowen was experienced at this technology long before coming to the Ottawa lab so his training was of a different sort than somebody who wasn't initiated in doing RFLP technology.

THE COURT: Quite a portion of Dr. Fourney's evidence was devoted to that very point, I think, Mr. Furlotte, earlier today.

MR. FURLOTTE: Yes, but since I understood they were both training Dr. Bowen but -

THE COURT: Well, I think Dr. Fourney made the point, as this witness has just done, that Dr. Bowen came in as a person with very considerable experience in DNA testing through his other work before he joined the R.C.M.P. lab.

MR. FURLOTTE: Page 95 of the OTA Report it says that: "Workers in a novel area sharing a common goal can develop a technique that furthers their professional end and they can generally accept it regardless of its scientific reliability". Would you agree with that statement, Doctor? Basically what it's saying, I assume, is that the scientists in the forensic units testing DNA could generally accept everything about it, but that necessarily would not prove its reliability, would it?

A. If they weren't credible scientists and if they weren't doing their job properly I think - certainly not specifically with forensics or forensic DNA typing but if somebody had a common interest and they were blinded by that common goal you could do that. I think that's the caution that they're laying out, that the Courts need to look at both sides.

Q. And basically here it says: "Here general acceptance does not equate with scientific reliability and validity". If you have a special

interest in something, then it's reasonable to believe that you could be blinded by your interest?

A. Some people if they're not good scientists and they're not following good scientific practice, if they misapplied the principles of science and went to that extent. I don't think they're even talking about DNA here.

Q. No, that's just in general, any science in general. I would assume that statement would apply to all scientists in general.

A. Well, if people do things wrong they run the risk of coming up with wrong answers.

Q. And being proven wrong in the end. At Page 104 it states under "Reliability": "Although there is a consensus regarding the uniqueness of each individual's DNA and the ability to type an individual's DNA for identification purposes, debate still exists regarding experimental verification, adequate population data, the reliability of different laboratories testing and analytical protocols, the error rate of tests that are performed and the quality control of laboratories performing the tests", so would you admit that there is still general debate over these issues?

A. With some people I don't think these things will ever go away, they make their living debating them. Again if you're asking my opinion and not the general scientific or the defence experts' union view about this matter, I think a lot of these issues have passed by the wayside since 1989.

Q. In that report at Page 107 Dr. Lander had stated: "It is my belief that we, the scientific community" - and he's talking about the scientific community in general, not the forensic scientific community - "have failed to set rigorous standards to which courts, attorneys, and forensic testing laboratories can look for guidance with the result that some of the conclusions presented to the courts are quite unreliable".

A. Yes, that's Dr. Lander's view.

Q. That's Dr. Lander's view and opinion, right.

A. That's his view and opinion, yes.

Q. And has anything really changed since this report came out?

A. With regards to Dr. Lander?

Q. No, with the respect of forensic laboratories changing their attitudes and standards.

A. Again I have been out of that business since this report came out so I haven't been privy to changes or non-changes that have occurred or not occurred in forensic typing protocols. We've gone through what happens at the R.C.M.P., I'm aware of some of the things that have changed there, and again they're for the most part cosmetic and designed to ensure that the technique works better and works more efficiently. I'm not well enough informed to give you an opinion as to whether things have changed or stayed the same in the other labs and why that is.

Q. At Page 109 it states: "Several concerns have been expressed regarding DNA as evidence, including (1), the weight of the statistical data; (2), the

lack of standards to ensure reliability of the evidence; (3), potential bias of expert witnesses whose livelihood depends on the success of the technology; and (4), the inability of defendants to defend against such technical and unreliable evidence". Are these still concerns within the general scientific community, Doctor?

A. Again I can only speak for myself. Unlike some of these people I don't like to assume that I know what the rest of the world is thinking, but you know, it's quite true that at that time and I think it's been in evidence in this trial and other trials I've been involved in that many of these things are still being debated in courts. DNA as evidence, well, certainly that's a debate where it's the purpose of trials such as this. The weight of statistical data, well, that comes up yet again in another case. The potential bias of expert witnesses making a livelihood, well, there certainly are many of those, and that again comes up. Civil liberties considerations, these are all - they're just stating the obvious. These are always points of concern and points of debate.

Q. Doctor, I show you a copy of a paper by yourself, Ron M. Fourney and John H. Bowen titled "Forensic Analysis of Restriction Fragment Length Polymorphism, Theoretical and Practical Considerations for Design and Implementation". You've authored this paper?

A. I wrote it, yes.

MR. WALSH: It's the Promega Paper, My Lord. I think it's called the Promega Paper, it's in evidence, I

believe.

MR. FURLOTTE: It is in evidence.

MR. WALSH: Maybe I could find it for you in a moment.

THE COURT: Well, maybe we can just call it the Promega Paper for the present.

MR. FURLOTTE: Yes, if I just show him my copy I'm sure he'll recognize it.

THE COURT: I know what it is, I was just trying to get on the record what we're talking about.

MR. FURLOTTE: At Page 119, Doctor, it states: "This report provides an overview of the DNA typing system utilized by the molecular genetic section of the Royal Canadian Mounted Police. Theoretical and practical considerations for the design and implementation of the DNA typing system are discussed with particular emphasis placed on aspects of the system that address controversies associated with forensic applications. Recent debates have brought into question the ability to achieve genetic individualizations based on the analysis of a limited number of genetic loci. Quote King, 1989, Lander, 1989, and Lewin, 1989. Apart from quality control and technical efficiencies there are several" - and you underline - "bona fide scientific issues at the heart of this controversy".

A. That's underlined just to indicate italics.

Q. Right, these are several bona fide, and you underline bona fide.

A. Yes, not to emphasize, not for emphasis, just to point out that it should be in italics.

Q. But you admit that they are bona fide scientific issues at the heart of the controversy?

A. Yes.

Q. And, "These include concerns regarding (1), the number and types of loci being analyzed and the criteria used to define an RFLP match, the degree to which allele frequency population data bases are representative of the relevant populations, and the validity of the statistical methods used to assess the significance of RFLP inclusions". So, Doctor, when this paper was prepared those were bona fide issues within the scientific community?

A. Those had been, and I was quoting commentaries made prior to writing this.

Q. They still are, are they not?

A. I'm certain you can find people who think they still are, yes.

Q. Yes, so you would have to say that aspect of DNA forensics has not been accepted within the general scientific community?

A. That's not what I'm saying here. I'm pointing out why we wrote the paper and some of the things that we were going to address. I've never taken the view that the world's perfect and that there's no controversy. I think that's head in the sand attitude. People were making criticisms, I quoted those people, and their little commentaries that they had written. I wrote down that some of the issues were actually bona fide scientific issues. I could have gone on to state that many of them aren't; I didn't, and I listed some of the concerns

that people have. I'm just stating a premise for even writing the paper.

Q. O.K., Doctor, but I believe you gave evidence in direct examination some weeks ago that the system used by the R.C.M.P. and the scientific theories, I suppose, to establish degrees of probability of frequencies, I believe you stated in direct examination that this was generally accepted in the scientific community as being reliable.

A. That was my opinion, yes.

Q. That was your opinion.

A. And I've quoted people here who have the opposite opinion, that's the nature of human beings. You're going to find people on both sides of the fence, some sitting on the fence.

Q. What do you mean by generally accepted?

A. You asked if it would be my opinion if it was generally accepted.

Q. That it was or would be or is?

A. You'll have to read it back, how the question was phrased. I can't remember what I said two weeks ago, how the question was phrased or whether you're giving it back to me properly or improperly or -

Q. Is the forensic application of RFLP analysis generally accepted in the scientific community as being reliable enough for the purpose of which forensic application is using it?

A. In my opinion, yes.

Q. The general scientific community out there accepts your opinion, that's what you're saying?

A. No.

MR. WALSH; No. Excuse me, My Lord, he's rephrased it to a

point I didn't understand that being the answer that Dr. -

THE COURT: Yes, we're sort of going to non sequiturs here, really, aren't we?

MR. FURLOTTE: I'm trying to establish what the doctor means when he says it is generally accepted in the scientific community.

A. Yes, that's the key part of that, what one person views as generally accepted. I've already said that I'm hesitant to say that my views are shared by everyone else, I know they're not.

Q. I'm not saying everyone. When we say generally, what do you mean by generally?

A. Amongst rational, thinking human beings who have a base of knowledge to -

Q. You mean by a majority?

A. Not necessarily.

Q. Not necessarily. Do you mean by 40%?

A. Again, people who have a basis upon which to form a relevant opinion. Certainly if I walked down the street and walked into a bowling alley and queried the people you'd get very different answers from if - you may get different answers than if you queried a scientific audience who has a knowledge upon which to base that opinion. In my opinion it's generally acceptable if you ask people who are properly informed and experienced in this particular application.

Q. So I assume, then, maybe what you mean, that the people that you've proposed your ideas to, those people generally accept it, is that what you're

saying?

THE COURT: When you say proposed to, who does he propose his opinions to?

MR. FURLOTTE: Well, probably to those people in the forensic community.

A. Well, the point is is that you don't poll people, you don't send out a newsletter or have an official vote or anything like that. It's not a Gallop Poll, is this generally accepted or not. Again you put things to peer review, you publish papers, you present your work at meetings, and again, you know, there's a variety of people there from prosecutors, defence attorneys, judges, all sorts of different people who are quite interested in this material there, and you get feedback from it. Upon that feedback you - that's how I bas my opinion of generally accepted.

Q. Right, and if you don't get any mass of objections to your work that you put out there for peer review, then you say it's generally accepted? Is that the standards of your generally accepted?

A. Not in an absolute sense. Again, if you published a paper and had to have everyone who read it agree 100% with everything you said you'd never achieve general acceptance. It's the nature of human beings.

THE COURT: The Supreme Court of Canada even experiences that problem.

Q. So when you say that it is your opinion that it is generally accepted in the scientific community you don't mean that the scientific community who knows

anything about RFLP - you don't mean that if you were to poll them that they would generally accept it?

A. I'd have to - if I went into, say, a wildlife biology department, somebody working out in the field with rodents or something, and presented all this to them, I'd have to walk into that department and actually give a seminar and see their views. I've given seminars to general scientific audiences.

Q. O.K., so you didn't poll everybody out there in the scientific community but you realize, Doctor, that there is lots of opposition out there in the scientific community who has a contrary opinion to yours as to its reliability?

A. Again, there are always dissenters.

Q. And there's a good number of them, is there not, Doctor - substantial?

A. They present their views on numerous occasions. Their views are fairly rigid. They have been rigid for several years and - but there's a limited number of them. The same names you see coming up in their travelling road shows from state to state and now into Canada.

Q. Something like the proponents of it? Travelling road shows maybe like Dr. Kidd, for example?

THE COURT: Well, I don't think we should get into personalities here too much.

Q. Do you know of anybody who's testified more in court than Dr. Kidd as a proponent of the forensic application?

A. Oh, I'm sure there's numerous people who have testified more than him. I'm sure it's something

that he doesn't like doing all the time.

Q. The number is growing all the time, too, is it not Doctor?

A. Number of what?

Q. As opponents, number of people coming to court, scientists, opposing the application of DNA forensics?

A. No, I think you made a realistic point that the number of people presenting the data - there's only so many people work in this field so the number of people presenting the data is fairly fixed. The number of people opposing the data, which generally aren't people who have anything to do with forensics and oftentimes people who have nothing to do with DNA analysis, it's a fairly fixed population of people.

Q. But it appears that at aleast from the case law - or maybe I'm wrong, but it appears on a general assessment of the proponents seem to be less able to go out into the general scientific community to get approval of it than anybody opposing it? If you were to take your independent and unbiased witnesses who are not involved in forensics there appears to be more opponents than proponents?

A. I'm not sure how you decide that. I've given numerous seminars to non-forensic proponent or opponent audiences, just general scientific audiences, both at the hospital and at the university, in different areas. I think that's a good way to find out whether people think what you're doing is absolutely scientifically unsound or whether they agree with what you're doing.

Again I don't poll them after the seminar but you generally have a question period.

Q. So when you say - again, when you say it's your opinion it's accepted in the general scientific community do you just dispell and again ignore all the opposition to the methods and its application?

A. No, you don't ignore criticism, not as a scientist. You evaluate the criticism, you evaluate both where it's coming from and what its substance is and what relevance it has.

Q. How much opposition would you need before you say, well, it's not generally accepted?

A. I'm not sure that's my decision to make. Again I'm not a pollster and nor am I involved in setting standards as to whether something is admissible or not admissible in a court of law. I don't think you'll find anyone who disagrees that this type of technology is both reliable and acceptable for use in diagnostics, which again have more dire consequences than the court room use of this technology.

Q. Diagnostics has more dire consequences?

A. In Canada it does, we don't have capital punishment.

MR. FURLOTTE: My Lord, if I may request, I would like to reserve the decision whether I want to ask Dr. Waye, you know, maybe a matter of half a dozen more questions at the most, but I would like to have until tomorrow morning to decide that and like I say, I will put a limit on myself of half an hour further cross-examination with Dr. Waye on this topic, but I would like this evening to go through my notes to save the Court's time.

THE COURT: When you say on this topic, surely you don't mean the matter of acceptance within the scientific community, do you?

MR. FURLOTTE: Well, but that may be part of it, but once I stop cross-examining Dr. Waye and I realize once the Crown puts him back on and he's back on for case specific evidence, then my cross-examination will be restricted to case specific evidence. I know we're about 15 minutes early but rather than me sit here for 15 minutes to see if I have an extra six questions or -

THE COURT: I'd sort of like to make good use of this time here. One of the things, I'm looking ahead and we want Dr. Kidd to get started first thing on Thursday morning because we've got to get that man out of here Friday afternoon, I would think, and even if it meant sitting Thursday evening to make progress with him.

MR. FURLOTTE: I would have no problem with sitting Thursday evening but -

THE COURT: No, but if he's just coming off a sickbed, as has been indicated, he probably isn't in much condition to be interrogated Thursday morning.

MR. FURLOTTE: I love that word, interrogated.

THE COURT: Interrogated? Well, that's a polite word I'm using. Thursday afternoon and Thursday night I think would be too - has he been very ill?

MR. FURLOTTE: I do not expect I'll be as long in cross-examination with Dr. Waye as I was with Dr. Fourney in the case specific evidence, and if the Crown is only going to take half a day with Dr. Waye tomorrow, then I expect I can finish up in

the other half.

MR. WALSH: In fact, I fully expect, My Lord, that I wouldn't even be a half a day, that the manner in which I'll approach the doctor's assessment of the case specific evidence, I don't intend to ask him to go through each individual item. He's reviewed it, I take it, and I'll just ask him for general statements associated with it. If Mr. Furlotte wishes to get into it, it will be his choice. I haven't been planning to have Dr. Waye on the stand very long on redirect in terms of the questions I have to ask him.

THE COURT: You have no objection to doing as Mr. Furlotte proposes?

MR. WALSH: No. In fact, I think what Mr. Furlotte is suggesting is very reasonable. I can see a situation where he doesn't want to - he wants to ensure that he has covered everything and it's probably the same request that I would probably make in the same position that he is now. I think it's reasonable, yes, My Lord.

THE COURT: When I say you won't want to go on on this topic, this business of acceptance in the scientific community, that's been rather well canvassed, I think, through this witness. Undoubtedly you'll want to ask Dr. Kidd questions on the same topic but - well, so we will adjourn now until tomorrow morning at nine-thirty. Mr. Furlotte will go on with his cross-examination on the earlier evidence of this witness, and then you'll have your re-examination which won't take too long, will it, on this?

MR. WALSH: No, My Lord.

THE COURT: And hopefully by tomorrow noon you will have finished your direct examination.

MR. WALSH: I fully expect that that will be no problem. I'll meet that deadline, yes, My Lord. In fact, that's when I had put on myself in any event.

THE COURT: And then hopefully tomorrow afternoon you don't see any difficulty in finishing with cross-examination?

MR. FURLOTTE: I can't foresee it.

THE COURT: Tomorrow afternoon?

MR. FURLOTTE: Yes.

MR. WALSH: My Lord, before we actually break, a housekeeping matter, I referred it to Mr. Furlotte. We have a document in evidence as VD-49. It's commonly called the fixed bin paper.

THE COURT: For the record, may I say that what we've just been talking about, the Promega Paper, is VD-50.

MR. WALSH: That's correct. VD-49 is commonly called the fixed bin paper. When we introduced it in evidence last week, I believe, or the week before, we had the final in-press draft of that particular paper. My understanding is that the journal, the American Journal of Human Genetics, where that paper is contained, has just come out this week, Dr. Waye, is that correct?

DR. WAYE: Yes.

MR. WALSH: And I have a copy of the actual published paper in its final form and I think as a housekeeping matter perhaps we could have it entered as 49A, and Mr. Furlotte, I believe, agrees to that.

MR. FURLOTTE: Yes.

THE COURT: Oh, the published version of that paper will be Exhibit VD-49A.

MR. WALSH: I have nothing further, My Lord. Thank you.

THE COURT: All right, so that ends everything for this afternoon.

(COURT ADJOURNED TO 9:30 a.m., MAY 15, 1991.)

COURT RECONVENES - 9:30 A.M., MAY 15, 1991

(Accused present in prisoner's dock.)

THE COURT: Now, Mr. Furlotte, you were going to complete your cross-examination.

CROSS-EXAMINATION OF DR. WAYE CONTINUED:

Q. Doctor Waye this morning I would like to refer you again to exhibit VD-50 which is entitled the - I suppose the "Promega Paper" for short, which was prepared by yourself and Ron Fourney and Doctor John Bowen, is that correct?

A. Yes, that's correct.

Q. I notice at page 150 of that paper, Table 4, the "Features of allele frequency population databases for a Caucasian population", and you have there the percentage of heterozygotes. Correct?

A. Yes.

Q. And what percentage is expected for heterozygotes, Caucasian data base?

A. Depends on the locus. Some of them are more polymorphic than others.

Q. Generally you expect it's about 90%?

A. Again, it would depend on the locus and how polymorphic it is.

Q. Okay. The D1S7 was 89% heterozygotes?

A. Yes.

Q. And for the D2S44 it was 91%?

A. Yes.

Q. D4S139 it was 86%?

A. Yes.

Q. And the D16S85 there was 69%?

A. Yes.

Q. And for the D17S79 there was 68%?

A. Yes.

Q. And I see over on page 152 for your table 6 for your "Expected and observed frequencies of homozygotes and heterozygotes" and to find out whether or not they were in equilibrium, using the D1S7 you rejected equilibrium?

A. If you take this test as a test of equilibrium.

Q. Yes, which is what you were doing in this paper?

A. That's the way the table is arranged, yes.

Q. And the D2S44, that was accepted to be within equilibrium?

A. Yes, expected and observed and using this statistical test you would accept the hypothesis.

Q. And D4S139, it was rejected. That they were not in equilibrium.

A. I didn't say that, no.

Q. Is this what the table says?

A. The table is arranged that way. Again, if you take this as a test of equilibrium, which it isn't, you reject.

Q. If it's not a test of equilibrium why would you put all this data in here and state which probes are accepted and which probes are rejected?

A. This was at that time a test that people were using as an indicator of equilibrium. If you go to the text there are a number of different alternatives raised about whether this is a true indicator of equilibrium or not. This is a standard piece of data.

Q. In this table and in this paper there was only one probe out of the five, the D2S44, which was accepted to be in equilibrium, is that correct?

A. If you were using this test as a test of equilibrium, which it's not.

Q. Now, Doctor, I am going to show you exhibit VD-49A which is titled "Fixed Bin Analysis for Statistical Evaluation of Continuous Distribution of Allelic Data - from VNTR Loci for use in Forensic Comparisons", and this study paper was produced by yourself, is that correct?

A. As a coauthor.

Q. Doctor Fourney --

A. The paper was written by Doctor Budowle and I was a coauthor.

Q. Doctor Budowle. And you were a coauthor with Doctor Budowle and Doctor Fourney and a number of other people in the FBI?

A. Yes.

Q. I may have a time finding some of the data in here because I have an old copy and I don't have the same page numbers so if you will bear with me for a minute. My Lord if you want to try to follow this one I can try to make comparisons with the copy Doctor Waye has.

THE COURT: No, here, that's all right, you probably need it more than I do.

MR. FURLOTTE: Up in the summary, doctor, this portion here it states:

> "Most important, the statistical analysis should not place undue weight on a genetic profile derived from an unknown sample that is attributed to an accused individual. The method must allow for limitations in conventional agarose-submarine-gel electrophoresis and Southern blotting procedure, limited sample population data, possible subpopulation differences and potential sampling error."

A. That's what it says, yes.

Q. Could you tell me how you allowed in your - I suppose the fixed bin approach the R.C.M.P. has - how you have allowed for the last one mentioned here, the potential sampling error. How is that calculated into your fixed bin approach?

A. Well by classifying alleles in blocks if you had a sampling error, say a sample that did not belong in the data base, say somebody inadvertently gave you a sample from a black person it would effectively be diluted out by incorporating in it a large block of alleles. I'm not saying that there were blacks or Hispanics put in the Caucasian data base but were there a sample misidentified by race by someone else and given to us and included in the data base that's a sampling error and what you are effectively doing by combining it with large blocks of alleles is you are diluting it out. You're diluting its impact out.

Q. On page 842 under the heading "Resolution" you state:

> "Resolution of alleles that differ by one to a few repeat sequences is not possible by using conventional agarose-submarine-gel electrophoresis and Southern blotting."

Is that correct?

A. That's what it says.

Q. And you still agree with that, do you?

A. Again, it would depend on the repeat size. Obviously if the repeat is - the repeat unit itself is a 100 base pairs and depending on how many repeat units there are sometimes you will be able to resolve and sometimes you won't. If you got very small repeat sizes, say on the order of nine base pairs or so which some of these loci are, it's quite difficult to distinguish the difference of one repeat unit out of several hundred.

Q. And you go on to state that:

> "This is particularly so when the overall size of the DNA fragment (or allele) is large and the core repeat sequence is short."

A. Yes, that is basically paraphrasing what I just said off the top of my head.

Q. Yes. You state also in there it says:

> "Small differences in allele sizes, combined with measurement error, cause measurements of alleles in a population sample to be a quasicontinuous distribution of allele sizes. Analysis of a quasi-continuous distribution of alleles differs significantly from analysis of the traditional genetic marker systems which provide discrete allele data."

A. That's what it says, yes.

Q. I notice in the original paper that I have here dated November of 1990 which was accepted for publication you also have in there, which I don't see in the latest, you state:

> "The resolution issue is complicated further by the fact that the resolving capability of the electrophoresis system changes continuously across the gel line."

Have you changed your opinion on that or why was it left out of this latest document? I don't see it in here.

A. It's something I would have a hard time answering. If you go to the beginning of the paper it says it was received January 30th, 1991. That's a typo. It should be 1990. That's when the paper was submitted. The draft of the paper that Doctor Budowle wrote and that I made comments on as a coauthor - that was the last draft of this paper I saw before it came out in the journal. In between that time it went through extensive peer review and several drafts were made and there was some editorial changes made. Again, I didn't make those editorial changes and I don't know who suggested them. Whether Doctor Budowle made them on his own or whether it was suggested by a reviewer or an editor. I wasn't consulted on those changes nor was there any need to consult me on those changes. I wasn't principal author.

Q. Okay. But originally it was stated in the original paper that:

> "The resolution issue is complicated further by the fact that the resolving capability of the electrophoresis system changes continuously across the gel line. This phenomena may not be easily addressed mathematically for matching alleles from two different specimens and may have to be calculated for such electophoretic run."

A. If you say that's what's in that version. I don't have that version with me and, again, that's a version that I didn't contribute to.

Q. Okay. Do you know of any reason why - or has this concern changed, or is it still a concern of the --

A. I think he's stating theoretical concerns. You know, it's theoretically possible that this could happen, that this could happen, and that something else could happen. I think he's overstating measurement and

precision. There are things that can happen so you can't define precise alleles and it's something admitted from the very beginning.

Q. Also it states -- I'll have to see if I can find it in the new one - if it's in the new one.

THE COURT: This earlier version, this is not something that is in evidence, is it?

MR. FURLOTTE: It is not --

THE COURT: Oh, this is 49.

MR. FURLOTTE: This is the 1990 draft copy and I believe there's been - I think there's been three different draft copies, has there?

MR. WALSH: I can't remember the date of the one that's in evidence here - 49.

MR. RYAN: I'm looking at VD-49, My Lord, and it says "Draft" on it and 3rd of January, 1991, and I believe the intials 'R.M.F.' on the top.

MR. FURLOTTE: And I have this of November, '90.

THE COURT: Would the witness like to see 49 and perhaps identify the date or --

MR. FURLOTTE: I think it's probably --

THE COURT: That was dated when? January, '90?

MR. RYAN: January 3rd, 1991 My Lord.

THE COURT: '91. I think the witness has suggested that the final -- No. You did suggest that the original draft had been prepared in 1990.

A. Yes.

MR. FURLOTTE: So, Doctor, I am going to refer to - it's probably easier to find in here - VD-49 rather than VD-49A. 49A I believe is the published version and 49 is the draft copy which was submitted for publication. On page 9 of the VD-49 it states:

"However, it has been observed by us, the FBI" --

MR. WALSH: I have an extra copy.

MR. FURLOTTE:

"However, it has been observed by us (FBI) that under the electrophoretic conditions described by Budowle and Baechtel (1990) bands within a lane of gel that contain degraded DNA will tend to migrate further than bands in a lane without degraded DNA."

Is that correct?

A. That's their observation.

Q. So degraded DNA doesn't necessarily mean that no bands will appear in the test?

A. I think they're talking about degrees of degradation.

Q. Yes, that they --

A. If you take degrade to mean a 100% degraded well of course no bands are going to be there. If you have a sample that's somewhat degraded they are saying in their particular system it has been their observation that you can't have band shifting. That's effectively what they are saying.

Q. But depending on the degrees of degradation the bands will migrate further in the gel?

A. In their particular system it has been their observation that in some degraded samples --

Q. And would that hold true in your particular system also?

A. That's not my experience, no. Band shifting can occur, I have gone over that several times, but it is not a general phenomena.

Q. Now, on page 22 under the heading "Hardy-Weinberg Equilibrium" it states:

> "The application of the conventional formulation of the Hardy-Weinberg rule requires discrete alleles and no measurement imprecision."

Is that correct?

A. That's what it says.

Q. And it says:

> "Neither of these requirements exists for VNTR loci that are analyzed by agarose submarine gel electrophoresis and Southern blotting."

Is that correct?

A. Again, that's what it says.

Q. Do you agree with that?

A. That we don't have discrete alleles and that there is measurement imprecision?

Q. Yes.

A. I've been saying that all along.

Q. And you also agree that to apply the Hardy-Weinberg rule the Hardy-Weinberg rule requires discrete alleles and no measurement imprecision?

A. The Hardy-Weinberg principle has a lot of requirements tagged to it, none of which fit natural populations. It's a theoretical model. It doesn't fit any populations.

Q. But it would still require discrete alleles and no measurement imprecision before you could use the Hardy-Weinberg rule?

A. If you follow the way those fellows wrote their paper and outlay their requirements at the beginning for an ideal situation I can't think of a population that would fit it, humans included.

Q. Right. On page 24 it states:

> "The fact that the present methodology permits correct phenotyping instead of genotyping and the existence of quasi-

> continuous data and measurement imprecision make the conventional approaches of the Hardy-Weinberg formulation inappropriate for addressing the genetic make-up of the sample population. 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."

Is that correct?

A. That's what it says.

Q. Do you agree with that?

A. Yes. I've been saying all along as we bring up these tests that that's not an appropriate test or that's not viewed as an appropriate test for defining Hardy-Weinberg equilibrium. And there is some difficulty with loci that have this many alleles to use conventional simple formulations to assess Hardy-Weinberg equilibrium. I think that's all they're stating here is that it's a difficult task.

Q. All right, but to use the Hardy-Weinberg rule, one, you stated in this paper that you have to have discrete alleles and there cannot be any measurement imprecision, and now you are saying that it is impossible to test for Hardy-Weinberg.

A. That's not what's said. You have, again, twisted what's being said. The application of conventional formulation of the Hardy-Weinberg rule requires discrete alleles. That doesn't say that you have to meet those criteria. Again, the Hardy-Weinberg rule has been applied for some 80 years to human populations and animal populations yet none of them fit all of those categories laid out in that theoretical model.

Q. But Doctor you will admit that the fixed bin approach system taken by the FBI and the R.C.M.P. is something new and it is definitely nothing conventional, is it?

A. Well it is conventional. You're defining alleles. An allele is just a classification. All the fixed bin approach does is define classifications. It's quite conventional.

Q. It goes 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. Further, the odds of discovering so many loci that are affected by some form of selection seem remote. 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)."

It continues on to state:

> "The purpose of applying statistical weight to a match is to convey a guideline for how common or rare an event is in the general population. It is obvious it is impractical to type pure ethnic groups (e.g., Caucasians). Additionally, since a suspect is innocent until proven guilty and the forensic scientist is characterizing the evidentiary sample (of unknown history) in most cases a general population estimate is all that can be used."

I believe that's a bit different than the original draft in 1990.

A. I can't even find the passage that you just read - I'm sorry.

Q. On page 26. Okay, that was at the top of page 25 - 24 and 25.

A. Yes, I think I found it.

Q. So it seems, Doctor, that in this paper it says, again:

> "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)."

I understand from this, Doctor, that it is recognized that there may be a problem if there is a significant difference within a race.

A. In its extreme form what you are worried about is the existence of a population of individuals that all look identical at VNTR loci. That's in its extreme form. That's what detractors of the technology would like to bring up that there is a population out there that are all identical, and I think what this passage goes on to say is that the bottom line is that you should look at enough populations to convince yourself and others that every population you look at is variable at these loci and you can distinguish individuals within that population using these tests, and that there aren't monomorphic populations.

Q. Page 27, last paragraph, you state:

> "Therefore, since U.S. population samples, particularly within a racial group (i.e., Caucasian or Black), are similar and conservative approaches such as binning are employed, a reasonable empirical assumption of random association of alleles can be made."

It states:

> "People are unaware of their VNTR genetic composition and their VNTR genotype does not enter into their decision to have offspring. Therefore, the algebraic approaches put forth in the Hardy-Weinberg rule can be applied."

That's based on the assumption, Doctor, that there are no statistical differences within Caucasians or Blacks or within any race, is it not?

A. That's how he is prefacing this - Doctor Budowle - that when you look at Caucasians both within the United States and elsewhere in the world you don't see glaring differences in VNTR frequencies but that are remarkably similar and --

Q. That's right. So I believe --

A. And it's obvious that --

Q. I believe studies are revealing that there is statistical differences within Blacks in the United States and there is statistical differences in other races that are spread out throughout the United States and other countries, even Canada, i.e., the Indians.

A. The Native Indian?

Q. The Native Indian.

A. Again, it's how you define a race. I think arguably the people who follow how the native Indians, quote, 'settled North America' many decades or many centuries ago and how they have settled in the various areas since then could argue that they could actually break that down into more discrete groups than just saying native Indian. So, again, it's your classification of a race. It's probably erroneous to group all people who are card-carrying native Indians as the same racial group. Plains Indians are clearly different from Indians of other areas.

Q. Doctor, in the final paper which you have and the draft copy from 1990, since this paragraph is left out of the copy you have - at least I cannot find it, on page 29 of my copy of the draft copy dated November, 1990, and you will have to read it from here because I don't believe it's in the new one, it states:

> "Ultimately, it would be desirable to define alleles discretely to be correctly genotyping, not just phenotyping VNTR profiles, and to reduce measurement imprecision. Then it would be legitimate to apply the Hardy-Weinberg equilibrium."

Have you changed your opinion on this? Apparently Mr. Budowle has.

A. Why do you say Doctor Budowle has changed his opinion?

Q. Well, I figured if he hadn't changed his opinion maybe he would have put it in the copy that you have in your hand.

A. I would have to ask the editor or the reviewers why that's not in there, or Doctor Budowle. He'd probably be able to tell me that. I'd be guessing.

Q. But I interpret this, Doctor Waye, that after - and this is just at the end of the paper - that the bottom line is that you realize it's not legitimate to apply the Hardy-Weinberg equilibrium rule.

A. That's certainly the way you've interpreted it.

Q. Certainly. Which way would you interpret it?

A. Looking at - and it's hard to read from here - but looking at the way it's written instead of starting with 'ultimately' he could have very well started off, if you were going to do it in a conversational way, started by saying "In a perfect world it would be

desirable for alleles to be defined discretely.' We can't do it with this system. To be correctly genotyping, again, we can't do it with this system. And to reduce measurement imprecision in a perfect world or ultimately as he has written it in the written form here.

Q. That's great so far.

A. Which is something I have said all along. Ultimately in a perfect world we would like to be able to sequence to the base part but it's not necessary.

Q. But isn't it an admission that it's not legitimate to use the Hardy-Weinberg rule unless you have that system?

A. It doesn't even mention the Hardy-Weinberg equation or the Hardy-Weinberg rule here.

Q. Well what do you mean by the Hardy-Weinberg rule if you can't associate it with the Hardy-Weinberg equation?

A. No, what he is talking about here and to place it all into context, he's talking about tests that are misapplied for evaluating Hardy-Weinberg equilibrium, not whether we should or should not use this algebraic formula.

Q. The necessary requirements, I understand from that paper, in order to use Hardy-Weinberg you must have discrete alleles and there cannot be any measurement imprecision.

A. Well the simple fact is that you misunderstood it.

Q. Well, I must have doctor.

A. Yes.

Q. Doctor Waye I refer you to your paper, again, "Suitable Restriction, Endonuclease Restriction Fragment Length Polymorphism Analysis of Biological Evidence Samples", again, you coauthored with Bruce Budowle of the FBI. Correct?

A. Yes.

MR. WALSH: I believe that's VD-35 My Lord.

MR. FURLOTTE: At the bottom of page 531 it says:

> "Thus, the Hae III-generated DNA fragments will be smaller than Pst I-generated fragments."

Correct?

A. Yes. Pst I is what we call a six cutter.

Q. And do you have -- The R.C.M.P. and the FBI because they use the Hae III do they basically generate the smallest fragments of all forensic labs?

A. I believe the standard for comparison are labs that use Pst I. That's a true statement, yes. Different restriction enzymes, depending on which one you would like to pick, give fragments of different sizes depending on how often the restriction enzyme cuts. Hae III cuts more frequently than Pst I.

Q. So you would end up with a lot of smaller minisatellites than other restrict enzymes would have?

A. Yes. The comparison of Pst I is that if you looked at a given locus cut with Pst I or cut with Hae III based on the frequency with which they cut the Hae III would generate - predict it would generate smaller fragments, and empirically that has been demonstrated.

Q. And would you agree that the probability of shared bands increases for smaller mini satellite fragments?

A. Probability of shared bands?

Q. Yes. Increases for smaller, mini satellite fragments.

A. That's an issue of resolution and actually the smaller the fragments get to a point the easier they are to tell apart. Certainly with our electrophoratic system if we use Pst I bands that are clearly distinguishable with Hae III would look very similar with Pst I. So in that context it's easier to tell them apart using Hae III and the Pst I. It's precisely the opposite of what you just said.

Q. At the top of page 532 it says:

> "Hae III-digested DNA yields RFLPs ranging from 700 base pairs (bp) to 7000 base pairs, while Pst I-digested DNA produces fragments in the range of 6600 base pairs to 400 base pairs."

Correct?

A. Yes. It's a general statement. That would be the range of fragment lengths that you generate at these particular loci. It's not an absolute. There are certainly fragments that are greater than 7000 and there's fragments that are less than 700. In general.

Q. You'll be getting into case specifics after but I notice in the profiles and the sizings for Mr. Legere's case that we have base pairs ranging from 500 to 13,000.

A. As I just said - in general.

Q. Pardon?

A. As I just said - in general. That's a range we're talking about.

Q. 700 to 7000.

A. We're talking about the majority. If you had to bet. When I cleave your DNA or my DNA where the fragments will fall at these loci that's a good range - empirical range, but certainly, as I just said, there's certainly fragments --

Q. What you mean here is an average range?

A. The distribution of fragment lengths, the majority of fragments will fall in that type of area.

Q. Okay.

A. Again, this paper was conceived and written prior to some of these loci even being added to the forensic repertoire so the range of fragments will certainly change as you add different probes. You have to put it in the time context.

MR. FURLOTTE: I have no further questions My Lord.

THE COURT: Thank you very much Mr. Furlotte. Now, you have some reexamination on this phase of the evidence.

MR. WALSH: Yes, My Lord.

REDIRECT EXAMINATION BY MR. WALSH:

Q. Perhaps, Doctor, if I could just for a moment, yesterday Mr. Furlotte referred you to -- and I wanted to clarify or get your full answer if I could. Mr. Furlotte referred you to page 34 of the decision of the United States V. Yee, and perhaps if you would turn to that - you have a copy in front of you - page 34, top of the page. Mr. Furlotte read you the statement:

> "On cross-examination Dr. Gilliam indicated that the larger FBI match window would increase the statistical likelihood that a match would be declared."

And your answer was that - as I paraphrase it - was that that is only part of how a match is declared. Do you remember that from yesterday?

A. Yes.

Q. Could you explain what you meant by that statement?

A. That meant matches are declared not solely based on a window. That's only one of the criteria used to define a match. It's a visual assessment not only of a locus, an individual locus, but of the overall pattern that you obtain at multiple loci. A match is a global concept that involves all the information at the end. Such a visual assessment - that's a qualitative assessment that a trained investigator makes and provides all the judgments to. Again, the matched window is only a part of that entire analytical process.

Q. Would you be able to assign relative degrees of importance in terms of the match made in terms of whether you could assign relative degrees of importance to the visual match versus the match window?

A. In my opinion the visual match is more definitive criteria for calling a match in most instances, at least in my experience, and I think it's the experience of other investigators. The match window has very little effect on whether a visual match is justified or not.

Q. I would refer you to the O.T.A. report, Doctor, briefly. I do not intend to go through it in the depth Mr. Furlotte did but I refer you to VD-24 which is the report of "The Office of Technology Assessment" and I would actually refer you to page 7, the second

column, bottom right-hand corner. I am going to read a statement to you Doctor. You had mentioned yesterday in answer to one of Mr. Furlotte's questions that you couldn't find a particular statement you wanted to refer to. I'll read this statement to you and I'm going to ask you a question in relation to it. It states at pages 7 and then continuing to page 8:

> "Genetic and molecular principles underlying DNA identification are solid and can be applied to DNA isolated from forensic evidence."

And in bold print it states:

> "The Office of Technology Assessment (OTA) finds that forensic uses of DNA tests are both reliable and valid when properly performed and analyzed by skilled personnel."

End of bold print. It goes on --

MR. FURLOTTE: My Lord I don't know if that's a proper way for the crown to put a question and I don't think it's a question. I think it's a very leading answer that he has given Doctor Waye rather than putting a question to him on redirect. You can't lead on direct evidence; you can't lead on redirect either.

MR. WALSH: I'm simply --

MR. FURLOTTE: If that's not leading I don't know what is.

MR. WALSH: I was simply referring him to the particular statement. I intend to ask him a question in relation to the statement. I don't want to play a guessing game like Mr. Furlotte does - I got a statement, guess what it is. I want to refer to it.

THE COURT: Well let's reserve the objection until the question is heard anyway. Go ahead with your --

MR. WALSH: Thank you My Lord. End of bold print.

> "Molecular genetics techniques can accurately disclose DNA patterns that reflect DNA differences among humans. Questions about the validity of DNA typing, either the knowledge base supporting technologies that detect genetic differences or the underlying principles applying the techniques per se are red herrings that do the courts and the public a disservice."

Do you remember reading that statement at any time Doctor?

A. Yes, I've read that statement.

Q. And yesterday you indicated that you were looking for a particular comment in that report. How does that statement compare with the comment that you were attempting to find?

A. I left out the red herring part but --

MR. FURLOTTE: If that's not putting the answer in his mouth what is?

THE COURT: Well that's being a bit leading I think Mr. Walsh.

MR. WALSH: Perhaps I could ask another question Doctor.

THE COURT: I recall the witness yesterday saying there was some statement in the report that he was trying to find and he didn't have an opportunity to find it.

MR. WALSH: Exactly.

THE COURT: You're suggesting --

MR. WALSH: I want to know --

THE COURT: What you are trying to find out is is this the question -- is this the statement --

MR. WALSH: The statement that he was looking for. That's correct My Lord. I didn't consider it to be --

THE COURT: Well why don't you perhaps put it in this way. Does that statement have any significance in relation to the evidence you have given in this case. And if

the witness says well that's the statement I was trying to find yesterday okay, but it may or may not be, I don't know. You have some reason to believe presumably that --

MR. WALSH: Well the major question I had in relation to this, My Lord, I'll put it in this particular fashion. Doctor you have read the OTA report?

A. Yes.

Q. You indicated that you read it. I just read you a statement from the OTA report that apparently extolls the virtues of DNA typing, am I correct?

A. Yes.

Q. Can you tell us, Doctor, having read the report whether or not there are other statements in this particular report that do the same thing?

A. Yes, there are, throughout the report.

Q. Thank you. Now, Doctor, I wish to go on to a couple other areas. Mr. Furlotte referred quite indepth with respect to band shifting and the probability of the bands shifting, etc. in his cross-examination. What, in your opinion Doctor, is the probability of band shifting going undetected in the R.C.M.P. RFLP system across multiple loci?

A. I think that's the beauty of looking at more than one locus where we say that band shifting can occur at an individual locus and it's theoretically possible that if you misinterpreted the results that you could draw an erroneous conclusion. When you look at multiple loci you would have to invoke band shifting consistently doing something that you would misinterpret at each and every locus. So I think that's the beauty

of the technology that you are looking at multiple tests and that anomalies would have to occur in a consistent manner and you would have to misinterpret them over and over again. It's just so unlikely that that would be a problem over multiple loci.

Q. What, Doctor, in your opinion is the probability of band shifting creating a false positive across multiple loci?

A. Again, you would have to repeatedly misinterpret the results over and over again for it to be a problem.

Q. What, if any, effect does the size of the match window of the R.C.M.P. RFLP system have on your opinion with respect to the possibility of false positives across several loci?

A. As I said before, the match window really has very little impact on calling the match itself. It's a tool to substantiate what you have called visually but it generally has no impact on what you have called visually.

Q. Mr. Furlotte referred you this morning to the Promega paper which I believe is VD-50, and he also referred you to the fixed bin paper which I believe was VD-54. With respect to VD-50 he referred you to some tables at the back of that particular publication, am I correct?

A. Yes.

Q. And those tables I understand, Doctor, refer to findings of excess homozygosity?

A. Excess observed single band patterns to be more correct.

Q. Okay. And you indicated that that is not an appropriate test or it has been a finding that it has not been an appropriate test.

A. Yes. There has been several publications to that effect since this was written that that really is not an appropriate test for defining whether a population is in Hardy-Weinberg equilibrium or not.

Q. And did that -- What does the term Wahlunds effect - Wahlund spelled W-a-h-l-u-n-d-s I believe - what does the Wahlunds effect - what does that mean in relation to that particular table or the findings there?

A. That is a situation or an observation that true excess homozygosity can be the result of subpopulation structure and a population that's not in Hardy-Weinberg equilibrium. Again, I emphasis that true excess homozygosity.

Q. And I want to refer you to VD-53. It's entitled "No Excess of Homozygosity at Loci Used for DNA Fingerprinting". What relevance does that paper have to your statements to Mr. Furlotte with respect to your findings in the Promega paper and in relation to your answers to me immediately preceding?

A. Well I think it's summarized quite nicely in the last paragraph of the paper what they did and what their conclusions and why they did when they say that:

> "It has been argued that a homozygote excess implies absence of Hardy-Weinberg, nullifying the validity of multiplication across loci as well as within loci."

And that was the arguments that were made by Doctor Lander several years ago in his initial criticisms of the statistical analyses of VNTR loci. It goes on to say:

> "Although the results presented here do not prove multiplicability across loci, they do prove that the arguments so far presented against it are incorrect."

So basically what they are saying is that they have done experiments that differentiate between this phenomenon of actual excess homozygosity and artificial or artifactual excess homozygosity as it applies to VNTRs and what they find out is that there really isn't a real excess homozygosity for the loci that we're using forensically. What it is, it's an artifact of the techniques being used.

Q. How does that paper impact on your thoughts at the time that you were writing the Promega paper at least as you have stated in the Promega paper?

A. On the Promega paper and in other papers presented at that time people had observed that there was an excess of single band patterns in the Promega paper as well as other peoples' publications rational reasons for this apparent excess of single band patterns were given. What they have done in this paper is they have actually taken it a little step further and tried to analyze just what is happening and they in fact did show why there was an apparent excess of homozygotes.

Q. How does that paper reflect your own opinions?

A. They formally prove one of the explanations that we had suggested for this observation.

Q. Are you familiar with the Jakobetz case - United States V. Jakobetz?

A. I have read parts of the proceedings, yes.

Q. I will read a statement from that particular case and I would ask you, if you would Doctor, please, to explain what relevance it would have to the VD-54 which I have just referred to you and to the part of the Promega paper dealing with real or artifactual single bands.

MR. FURLOTTE: Is that statement something I covered in cross-examination?

MR. WALSH: Well, I don't think it's necessary, My Lord, that I actually cover every statement provided I'm covering an area Mr. Furlotte raised in cross-examination that I had not raised in direct.

MR. FURLOTTE: Well, My Lord, I believe the crown introduced this paper into evidence through Doctor Waye and he covered it on direct examination. I don't think he should have the opportunity to cover it all over again after cross-examination.

THE COURT: What particular area of new evidence --

MR. WALSH: I'm dealing with the actual area that Mr. Furlotte dealt with this morning and he had dealt with previously, if you remember, the paper dealing with the "No Excess of Homozygosity" for VNTR loci. VD-54, was actually introduced during the cross-- 53, excuse me, 53 was actually introduced through Mr. Furlotte's cross-examination. During his cross-examination that paper was actually introduced into evidence and if you remember, My Lord, it was one of those situations where he had been dealing with it at some length and that he was given the opportunity to deal with it when he came back for cross-examination.

THE COURT: Well, I must confess I can't precisely recall how it went but go ahead and ask and if Mr. Furlotte wants an opportunity perhaps to ask a further question or two then we will give him that opportunity.

MR. WALSH: It says on page 260 of the United States V. Jakobetz, footnote 20:

> "In other DNA profiling cases, much debate centered on whether the population was in Hardy-Weinberg equilibrium, recognized as a prerequisite to using the product rule. See Castro; Wesley (and there is reference to the case citation). Recently, however, there has been general agreement that Hardy-Weinberg is a poor test for substructuring, at least with the sample sizes involved here. In this case, government experts Dr. Budowle and Dr. Conneally are in apparent agreement with defense experts Dr. Lewontin and Dr. Nadeau over the shortcomings of relying on Hardy-Weinberg equilibrium. In light of this consensus, it is unnecessary -- and this court happily declines -- to blaze a trail through this thicket of true homozygosity versus single bands."

Could you explain, Doctor, what, if any, relevance that statement has to the issues set out in VD-53 and tables in the Promega paper, VD-50?

A. What it does is it basically brings the controversy up to date. This is an issue that has been hashed over both in the courts and in the literature over and over again and I think the judge is just expressing his relief that both defence and prosecution have come - experts have come to an agreement that the tests that are being used to evaluate Hardy-Weinberg equilibrium are not appropriate nor are they relevant to this issue of population substructure.

Q. That summary that I have read, does that confirm or is it different than the opinions you have expressed with respect to VD-53 and the impact on the Promega paper?

A. They were done at different times. It doesn't - certainly doesn't change the views that we express. It was perceived as a problem and we investigated, as did others. I think at the end everyone agreed that it really isn't a big problem.

THE COURT: What was the date of the Jakobetz decision?

MR. WALSH: September 20th, 1990 My Lord. I have no further questions with respect to this aspect My Lord.

THE COURT: Thank you very much Mr. Walsh. Now, you are recalling Doctor Waye to the stand to examine on the case - his case specific knowledge or evidence.

MR. WALSH: That's correct My Lord.

THE COURT: It's 10 to 11; do you want a short break here before you start and then do it all up before lunch?

MR. WALSH: That's fine My Lord. That will be fine.

THE COURT: Is that more agreeable than carrying on for 10 minutes and then breaking?

MR. FURLOTTE: That's probably --

THE COURT: Well let's take a break then.

(RECESS - 10:50 - 11:20 A.M.)

COURT RESUMES: (Accused present in prisoner's dock.)

THE COURT: Okay Mr. Walsh.

DR. WAYE CONTINUED ON DIRECT EXAMINATION BY MR. WALSH:

Q. Doctor Waye did you have any involvement with respect to reviewing the case specific evidence, that is the case of The Queen V. Allan Joseph Legere?

A. At various times in the testing I have looked at the autorads.

Q. The original autorads?

A. Yes. I have looked at duplicates as well.

Q. I show you VD-54 Doctor. I'll take it out of its plastic sleeve. Would you look at that document for me, please, and tell me whether or not you recognize that.

A. Yes, I recognize it.

Q. And what is it?

A. It's a lab report relating to this case.

Q. Prepared by whom?

A. Doctor Bowen.

Q. You had occasion to review that report?

A. Yes, I have looked at this report.

Q. And have you had occasion to look at the original autorads from which that report was prepared?

A. Yes, I have looked at the autorads.

Q. And have you had an opportunity to review the calculations made with respect to the statistical significance of any of the matches that are shown there?

A. Yes, I have.

Q. Would you tell me, please, Doctor what opinion, if any, you have with respect to the conclusions that Doctor Bowen drew which are set out in that particular report?

A. I'm in agreement with the matches that were called by Doctor Bowen, the logic he used to define the matches, and the statistical approach he used to put frequencies to the matches.

Q. Do you have any reservations with respect to that opinion?

A. No.

Q. Have you had occasion to look at the computer quantification, that is the sizings, associated with the matches that were called by Doctor Bowen and that are set out in the report?

A. Yes, I have looked at the sizings of the bands, yes.

Q. And with respect to the first blot - and when I talk about first blot for the record it's set in the chart marked VD-88, blot 890L1191-6. Have you had occasion

to look at the sizings with respect to the matches that were called on that blot?

A. Yes, I have looked at the sizings.

Q. And could you tell me, please, what opinion you arrived at after looking at the sizings with respect to the match window of the R.C.M.P. in relation to the lane to lane comparisons that are set out in that blot?

A. The sizings were well within the match window and, as I said before, the match window generally has no effect on what you call visually and in this case it didn't as well.

Q. When you say well within the match window do you remember what the -- not each individual one, but do you - when you say well within what are you referring to?

A. Well the match window is 5.2% that was used at the time in this case and it is my recollection, and I can't quote specific numbers, but generally we are talking values that were somewhere between zero percent difference and 1 or 2% difference. They're well within that 5% window.

Q. Did you have occasion to review - you have indicated that you have - I want to refer you to the second blot, which we refer to as the second blot. The blot number is --

THE COURT: 1191-14.

MR. WALSH: 1191-13 My Lord.

THE COURT: 13.

MR. WALSH: 13. Do you remember looking at that particular blot Doctor?

A. I looked at a number of blots. I believe I looked at all of them so --

Q. I would refer you to VD-55 and perhaps if you would just look at the second section of VD-55. VD-55 has been shown to be duplicates of the originals.

A. Yes, I have looked at this before.

Q. And you are looking at the second section of VD-55. Do you remember having any occasion to look at the sizings with respect to the lane to lane comparisons made in that particular blot?

A. Yes, I looked at the sizings.

Q. And what conclusion did you arrive at with respect to the sizings associated with the lane to lane comparisons made in that blot?

A. Again, they simply verify what my eyes had already told me, that they were matches and they would fall within the window. That was the expectation; that was in fact what was observed.

Q. And do you remember how far inside the window they fell?

A. It is my recollection that it was pretty much the same situation as with the first blot. They were well inside that 5.2% match window that was used at this time.

Q. Did you have occasion to make any comparison between this particular blot - the second blot - and the blot marked on the chart VD-88?

A. A comparison of the sizes?

Q. Of the standards. Of the standards set out in that particular blot compared to the standards set out in VD-88?

A. I made those comparisons, yes.

Q. And did you look at the sizings associated with that comparison?

A. Yes.

Q. And, first of all, what conclusion did you draw with respect to as to whether or not there was any matches?

A. Again, the sizing had very little effect on the judgments that had been made visually just looking at the patterns and comparing blot to blot. Again, that's not the optimal way to do a comparison blot to blot but at times you are forced into that situation where DNAs are analyzed on different blots. What generally happens and what we have published prior as an observation is that the sizing differences tend to increase when you are comparing things that are either on the same gel but between different flanking markers or on different gels.

Q. And with respect to the gel to gel comparison that you made does this observation hold true in terms of the size difference within the match window?

A. Yes.

Q. Doctor did you have occasion to look -- Perhaps I'll refer you to VD-56, the first section gel number 3, membrane number 3. Would you look at that for me, please, and tell me the first section of VD-56 whether or not you had occasion to review the originals, duplicates of which are set out in that particular exhibit?

A. Yeah. I can't remember whether I actually looked at duplicates or originals but I looked at a series of autorads. It really doesn't matter whether it's a duplicate or original.

Q. In this particular case, Doctor, the evidence or at least from the report and the evidence that there was an exclusion between the standard run and the one evidence sample, did you make any notes with respect to the sizings or the comparison between the standards - the known standard purporting to come from Allan Legere on that particular blot and the first blot - the known standard on the first blot?

A. Yes. Those were amongst the data that I looked at. I didn't analyze it myself.

Q. Did you notice -- Were you able to determine if there was any difference in terms of the match window whether or not any of the standards or samples fell outside or were inside the match window on the third blot when it's compared to the first blot?

A. I believe there was one value that exceeded the 5.2 window. One difference between a standard on this particular autorad and the previous one.

Q. What if any effect would that have on your opinion with respect to the validity of the matches found in the first blot?

A. Doesn't compromise it in any way. In fact, as we said before, these differences increase when you are making blot to blot comparisons and that's well within observed values that we have generated in the lab.

Q. What, if any, opinion - or what, if any, effect does the fact that one of the bands fell outside the match window on the third blot - one of the purportedly known standards of Allan Legere fell outside the match window, what effect does that have on your opinion with respect to the validity of the R.C.M.P. system

to produce reproducible results?

A. There is absolutely no effect. It doesn't compromise or test its reliability or its validity.

Q. What conclusions, Doctor, would you draw from the matches -- I refer you again to VD-54. I refer you to page 5 of that particular report. With respect to the matches at page 5 what, if any, conclusions would you draw from the statement that:

> "For the DNA typing profile obtained from exhibit 1J (D1S7, D4S139, D10S28 and D17S79 match that of exhibit 56A-69A) the estimated frequency of occurrence in the Caucasian population is less than 1 in 5.2 million male Caucasians."

What conclusions do you draw from that particular statement for which you have already indicated that you agree?

A. What would be my opinion or conclusion or --

Q. Yes, what is your opinion with respect to the statistical significance that's associated with those matches?

A. Well, it's --

Q. What does that mean to you between the exhibit 1J and the exhibit 56A-69A?

A. To my mind what this says in a very scientific manner is that you have associated - you have matched one exhibit to another exhibit and you have defined that. The chances of that match being fortuitous is very rare, 1 in 5.2 million. Extremely rare.

Q. I refer you again on page 5 to the statement:

> "For the DNA typing profile obtained from exhibit 135 (D1S7, D2S44, D4S139, D10S28 and D17S79 match that of exhibit 56A-69A), the estimated frequency of occurrence in the Caucasian population is less than 1 in 310 million male Caucasians."

What, if any, conclusions do you draw or opinions you have with respect to that statement for which you have indicated that you agree as to the meaning to be associated between that finding in relation to exhibit 135 and exhibit 56A-69A?

A. Again, a forensic exhibit has been linked to a standard and the analysis - a match at 5 such loci is even more rare than the previous 4 probe matching. In fact in this case it's some sixty fold more rare than the one in 5.2 million events so it's an even rarer occurrence.

THE COURT: Your questions have become a little convoluted there, Mr. Walsh, and I'm not sure just what it is that the witness is agreeing with. Is he agreeing with the fact that the 1 in 310 million figure is the correct figure to use or --

MR. WALSH: My understanding, My Lord, I apologize if my questions have come out convoluted --

THE COURT: Well only because you were trying to crowd too much into the one --

MR. WALSH: I wanted to make sure that it was phrased correctly and sometimes it's necessary to add qualifiers. My understanding of the doctor's testimony up until this point when he indicated that he reviewed the report and that he agreed with the conclusions that the Doctor had drawn in that report - what I was attempting to elicit from the doctor is what in his mind what, if any, qualitative statement he would associate with that particular finding. And he has answered the question that I had put to him in the terms that he's associated - a qualitative statement associated with rareness.

MR. FURLOTTE: My Lord for the record I would object to the expert witnesses giving their qualitative statements associated with rare, extremely rare, remote or extremely remote or anything else. I don't think they have been qualified as experts to give that opinion and that's an opinion that any man off the street can give. You don't have to be an expert to qualify a figure as to whether it's rare or extremely rare. And I don't think this is a proper matter for these expert witnesses.

THE COURT: Well, that's sort of by the way here. The figure you're using or the figure you are essentially interested in is the figure of 1 in 310 million.

MR. WALSH: Yes, My Lord. Just so I can clarify the crown's position, we will be arguing, My Lord, that the expert witness — The position the crown will be taking is that the expert witnesses should be entitled to express their opinion in a qualitative form as to what a particular match means to them. Their own opinion. Whatever phraseology or phrases they wish to use. That that particular opinion should be supported by reference to probability figures. Statistical significance. So that the statement that's made by the expert can be weighed by the fact-finder in terms of comparing the opinion that's been given with the --

THE COURT: Well what would you want - or I guess what the witness has said is that he considers 1 in 310 million extremely rare. And I think we would all agree, Mr. Furlotte, that surely that would be extremely rare, wouldn't it?

MR. FURLOTTE: Well, Doctor Carmody figures a figure of 1 in --

THE COURT: Well you say that any man on the street --

MR. FURLOTTE: Yeah, but Doctor Carmody figures the figure of 1 in 10,000 rare enough to convict beyond a reasonable doubt and I don't think we should be getting into this. This is not what they were called on this hearing to give.

THE COURT: Well I'm not greatly concerned here with --

MR. FURLOTTE: It's whether the figures are valid or not. It's not whether their opinion is valid.

THE COURT: Well, I can see no harm in the witness saying look, I look on that as extremely rare. If the time comes in this trial that I've got to charge a jury on these figures or on relativity of rareness I'll have to concoct my own definitions anyway.

MR. WALSH: Yes, My Lord. Again, so Mr. Furlotte understands, we're not asking and we're not attempting to get the witness to make any statements with respect to what is or is not beyond a reasonable doubt or what is or is not beyond a reasonable doubt associated with guilt. Those are all things that Mr. Furlotte has raised in relation to Doctor Carmody. We're simply attempting to find out here what the significance is of a declared match.

THE COURT: Well, go ahead here. Go ahead.

MR. WALSH: Well, if I am correct My Lord, if I understand correctly I believe the doctor has answered the question. I apologize if they were convoluted but that was the purpose behind the questions, to get a qualitative statement associated with it.

THE COURT: Okay.

MR. WALSH: Doctor, what, if any, band shifting did you observe with respect to VD-88. This is the first blot here.

A. When I scored those blots there was no apparent visible band shifting.

Q. And what, if any, band shifting did appear to you with respect to the second blot, that would be 890L1191-13 I believe it was.

A. That was the standards compared to the standards?

Q. Yes.

A. There was no significant band shifting as well.

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

THE COURT: Now, cross-examination Mr. Furlotte.

MR. FURLOTTE: Can I have a short recess My Lord? I wasn't expecting --

THE COURT: We just had --

MR. FURLOTTE: I wasn't expecting Mr. Walsh to finish up so quick. Five minutes.

THE COURT: All right then.

(RECESS - 11:40 A.M. - 12:05 P.M.)

COURT RESUMES: (Accused present in prisoner's dock.)

THE COURT: Now Mr. Furlotte.

MR. FURLOTTE: Yes, My Lord. My Lord I have the November, 1990 draft of the Fixed Bin Analysis for Statistical Evaluation.

THE COURT: This is the draft of VD-54, is it?

MR. FURLOTTE: 49A. Yes, it's a draft of exhibit VD-49. 49A is the published version and this is the original draft version which maybe we can just put it as 49B.

THE COURT: All right, but is it acknowledged by the crown as --

MR. WALSH: I have no objections to that being entered My Lord.

THE COURT: As a draft.

MR. WALSH: As a draft.

THE COURT: And this is recognized as a draft version of VD-49A.

MR. FURLOTTE: Yes.

THE COURT: So we will call that VD-49B.

CROSS-EXAMINATION BY MR. FURLOTTE:

Q. Now, Doctor Waye, when were you contacted to review the reports and the autorads prepared by Doctor Bowen?

A. At various times I surveyed some of the work that was done. First, while I was still in the employ of the R.C.M.P. so that would be prior to January 15th, 1990. I looked at results that were obtained up to that date.

Q. Up to that time?

A. I believe at some point I was in Ottawa on an unrelated matter in December of last year and I looked at data that had been collected to that point. And the last time that I was in this court I looked at materials that were done I guess up to that point.

Q. Do you have any notes as to which day in December that you had did another review?

A. If I look at my calendar I can tell you the days that I was -- I might be able to tell you the days that I was --

Q. Okay.

A. This is my 1991 calendar. So I don't -- I would have that information at home, and I certainly would have it.

Q. Was it before or after Doctor Bowen made his final report?

A. I can't recall.

THE COURT: Are you talking about -- You're talking about '91?

MR. FURLOTTE: I'm talking about 1990. December, 1990.

THE COURT: '90, rather.

MR FURLOTTE: It appears, Doctor, that this project was put on hold in December of 1989 before you left the Ottawa Lab.

A. Again, I didn't do the case. I don't know the exact flow of when the experiments were done.

Q. After D16S85 was probed in December, roughly December 5th, 1989, nothing further was done until November, 1990 - or I believe October of 1990.

A. That may or may not be the case. Again, I --

Q. You don't know.

A. I don't know. I don't know whether that in fact happened or what the reason was if it did happen.

Q. Do you recall the reason why you found D16S85 inconclusive?

A. Why I found it inconclusive?

Q. Yes.

A. I didn't score any matches.

Q. But you reviewed Doctor Bowen's notes; you reviewed the autorads; and you agreed with his assessment?

A. Well what I did - precisely what I did was I looked at the autorads by myself and made visual calls independent of Doctor Bowen.

Q. Did you make any notes of what your calls were?

A. No.

Q. You didn't make any notes. All you can say is that you agreed with everything Doctor Bowen found.

A. I made the same calls that he made, issued in his report.

Q. Okay. He called D16S85 inconclusive. Did you make the same call?

A. Again, I would have to look at what I scored. What I scored as matches were the same as his. I can't tell you right now which lane and which things I didn't call matched. I don't even know what the exhibit numbers meant when I called them. So --

Q. So basically what you are saying, Doctor Bowen - you knew which matches that he scored as a match and you said yup, that's fine with me?

A. No, I didn't.

Q. Is that basically the way you did it?

A. I'm pretty much -- I'm pretty convinced that that's not what I just said. What I did is I looked at the auto-rads without him present and made my calls and was told after each call I made that yes, that's an agreement. That's how I know that it was an agreement. I didn't look at the end result, look at the autorad and say yeah, I agree.

Q. So you would have looked at all these here, D2S44, for each exhibit item and you would have made the call inconclusive, inconclusive, inconclusive, and then match. Is that the way you went about it or did you just know which matches he made and just decided on the matches?

A. I just finished saying that I didn't know which matches he made.

Q. But yet you made all the same calls he did.

A. I said I made the same matches and went through the same thought processes as Doctor Bowen.

Q. Did you make any matches that he didn't make?

A. No. Matches that I called I was informed that they were the same matches that he called after I had made them.

Q. So you don't recall why you didn't make any -- why you ruled some of these were inconclusive in your mind?

A. For the --

Q. All the little stars are inconclusive.

A. As I said, I looked at the autorads that were given to me. I can't remember each lane. I can't even remember what these codes in fact mean. So recalling what each little star is is an exercise in futility. I haven't committed what I did to memory.

Q. And you didn't make any notes?

A. No, I didn't.

MR. FURLOTTE: I have no further questions.

THE COURT: Reexamination?

MR. WALSH: No, My Lord.

THE COURT: Well, thank you very much Doctor Waye. That's all for you, at last. Now you can go and attend to - what did I describe it - your family life.

MR. WALSH: My Lord I would inform the court, I had made a promise earlier that we would not have any disruptions. I'm in a situation now where we have completed somewhat earlier than I had anticipated. I have Doctor Kidd here - he just arrived - however, I haven't had an opportunity to prepare with Doctor Kidd my direct examination and I would ask the court for that

indulgence. I had projected to start tomorrow morning and that's the schedule that I'm on. Doctor Kidd needs some time to review some of the exhibits that are filed and things of that particular nature. I would ask the court's indulgence to be able to begin tomorrow morning and I'm prepared to begin early tomorrow morning if the court would so wish to sit early.

THE COURT: Have you talked to your witness, Dr. Kidd?

MR. WALSH: I just said hello to him just before I came into court here a few minutes ago. He just arrived.

THE COURT: But is he - how is his physical condition? You indicated earlier he had been ill.

MR. WALSH: Yes, he's prepared to testify. I haven't had a chance other than to simply say hello to him.

THE COURT: I'm just wondering about a long day tomorrow. Perhaps he would prefer to do an hour this afternoon, later, or an hour and a half --

MR. WALSH: If the court would excuse me just for a couple of minutes and I'll go out and see if he is still in my office and if he is I will ask him.

THE COURT: Well just hold on a minute until we consider this though. What I would very much like to see happen is if we would deal with him completely by Friday afternoon - be finished with him Friday afternoon so, (a) so he could get away and so the rest of us can get away, and we don't want to be dragging over the weekend and having to bring him back or keep him here for the weekend.

(Discussion re calling of Dr. Kidd.)

MR. WALSH: I spoke to Dr. Kidd. He is prepared to - he says to give a cushion on the other end he's prepared to start at 3 o'clock today if it is agreeable to the court. There would only be one condition. Dr. Kidd needs time, and he was going to devote it this afternoon, so he will do it tonight, he needs time to go over the original autorads and to refresh his memory with respect to the case specific evidence. Now if the court would agree I can put him on the stand beginning at 3 o'clock. I can cover my area of direct examination up to the case specific evidence but then Dr. Kidd would need the permission of the court to review this evidence this evening before I went through that direct tomorrow morning with him. If that's fair. Because normally the rule is that once I put him on --

THE COURT: That sounds -- Your examination this afternoon would be as to the general aspects of DNA typing.

MR. WALSH: Yes, and I would get as far as I possibly can on that and then tomorrow morning I will either finish off on that aspect and then go into the case specific or I may get to a point this afternoon up to the case specific. The only condition would be that Dr. Kidd be entitled to review this evening the case specific evidence. He says normally he would like to do that. And he would devote this afternoon to doing that. So that would be the only condition. If the court doesn't feel that's appropriate then I would ask the court permission to start at 9 o'clock in the morning.

THE COURT: Well I see no problem with it myself. Mr. Furlotte can we accept Mr. Walsh's undertaking that he won't coach Dr. Kidd as to anything he might have forgotten to say this afternoon?

MR. FURLOTTE: I hardly think it would be Mr. Walsh that would be coaching Dr. Kidd. It might be vice versa maybe.

MR. WALSH: There's very few things, My Lord, that I would be able to say to Dr. Kidd that, even if I wanted to, would have any bearing on this particular matter.

(NOON RECESS - 12:30 to 3:00 P.M.)

COURT RESUMES: (Accused present in prisoner's dock.)

THE COURT: Now, you had another witness Mr. Walsh.

MR. WALSH: Yes, My Lord, I call Doctor Kenneth Kidd.

DOCTOR KENNETH KIDD, called as a witness on the voir dire, having been duly sworn, testified as follows:

DIRECT EXAMINATION BY MR. WALSH:

Q. Would you give the court your name, please?

A. Kenneth K. Kidd.

Q. Doctor Kidd my understanding is you are a Professor of Human Genetics, Psychiatry, and Biology, at the Yale University School of Medicine, is that correct?

A. That's correct.

Q. I show you this document here Doctor. Would you look at it and tell me if you can identify it?

A. Yes. This is a copy of my curriculum vitae.

MR. WALSH: My Lord I move to have this entered.

THE COURT: Okay, that would be exhibit VD-114.

(Clerk marks C.V. of Dr. Kidd VD-114.)

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

THE COURT: Yes, go ahead.

MR. WALSH: Doctor, you have a Masters and a Ph.D. both in Genetics from the University of Wisconsin, is that correct?

A. That's correct.

Q. Your major or your specializations were in immunogenetics and population genetics, am I correct?

A. That's correct.

Q. That you did - you were an NIH Postdoctoral Fellow with L.L. Cavalli-Sforza at the Institute of Genetics at the University of Pavia, in Pavia, Italy.

A. Correct. And also with him at Stanford University. During the middle of my time with him he moved and became a Professor of Genetics at Stanford and I moved with him back to the United States.

Q. And my understanding that your Postdoctoral Fellowship was in Human Population Genetics?

A. That's correct.

Q. And who is Cavalli-Sforza in terms of the scientific community? What reputation does he have in relation to Human Population genetics?

A. He is one of the foremost experts in human population genetics. He wrote with Walter Bodmer, published in 1971, a book entitled "The Genetics of Human Populations" which was virtually the bible of the field and has yet to be completely superseded despite all the 20 years of accumulated knowledge since then. He's a member of the National Academy of Sciences and a very senior and well respected person.

Q. Doctor, what if any difference would there be between a population geneticist and a human population geneticist?

A. Certainly the mere inclusion of the word human population genetics the word human in that limits it more to the specific problems of the population

genetics of humans as a species. Population genetics can range all the way from very theoretical and purely mathematical population genetics to studies of individual organisms, drosophila, plants, fish. In this case the specialty is humans and every different kind of organism has its unique characteristics that affect how one has to apply population genetics theory in studying that organism.

Q. The C.V. shows that during your time at Stanford and Italy that you were an NIH Postdoctoral Fellow. Could you tell the court what that is, please?

A. The United States National Institutes of Health awards Postdoctoral Fellowships to individual students on the basis of competition. A relatively small number are awarded. And I applied for one and was one of those who was awarded such a fellowship.

Q. You were also a Research Associate, Department of Genetics at Stanford University School of Medicine with Professor Cavalli-Sforza?

A. Right. The NIH Fellowship was for two years and I stayed on working with him for a third year and so my title changed but the kind of work I was doing did not.

Q. You were also Assistant Professor of Anthropology and Pediatrics at Washington University and the Washington University School of Medicine in St. Louis?

A. Right. That was my first faculty appointment which reflects the two different areas of specialty I have; one is human evolution and human population genetics and the other is more medically-oriented human genetics. So I had appointments both in the medical school and in anthropology.

Q. I see, Doctor, you were at one time Assistant Professor of Human Genetics at Yale University School of Medicine and that was between 1973 and 1978, is that correct?

A. Right. I was recruited away from St. Louis by Yale and moved there in 1973 and I have been there ever since, first as Assistant Professor, then Associate Professor, and now as full professor with also joint appointments in Psychiatry and Biology.

Q. And, as well, you were - or I see Doctor that you were at one period between 1981 and 1982 a Visiting Associate Professor at the Harvard Medical School and a visiting scientist in the Biology Department of MIT, is that correct?

A. That's correct. That was the year I was on sabbatical from Yale and I was retraining myself in the new molecular genetic techniques and was studying at both Harvard and MIT.

Q. And as a Professor of Human Genetics, Psychiatry and Biology at the Yale University School of Medicine what role do you play there or do your duties involve there in relation to DNA or DNA typing?

A. Yale is very much a research university and in the medical school I have little obligation for undergraduate teaching so that most of my teaching role is in conjunction with conducting research, and my research is almost entirely related to molecular biology and human population genetics.

Q. You work in a particular lab there and I understand that is called the Kidd Lab.

A. That's simply the name the people working in my lab give it to distinguish it from the Eisenstat lab down the hall headed by Professor Eisenstat. I have -- It varies almost every month with students and post-docs arriving and leaving but somewhere between 16 and 21 people in my laboratory, including postdoctoral fellows, graduate students, visiting scientists, technicians, research faculty who work in my lab under me, people who also have a Ph.D. but work for me.

Q. What are the major areas of research interest of your lab Doctor?

A. Right now I commonly think of it as three or four different areas. We're doing a great deal of work on genetic linkage mapping, putting together the genetic map of Homo sapiens using DNA polymorphisms as the markers. We have used and are using that technique to try to identify genes that cause complex human disorders. Some of those are the neuropsychiatric disorders like schizophrenia and Tourette syndrome but one of them is an inherited form of cancer where we have mapped the gene to a small region of a particular chromosome and are now trying to use molecular biology techniques to isolate the gene the way the cystic fibrosis gene and the neurofibromatosis genes have been isolated in the last couple of years. And --

Q. These molecular -- Go ahead Doctor.

A. And then the final area involves -- Well actually I skipped one area. One is a very detailed molecular study of a particular region of a particular chromosome that we are interested in because of its developmental significance in early human development.

And the final area is the human population studies where we have continued to collaborate with Cavalli-Sforza and his lab and my lab have now assembled a collection of something in excess of 800 cell lines established on humans from around the world and we are studying those samples for dozens to a hundred or more different DNA markers.

Q. You indicated that, for example, you are attempting to isolate the genetic cause for this particular form of cancer. You indicated, Doctor, that you were using molecular biological techniques to do this. What kind of techniques would you be using?

A. The whole panoply of modern recombinant DNA and molecular techniques, cloning, PCR - polymerase chain reaction. We are screening yak libraries, yeast artificial chromosomes. We're doing DNA sequencing.

Q. What, if any, work do you do with RFLP?

A. Well, the RFLPs are the way in which we found where that gene was initially. It's the work we are doing with the population studies. It's the work we're doing with the psychiatric studies. We have identified and characterized a large number of new RFLPs and published them. We have used a large number of RFLPs identified by other people. We have currently studied - I think the latest estimate we have studied we have used in the laboratory more than 250 different RFLP systems, each one typed on between 100 and 500 people. So we have done in my laboratory over the last six years several hundred thousand RFLP typings.

Q. Doctor I see in your memberships and professional organizations that you are a member of the "Genetics Society of America".

A. Yes.

Q. And the "American Genetic Association" you're a council member?

A. Correct.

Q. Is there any difference between simply being a council member or a member of that particular organization?

A. The council is the governing board of that society and there is a ballot among the members to elect members for three year terms and I was elected for a three year term.

Q. You are also a fellow of the "American Association for the Advancement of Science", am I correct?

A. That's correct.

Q. What, if any, differences are there between simply being a member which you were for a period and now being a fellow of that society? Or of that Association.

A. Being elected a fellow is considered an honor and is based on nomination and evaluation of credentials for having made a major contribution to American science, and being a fellow is limited to no more than 10% of the membership.

Q. You are also, Doctor, a member of the "Human Genome Organization", the acronym being HUGO?

A. Correct.

Q. Could you explain what the Human Genome Organization is Doctor, and the extent of its membership and how you become a member?

A. It is an organization - an international organization that has been formed to try to coordinate human genome research on an international scale and its membership is limited to only people who are very active in that area of research and already contributing significantly to the advancement of knowledge in that area. Membership is by nomination and election and I think at the moment there are only about three hundred people who belong to it around the world.

Q. Doctor you are also, I see, a member of the "Mammalian Genetics Study Section", NIH. I understand that you were a charter member of that organization.

A. The study sections at NIH are the grant-reviewing boards of scientists and in the late 1970s it was clear that human genetics and mouse genetics were becoming very specialized and very important areas of genetics so a new study section was formed of people who had expertise in that area to review forthcoming scientific studies for funding, and I was a member of that for four years.

Q. You also, Doctor, were a member of the Board of Directors of the "American Board of Medical Genetics".

A. Right.

Q. Would you explain medical genetics and how it applies in terms of the field of molecular genetics for example?

A. Well molecular genetics is revolutionizing medical genetics right now but medical genetics is inherited human disease. How to identify it; how to treat it; how to study it; interacting with patients. And the

American Board of Medical Genetics is the accreditation agency that certifies individuals as having expertise so that they can meet the legal requirements for being reimbursed by insurance agencies; meet the legal requirements for holding positions as director of a clinic in a hospital setting; and I was certified by that and board membership is by election, again, among the individuals who are certified, and the board is responsible for keeping the exam up to date and administering and in turn certifying other people.

Q. You are yourself board-certified with the American Board of Medical Genetics as a medical geneticist?

A. Correct. Which means that I am considered by that board qualified to supervise a genetics clinic.

Q. You are also on the Editorial Board of the Journal of Genetics?

A. Yes.

Q. You were on the Editorial Board of Genomics. You are not a member now?

A. That's correct. I rotated off. It's a rotating position.

Q. You were, I see, a Special Consultant to the Howard Hughes Medical Institute serving as Scientific Director for the Human Gene Mapping Library. Would you explain what that is, Doctor, and what relevance it would have to what we are dealing with here?

A. The Human Gene Mapping Library started at Yale in the mid seventies as a computer data base on human gene mapping and grew quite rapidly in the early eighties. It was funded by the National Institutes of Health for several years and then funding for a few years

was taken over by the Howard Hughes Medical Institute. I was part of the scientific direction of that for many years and then I took over basically for two years, the final two years before the project ended, and ran the entire operation. In part, it was a staff of 15 people and a huge data base and my particular responsibility in that data base was the design and the management of the RFLP component of the data base. I started working with RFLPs when there were only 16 total known and at the time the data base ended and the data were transferred into a different more elaborate system we had two thousand five hundred RFLP systems catalogued in the computer system.

Q. I show you, Doctor, VD-27 which is a chart presently hidden and I'll reveal it. It's a chart depicting Schematic of chromosomes or probes in relation to chromosomes, and the human gene mapping library - what relevance would that have to the probe designations that you see on VD-27?

THE COURT: Perhaps you would like to give that a little twist there.

A. I can see it fine.

THE COURT: Can you see it all right?

A. Yes. I don't need to see it too closely to know what it's all about because at the time those designations were assigned I was the one responsible for assigning those symbols like D10S28. Those are catalog names, if you will, and for a period of four years I was responsible, given my role in the International Gene Mapping Workshop DNA Committee - I was a member and then chairman of that Committee, it was my responsibility to supervise assigning those numbers.

Q. What do those numbers, if you were looking at this number say D10S28, what does that mean? What are the letter and number designations?

A. I helped devise the symbolism. "D" stands for DNA segment or DNA probe. 10 stands for the chromosome number. The "S" stands for single copy meaning it is a piece of DNA that really occurs only once in the genome. And 28 is the sequential number in which they were entered into the large data base. Sequential single copy probe on chromosome 10. All of the others are the same. D1S7: single copy, DNA segment on chromosome 1, number 7 in the catalog. The only one that's -- The two that are different there, D7Z2 - I guess "Z" - I'm in Canada now - the "Z" stands for a form of repetitive DNA that is isolated into a particular region as opposed to single copy. And the DYZ1 is a form of repetitive DNA on the "Y" chromosome, again, not single copy.

Q. You have touched on it Doctor, I see here that you were Co-Organizer with Frank H. Ruddle of the Tenth International Human Gene Mapping Workshop.

A. That's right.

Q. Would you explain what the Human Gene Mapping Workshop what it is and what it does?

A. The Human Gene Mapping Workshops have been running since 1973 when the first one was held. They moved to different locations every two years and the first one was held at Yale. I attended it. Frank Ruddle organized it. And by the time of the 10th one we requested that it be back at Yale. At that time we had the computer data base located at Yale in which we

cataloging all of these DNA segments and other loci and we used that as support for the meeting. It was an international meeting attended by 700 scientists from around the world. It lasted almost a full week. Frank Ruddle and I were -- He is Chairman of the Biology Department and Professor at Yale. We co-organized it and sort of shared the responsibility of organizing and hosting that meeting. And I also was Chairman of the DNA committee at that meeting and so ran that part of the workshop - that scientific part of the workshop as well.

Q. What application would that have to what we are dealing with here Doctor?

A. Well, it is that body of scientists that really gives the stamp of approval, sort of the ultimate in peer review, that a locus is indeed, as D10S28 is hatched there on the short arm of chromosome 10, that body of scientists will look at the evidence, the publications related to that, and will say yes we accept this as confirmed solid evidence; looks good but it's still provisional; very tentative; we're not ready to accept it yet; or no, not at all, we don't agree. And all of these are confirmed assignments and very well supported in the scientific literature.

Q. Doctor I see from your C.V. that what's here is 236 publications. I understand, Doctor, since this C.V. has been prepared there has been approximately another 20 added to your C.V.?

A. I think it's around 255 right now. I never remember the exact number because it changes every week.

Q. If I could ask you, instead of going through each one, I would just ask you a general question and if you could give me perhaps the percentage of these publications that pertain to DNA markers and/or human population genetics?

A. Let me qualify that slightly and give an estimate for the last hundred because I was not doing any DNA work until 1982 and then it was a couple of years before I started publishing extensively out of my own lab as we got the lab started. But since the last hundred publications, basically the last five or six years, 80 or 90% of those deal with DNA or human population genetics. Some deal with computer data base design; some deal with familial patterns of certain psychiatric disorders; other areas of research; but the overwhelming majority are on DNA.

Q. And I understand, Doctor, as well from your C.V. that you have been into -- you have been dealing with human population genetics since about 1968.

A. I first started working in human population genetics as a graduate student and my first paper is I think number 10 in my C.V. It actually came out, I believe, in 1972 but on analyses of the populations on the Island of Bougainville.

Q. You have, Doctor, given testimony in court on the forensic application of RFLP typing and the human population genetics issues associated therewith, am I correct?

A. Yes. Several times.

Q. And could you just first of all could you tell us what-- I take it that has been in the United States?

A. Yes.

Q. How many States - or could you name some States that you have actually given expert testimony in those fields?

A. I can't tell you the total but I can start enumerating them. New York. Virginia. Colorado. California. Vermont in a federal case. Cleveland in a federal case. That's Ohio. There were actually three in Virginia and two different cases in California.

Q. Are you the same Doctor Kidd who testified in New York V. Wesley?

A. Yes.

Q. Virginia V. Spencer?

A. Yes.

Q. United States V. Jakobetz?

A. Yes.

Q. And United States V. Yee?

A. Yes.

Q. Have you ever consulted for the defence, Doctor?

A. Yes.

Q. And under what circumstances would that have been?

A. I have been asked to evaluate autorads and give an evaluation to defence attorneys in at least three different cases and in none of those cases did the Defence want to put me on the stand so I did not testify but I pointed out to the defence the weaknesses, if any, that I saw in the evidence and advised them as to what I thought their best strategy would be.

Q. Doctor, are you testifying regularly now or have you changed your routine with respect to going to court?

A. I --

Q. If you had a routine going to court.

A. I will be quite frank and say that I have gotten very annoyed at the legal system in the United States and I simply am refusing almost all requests. I must get at least one a week to testify. I could spend all of my time testifying, going over issues that have already been covered in several transcripts that exist but they're in a different jurisdiction so it all has to be done again, and I don't have the time to do it.

Q. Have you been asked to testify in other cases in Canada?

A. Yes.

Q. And have you agreed?

A. No.

Q. Perhaps if you could just touch on when were you requested to assist in this particular case?

A. A year and a half ago. It's well over a year ago.

Q. Does that have a bearing on the fact that you're testifying today?

A. Yes, because I had made a commitment. If I were to be asked today I would almost certainly say no.

Q. Doctor, what is demography, if I have pronounced it right, and what application would that have to population genetics and human population genetics in particular?

A. Demography would be the study of population structure with respect to age and sex differences, reproductive patterns, stratification, and in many of those ways it is very intimately related to human population genetics in terms of issues of stratification; in

terms of population size; and in terms of mating patterns; so that much of population genetics applications to humans have to take into account human demography, and just as if you were a drosophila population geneticist you would have to take into account the various aspects of drosophila reproduction and migration. Drosophila fly; humans sometimes fly, sometimes take boats; but certainly humans also migrate.

Q. What experience have you had with respect to that particular aspect of demography? Have you had any experience in that area?

A. I studied -- Because I studied human population genetics I studied theoretical demography. I even gave lectures in graduate courses when I was a post-doc at Stanford in theoretical demography. I have always taught a section on human demography in my population genetics classes when I teach them at St. Louis or at Yale. I have written computer programs to simulate demographic processes that are used; have been used for research purposes and have been used for teaching purposes.

Q. Would demography come under the umbrella of human population genetics?

A. Certainly the aspects of demography related to humans would.

MR. WALSH: My Lord at this time I am going to ask that Doctor Kidd be declared an expert in molecular genetics, DNA technology and testing procedures, and human population genetics.

THE COURT: Your second item was DNA --

MR. WALSH: Technology and testing procedures. And human population genetics.

THE COURT: Mr. Furlotte have you any questions to ask of Doctor Kidd?

MR. FURLOTTE: No questions.

THE COURT: No. Well, I think it has been adequately established that for the purposes of this trial, at any rate, Doctor Kidd is declared an expert in these fields. That doesn't entitle you to charge more for consultations you know.

A. I'll accept that.

THE COURT: It doesn't even make you an expert; it's just for the purpose of this trial.

MR. WALSH: Doctor, are you aware of the RFLP typing system in place at the R.C.M.P. DNA lab in Ottawa?

A. Yes, I am.

Q. Would you tell the judge, please, and the court how you became aware of this particular system?

A. In two separate ways. First, I became aware of some of what they were doing through meetings that were organized by the FBI in Quantico where I was invited down to advise them on statistical procedures in a workshop setting and representatives from the R.C.M.P., Ron Fourney and I'm not sure who else, I guess John Bowen also was there, and they discussed the procedures they were doing because this statistical analysis and the appropriate way of dealing with the statistics has to take into account the methodologies that are being applied. So in discussions there I became aware of some of their techniques. And then

I have visited their labs in Ottawa on two occasions. One was just a year ago and the other was last October, and especially on the first occasion I was given a very thorough tour and description of the laboratory procedures, shown the way they maintain records of samples in terms of chain of custody and documentation of samples. Was shown their protocols; their manuals; and looked at a lot of their results; and asked a lot of questions both relevant to the forensics but also out of my own self-interest. One always learns new techniques and better ways of doing things in your own lab when you visit some other lab. So I guess I -- I think I know about their procedures quite well.

Q. Did you have an opportunity to review their protocols?

A. Yes.

Q. And have you had discussions with people like Doctor Bowen?

A. Yes.

Q. Could you tell us, Doctor, in the scientific community what, if any, reputation does the DNA forensic lab in Ottawa - the R.C.M.P. DNA forensic lab in Ottawa have in the scientific community?

A. As far as I know it has an excellent reputation. They have good people who are respected for their ability and knowledge and they do very good quality work.

Q. Do you have any opinion Doctor - or what, if any, opinion do you have as to the system's ability - the RFLP system in place with the R.C.M.P. - their ability to produce accurate, reliable and reproducible results?

A. I think their ability is excellent to do that. The results that I saw were quite high quality which means accurate. I know they are reproducible from other data that I have seen. And what was the third aspect?

Q. Accurate, reliable and reproducible was the question.

A. Okay. I'm not sure how reliable differs from accurate and reproducible but I would agree to all three words.

Q. Fine. Well, that's the lawyer in me, unfortunately, Doctor, covering all bases.

I would refer you to -- There was evidence in this particular hearing, Doctor, that the probes in use, particularly the probes in use at the R.C.M.P. Laboratory, some of the probes in use are D2S44, D1S7, D4S139, D17S79, D16S85, D10S28 and the monomorphic probe being D7Z2, and the sex typing probe being DYZ1. Are you familiar with those particular probes?

A. To varying degrees I know something and have read about all of them.

Q. And in your opinion the validity of using these particular kinds of probes for forensic DNA work?

A. Is in my opinion not questioned. They are as good as any of the VNTR markers that exist.

Q. And the other evidence, Doctor, in this hearing to date has been that they use these probes in conjunction with the enzyme Hae III. Are you familiar with that enzyme and its relationship to the use of these particular probes?

A. Yes, I am.

Q. And your opinion with respect to the use of that particular enzyme for forensic work?

A. It's a very good enzyme and it cuts appropriately for use with these probes. It's a very reliable enzyme. It does not give nonspecific activity. Its activity is highly specific under robust conditions so that one does not find spurious artifacts when using it.

Q. You use the term 'robust'; what does that mean? Does it have any particular meaning in the science world?

A. I'm using it in English language sense there that one can have slightly different concentrations than you think you have; slightly different pH than you think you have; slightly different buffers; different salt concentrations; and it will still work. That's something that I as a teacher with graduate students and postdocs learning the methodology have to be very concerned about because when they are learning they are making all kinds -- Every error that can be made has been made. And it's probably not quite as relevant in the case of the R.C.M.P. Lab where you have at least doing the case work people who are already very thoroughly trained and skilled and a very fixed protocol. But, nonetheless, this use of an enzyme that's robust gives an extra margin of safety.

Q. And the use of the monomorphic marker, in this case D7Z2, what is your opinion with respect to the use of a monomorphic marker in the forensic system?

A. I originally advised the FBI several years ago that they should add a monomorphic marker to their system. It's an excellent check that everything has worked as

one thinks it should have worked and provides an extra degree of confirmation that there are no unidentified problems in the test.

Q. And the use of the sex typing probe -- I use the phrase 'sex typing probe' because that's the way it has been explained to me, DYZ1, what opinion do you have with respect to the use of that in the forensic system?

A. It's a very commonly used probe that is "Y" chromosome specific so that it will allow one to distinguish between DNA that is entirely female in origin and DNA that is male in origin. So obviously in many forensic settings that's a useful, additional confirmation that the DNA matches by sex as well.

Q. And I understand also the evidence to this point, Doctor, has been that the R.C.M.P. run a male and female DNA control in their gels. What, if any, opinion do you have with respect to that?

A. It is always advisable to run controls. They are running samples of known size and if in any particular forensic application they found that the controls did not by their measurement techniques give the size they are known to have then you would know something went wrong with that test. So it's an additional important test or control that everything in the test has gone as one wants it to.

Q. Are you familiar, Doctor, with the match criteria for the interpretation of autorads generated by the R.C.M.P. RFLP system? That is the visual match confirmed by a monomorphic probe, backed up by computer quantification using a 5.2% match window. Could you provide an opinion with respect to the validity of that type of interpretation?

A. I think that is the proper way to go about such a test. There, I know, has been discussion about whether or not a visual match or a purely computer-generated match should be used in these situations and I feel that a visual match is probably the more powerful. The human brain is an exceptionally good pattern recognition system. The follow-up of confirming that everything is within the window, that the monomorphic marker shows no aberrations is an excellent safeguard against somehow deluding oneself but it's no guarantee. In fact there can be visually distinct patterns that nonetheless fall within the match window and so the match window is not a sufficient match criteria. The visual check is the preferable one.

Q. Would you or should you expect variation from lab to lab - forensic lab to forensic lab with respect to a match window, and I say that because I know that from the evidence that the FBI I believe have a 5% match window and the R.C.M.P. have a 5.2%. Would you expect such variation and how would it --

A. The difference between 5% and 5.2% is essentially trivial but I would expect such differences. Laboratories have slightly different ways of performing the techniques and these give rise to slightly different amounts of variation from test to test. At this point I am more familiar with the basis for the 5.2 in the R.C.M.P. lab than I am familiar with the basis for the 5% in the FBI lab. The 5.2 is a very conservative -- No, I don't want to use the word 'conservative'. It is an empirically-based window that 99% of true matches actually fall within that range. So it is a measure of how much variation

actually does occur from when the same sample is re-tested and an attempt is made at a match.

Q. Is that window appropriate to the R.C.M.P. system - that 5.2% in your opinion?

A. Yes. It's based on their technology and the way they do the test in their lab.

Q. Would you explain, doctor, what a band shift is?

A. A band shift is a phenomenon that arises probably because the ionic strength of a particular sample is different from what it should be and this causes the DNA in that particular lane to either migrate faster or slower than one expects it to under the standard conditions. So that one sees the band either not quite as far down or a bit further down than you would expect to see it. And if a comparable shift has not occurred in the marker lane then one would get a slightly different size estimate or, if one has two samples that are identical DNA but one has band shift because it's too concentrated, for example, then one would see the bands actually lining up not in the same place but the bands would be offset. One would have migrated differently and they would not match.

Q. What, if any, opinion do you have doctor with respect the likelihood of band shifting going undetected in the R.C.M.P. RFLP system?

A. It is very low. They have the monomorphic marker, D7Z2, in the system and since that is present in all of the sample lanes if it does not show a shift it is very unlikely that there would be any appreciable shift in another part of the gel. So that it is a control.

Q. What, if any, opinion do you hold with respect to band shifting falsely matching samples across multiple loci?

A. What I didn't say before when I talked about the identical sample, one shifted and the other not looking different, is the question you are raising now - what if there are two samples that are really different and one of them undergoes band shift so that they appear to line up when they are really different. That certainly can occur but for it to cause alignment across multiple loci is a vanishingly small probability. It may occur on one locus or in one pair of lanes on a given filter at one locus, but unless the samples in the two lanes are offset by a comparable amount all in the same direction they can't be brought into alignment by band shifting. So that band shifting, to bring all of the bands at all of the loci into alignment, is a theoretical possibility but it would require, first, that a very rare pattern actually existed in that it was identical to the one you wanted. Your known sample was identical except shifted for all bands by a comparable amount in the same direction. Not just any random pattern could be brought into alignment. It then would have to be a second very rare event and that is all actually shifting without the constant marker - without the monomorphic probe showing any evidence of a band shift. And I think for that to occur is just a virtual impossibility.

Q. What, if any, Doctor, opinion do you have as to the risks of a false positive, and I use the term false positive to mean that is declaring a pattern of bands in separate lanes or gels across multiple loci to be

indistinguishable when they are in fact not? What opinion do you have as to the risk of that occurring in the R.C.M.P.'s RFLP system?

A. I want to distinguish very carefully what I mean by a false positive which - so I will elaborate on what you said slightly. Patterns that could be distinguished, that really are different from two different individuals, and under ideal circumstances could be distinguished, happening to be indistinguishable by the R.C.M.P. system I think is a vanishingly small chance. It would require a combination of circumstances that I think is of the sort I just mentioned with the band shifting across multiple loci, rare event confounded by simultaneous occurrence of another rare event. And so I would dismiss that as a possibility.

Q. What, if any, opinion would you hold doctor as to the risk of a false negative, that is, as I use it, declaring a pattern of bands in separate lanes or gels across multiple loci to be different when they are in fact indistinguishable?

A. That's a significant risk. The nature of the technology is such that's why there's a 5.2% window. There can be variation. And so I don't know how to give it a numeric value but it is a real possibility. It is nearly impossible to determine what the risk is and I'm not aware that many tests have been done to try to determine that risk. It always operates in a forensic situation in the defendant's favor because the DNA then is interpreted as saying these aren't from the same person and that ends the situation.

So in a forensic and legal setting it's a very acceptable risk and I think it's low, probably way less than 1%, but it's certainly present.

Q. What, if any, opinion, Doctor, do you have with respect as to the reasonable reliability of the R.C.M.P.'s forensic RFLP system including the interpretation of the autorads?

A. I think it's very good. It's highly reliable. I think the interpretation of the autorads is done properly by skilled people using essentially the best techniques currently available for applications to these loci.

Q. A final question, Doctor, I have on this particular area is what, if any, opinion do you have as to the general acceptance of this RFLP system that the R.C.M.P. have in place including the interpretation of the autorads? What opinion do you have as to the general acceptance of this system in the scientific community?

A. The basic scientific framework in which this is taking place is unquestionably accepted in the broad scientific community. Research laboratories, medical diagnostic laboratories around the world are using RFLP technology, many with some of the same loci for nonforensic purposes on a daily basis in hundreds of labs. So that there is really no question about the general acceptance in the scientific community of the basic principals involved in this technology. I think any molecular biologist or person who is doing this kind of work who looked at the specific protocols and results from the R.C.M.P. Lab would say yes, these meet all

the standards that we would want to see for reliability and quality and that the results are done very well.

Q. Doctor I am going to enter the area of population genetics as it applies to what we are dealing with here. The first question I have, Doctor, is what is the significance of patterns being declared indistinguishable? What is the significance of that if a scientist was to look at a blot and make a declaration that a certain pattern of bands were indistinguishable?

A. The word that's usually used in the forensic setting is a match. I much prefer the word you used, indistinguishable, partly because there is semantic confusion I think in some peoples' minds that a match means identity. In fact when the two patterns are indistinguishable there are two possible explanations. One of them is that they are indistinguishable because the DNA in the two lanes came from the same person and so that you are really looking at the same DNA and, of course, then it's indistinguishable. The other possibility is that it is DNA from two different individuals but they just happen to have patterns that are indistinguishable. And I want to clarify right now, that is not a false positive. That is simply two people happen to have patterns that are indistinguishable by this technology. And that is the point at which population genetics enters in because this is a coincidence and in a forensic setting one wants to know how likely is this. Is this a very rare event or is this a very common event? And population genetics enters in in terms of trying to estimate

this alternative explanation. We have the two. It's a coincidence or they're the same person. And if the probability or chance that it's a coincidence is relatively large, say 1 in 2, 1 in 5, then sure it could be a coincidence. There's nothing to distinguish between those two explanations. But if the chance that it's a coincidence is very small, 1 in 100, 1 in 1000, 1 in 100,000, 1 in 1,000,000, then one says oh, well maybe it wasn't a coincidence. Maybe it's really from the same person. And one places different weights on those two explanations depending upon what that probability is.

Q. In order to assess or to put a statistical significance associated with a declaration that certain bands are indistinguishable or certain pattern of bands are indistinguishable, what is it that a forensic laboratory must first compile?

A. You basically need a data base. You need to know how frequently those patterns occur in the population at large.

Q. What considerations, Doctor, would go into the selection of a sample population to determine VNTR allele frequency?

A. One slight caveat and then I'll answer the question. We are not specifically determining allele frequencies with VNTRs because we don't have the ability to identify individual alleles. We can only identify sizes of alleles which is one of the reasons we go into binning. But what one would need for a data base is to decide upon the relevant population. If one is interested in Chinese then one clearly has to have a data base of Chinese. If one is interested in,

hypothetically, a rape in Minneapolis, then one needs to know the sample of males who were in the Minneapolis area at the time the rape occurred. If one is dealing with Blacks or Caucasians one needs to define those because it's a well-known fact in human population genetics that allele frequencies, and hence bin frequencies, can vary among populations, so one should use a reasonably appropriate population. One then needs to identify by sampling, using some sort of sampling theory, a random selection of individuals from that population and test them. They should ideally be unrelated and there should be a moderate number of them.

Q. You say moderate. What do you mean Doctor? Moderate number.

A. Moderate number I'm saying in terms of a forensic application. In fact in part what you need in the data base is determined by what purpose you are going to put the data to. But for a forensic situation something on the order of a hundred to two hundred people, minimum, is a quite adequate sample.

Q. What about ethnic diversity Doctor?

A. Well, certainly I mention major ethnic groups. If we're talking about within Caucasians, the Canadian white population or Caucasian population is of mixed European ancestry. It's a higher proportion of English ancestry than we have in the U.S. but it is a mixed European ancestry. So one would want some representation of that but that's almost going to happen automatically because the population is fairly randomly distributed in terms of any of the major groups. One does not

need geographic representation because there is no strong indication that the population is subdivided geographically in a population like Canada or the U.S. whereas in Africa one might very well want some geographic representation because the gene frequencies in the Masai in Kenya might be very different from those in the Pygmies in the Central African Republic for example.

Q. Are there any other considerations Doctor?

A. There probably are but I can't think of any at the moment.

Q. How would you actually go about obtaining such a sample for these particular purposes? What would you consider to be an appropriate way to go about doing that?

A. There are dozens of ways one could go about doing it. And I'm aware of how the R.C.M.P. went about doing it; I'm aware of how the FBI went about doing it. The FBI took recruits coming for training at Quantico and sampled them and they represented people from around the U.S. They represented, on average, a higher socioeconomic and educational grouping but there is no reason to think alleles of these loci have anything to do with IQ or education so that's irrelevant. The R.C.M.P. looked at blood donors - random selection of blood donors. Also looked at army recruits. Both of those are perfectly reasonable ways to get a large number of people.

Q. Doctor, I am going to refer you to a number of exhibits because I want to know - you indicated that you are aware of the R.C.M.P. Caucasian data base and

I want to establish if you have seen some material that has been filed in court here.

Doctor I am going to refer you to an exhibit that has been marked on this particular hearing exhibit VD-58. Would you look at it for me, please, and tell me whether or not you have seen that before.

A. Yes.

Q. I show you exhibit VD-61. Have you reviewed that as well?

A. Yes.

Q. VD-60A?

A. Yes.

Q. VD-59A?

A. Yes.

Q. 63A?

A. Yes.

Q. 62A?

A. Yes.

Q. Doctor, that is evidence that was entered through, I believe, Doctor Carmody and Doctor Fourney in relation to the R.C.M.P. Caucasian data base. Is that your understanding as well?

A. Yes, that's correct.

Q. What, if any, opinion, Doctor, do you hold as to how representative the R.C.M.P. Caucasian data base is of the Canadian population as a whole and New Brunswick in particular as it pertains to VNTR loci?

A. I think it's quite representative of the population as a whole. It's not only large so that it's going to be quite accurate because of its size, but it also has a quite close approximation to the provincial distribution of population so that if there were any geographic

variation based on different provinces having different gene frequencies because they came from founders with very different gene frequencies this would essentially control for that. There is, however, because I know that the comparisons were made among the different samples which were obtained in different provinces by different means, by different sampling strategies, those were all identical and so there's really no evidence that there's any variation by province.

Q. You are referring to Doctor Carmody's work?

A. Yes.

Q. Doctor what, if any, opinion do you have with respect to the -- What, if any, concerns would you have with respect to the R.C.M.P. Caucasian data base since no small communities have been sampled? Would that affect your opinion?

A. No, not if they are small Caucasian communities. There are not great differences throughout Europe for these systems. In my experience, for example, we're doing a lot of studies on an isolated Mennonite community in Saskatchewan and Alberta and we have found that they have a lot of DNA variation. There is no evidence of any unusual character. They are a religious isolate and they're in small communities but genetically they're no different from you or me.

Q. What, if any, necessity in your opinion is there to sample the population in the area where the crime is committed and to use that as your data base?

A. Only if there is some reason to suspect that the population in that area is somehow very unusual, and

everything I knew about the Canadian population in this area is that it's not.

Q. Do you have any experience in relation to particular areas other than the Mennonites?

A. We have done work on isolated populations from around the world. We are studying the Druze, a religious isolate in the Middle East that's been reproductively isolated for at least six hundred years. They have lots of genetic variation. We are looking at very primitive tribal populations in the Amazon Basin and even though all children born in the last 15 years or 20 years, I don't remember the exact date, are descended from one man three to four generations ago, because he was the tribal chief and had five wives, still at the DNA loci every individual that we studied had a distinct DNA pattern so that the frequencies there might differ but the patterns are - there are still lots of variation and lots of patterns so that small variations in frequencies become very unimportant. And that, I might add, that's probably the most extreme sample example that I know of that's ever been studied in humans for being a very tight, closed, in-bred population.

Q. At the risk of being redundant I'll ask this question anyway Doctor: what, if any, opinion do you have as to the reasonable reliability of the methodology used in selecting a data base as the R.C.M.P. have and as to its general acceptance in the scientific community for the purpose for which it is put?

A. I have no problems whatsoever with the methods that were used. I think they are appropriate. I think it's

an appropriate data base. The general acceptance in the scientific community I am sure that there will be people who will criticize it but I would have to say that of the criticisms I have seen in court transcripts or in other cases in which I have been involved, most of the criticisms of this kind of data base are inappropriate and that most people would accept it for forensic applications in the way that the R.C.M.P. does.

Q. Doctor, the evidence to this point in the hearing as to the method of frequency calculations using the R.C.M.P. Caucasian data base was that the allele bin frequencies were determined using the fixed bin method. The fixed bin method was described in VD-49A. I will show you what has been marked VD-49A. It's entitled "Fixed Bin Analysis for Statistical Evaluation of Continuous Distribution of Allelic Data". Are you familiar with that particular publication?

A. Yes. I have known of this work in its various draft and developmental stages up until publication.

Q. And the other evidence, Doctor, was that the probe frequencies were determined using the Hardy-Weinberg equation and that the overall genotype frequency across several loci is determined using the product rule. Are you familiar with this method of calculation for these forensic purposes?

A. Yes, very familiar.

Q. What is the effect of the binning method - or the fixed bin method on estimating the frequency of a particular band pattern?

A. It vastly, extravagantly overestimates the frequency of the band pattern. The fixed bin method is a specific method. There are many that one could use but it is one specific method for dealing with the problem that these systems show with this technique essentially continuous variation so that one cannot say with any certainty that a band measured as 3.152 kilobases is or is not different from a band measured as 3.159 or 3.148 kilobases. This is the level of measuring error in this technology and it is greater than the real difference between alleles, so that one cannot calculate allele frequencies specifically because one cannot identify a specific allele. When one sees a pattern where the bands match one wants to calculate conservatively what is the largest possible frequency in the population of alleles that given this measurement error might be in the given experiment indistinguishable from my known standard allele, given that the nonstandard allele has this small amount of measurement error in it as well.

One approach used by some companies, Lifecode and Cellmark, has been a floating bin approach. They take their estimate and they take the bin measured around it and say, okay, any of these might be indistinguishable, often will be very distinguishable but since they sometimes might be - will collapse or pool all their frequencies the fixed bin approach is even more conservative. It defines the bins in advance and there are many very distinguishable alleles in those bins but they're bins defined for convenience. And then if you are near the boundary

it always takes the bin with the higher frequency. But in fact the real frequency of that band in the population is far less than the bin frequency that is used. So it may be an order of magnitude bias a factor of ten per band bias in favor of the defendant. It's a built-in bias. So that when Hardy-Weinberg is used and then the product rule is used you are always at every step using a frequency that you know to be an overestimate of the true frequency. You don't necessarily know how much of an overestimate but you know it's an overestimate and, therefore, the final number you get is designed to be an overestimate of the true frequency. What one is really calculating is the probability of another pattern in which all of the bands fell into the same bins as the pattern just observed or the known pattern. And the overwhelming majority of those patterns that meet that criteria will fail on the visual and statistical match rules. Will be quite distinguishable so that the true frequency is very much less.

Q. What, Doctor, if any, conditions must be met or what assumptions must apply before the Hardy-Weinberg equation or the product rule can be used?

A. There are a large number of formal assumptions underlying the Hardy-Weinberg rule. One of them is that there is no deviation from random mating. Clearly, we know non-random mating occurs for height, for amount of education, for socioeconomic status, but the Hardy-Weinberg rule says that kind of non-random mating is irrelevant unless this gene is related to those characteristics, and none of these genes - these

are all in fact not functional genes. These are simply variant in nonfunctional DNA. So there is no reason to expect any of those to be related to these sorts of social factors. So that non-random mating becomes a reasonable assumption. I mean random mating becomes a reasonable assumption to make in looking at these loci. One can further try to test it and for some of these loci, I think D2S44 and D17S79 but I'm not certain of that, a colleague of mine at Yale has looked at the data base that was generated by the Lifecode Corporation and did appropriate statistical analyses of a very sophisticated sort. It was published in science for all of the loci that were examined and they met with no problems.

Q. That is - I believe for your information, Doctor, it's VD-53. Is this the paper by Devlin and Risch?

A. Yes.

Q. Would you look at VD-53 and tell us whether that is in fact the same paper?

A. That's the paper and -- Yes, D2S44, D17S79. I got it right. And also D14S13 which is not one of those there. They essentially found for all of these in Caucasians that there was no evidence of deviation from Hardy-Weinberg. And whenever tests have been done, and I understand though it was not as statistically powerful a test as the Devlin et al test, I understand that Doctor Carmody did some tests of the R.C.M.P. data base and it similarly showed no evidence of deviation from the frequency distributions expected under the assumption of Hardy-Weinberg. And one does not need to show that all of the formal assumptions

underlying Hardy-Weinberg are true if one shows that the data are in agreement with that expectation, and the data appeared to be in quite close agreement with that expectation. The product rule is the extension of the same logic to multiple loci and as this chart quite clearly shows, every one of these loci is on a different chromosome.

Q. You are referring to VD-27 which is --

A. VD-27, yes. That gives a priori very strong indication that these loci would show no association in the population because they are transmitted from parent to child quite independently. The so-called multi locus linkage disequilibrium is in fact, in my opinion, not a relevant issue in this case because for that to be present and hence cause some problem with the product rule it would be necessary for there to be very marked substructuring within the population, quite marked deviation from Hardy-Weinberg mating, and in addition it would be necessary for those two or more sub-groups to have markedly different bin frequencies for the particular bins in which the evidentiary sample, or whatever the particular case is. If they do not differ in bin frequencies for the bins relevant to the particular case multi locus disequilibrium is irrelevant. They must differ for both bands - for the bins for both bands at a particular locus. Even if they differ at only one bin but not at the other you will not get the effect. So that the multi locus disequilibrium with these highly polymorphic loci is a vastly different statistical phenomenon from the multi locus disequilibrium that is present in all elementary population genetics textbooks where it's

based on two alleles at one locus and populations with very different frequencies at those two. Once once gets to a multi locus system it's a very different set of statistics. And in my previous testimony there has -- or in the trials or Frye hearings that I previously testified in there has been a great deal of confusion over that where witnesses attempting to discredit DNA evidence, or the product rule, have used these simplistic textbook examples without recognizing that this is a vastly more complex situation and requires phenomena of a magnitude that we can say by looking at the data do not exist.

Q. If I could perhaps with respect to that testimony, Doctor, Doctor Carmody's evidence was that he compared the Vancouver with the Canadian Forces Base Kingston with Ottawa, that data, he compared it and found no statistical difference in their bin frequencies. What does that tell you?

A. It tells me, one, that there is unlikely to be any substantial substructuring in the Canadian population that is relevant to these loci because even if there were substructure if the frequencies are the same it's irrelevant.

Q. Doctor Carmody's evidence was also that he compared the R.C.M.P. Caucasian data base, the bin frequencies, with some Caucasian data from Dade County in Florida, Fort Worth in Texas, with the FBI Caucasian data and he found some statistically signficant bin frequency differences but no forensic difference. Could you explain that - what that indicates to you?

A. Statistical significance simply means that it is very likely that the difference is real but if one does a large enough study a difference in frequency, I'll say 5.25% for the bin in one study and 5.28% in another study, if the studies are large enough that will be a significant difference from a statistical point of view. But when we're talking about bins in the first place we're not talking about accurate estimates of alleles. We're talking about a deliberate gross overestimation for the frequency of a pool of allele. The difference between 5.25 and 5.28 is trivial and meaningless in that context. It is largely irrelevant to the application. I would certainly not be at all surprised if there were differences; the magnitude of the differences though was relatively small. Now it was in some of the cases - it was clearly larger than that example I just gave. It may have been the difference between 6% and 8%. But still the difference between 6% and 8% in most of these forensic applications is not of concern. One is not attempting to get an accurate estimate. One is attempting to get a reliable meaningful overestimate.

Q. I am going to refer you, Doctor, to VD-65. Would you look at that for me and tell me whether or not you have seen this before?

A. Yes, I have seen this. This is the comparison that Doctor Carmody did recalculating the statistics in this case using the other data bases.

Q. And how does that -- The summary of the statistics that are shown there with respect to the comparisons of the statistics in this case with the FBI Florida,

Texas, Minnesota, what does that tell you Doctor?

A. Take the first locus, D1S7. There is a clear difference; one in 78 for the Canadian; one in 96 for the FBI; one in 80 for Florida; one in 76 for Minnesota. But when one takes the 99% confidence interval for the Canadian sample all of the other samples fall within it - within that 99% confidence interval. So that says to me those are not particularly meaningful differences. The most important thing -- And I don't see any really marked differences here at all. It's the sort of statistical fluctuation one finds with different samples. What is really important is when one takes those 99% confidence intervals and then does the four or five locus calculations and one gets values ranging from 1 in 3.1 million as the largest number down to 1 in 17 million for the smallest number. On the Canadian data base that basically says to me from a statistical point of view all of this is estimation, and recognizing that I have already overestimated by using bin frequencies I am now taking confidence intervals on the bin frequencies. If I take the most bias in favour of the defendant, i.e., the largest number in every case I have 99% certainty just on the confidence intervals that the true value is smaller. From the bin frequency I have essentially -- from the binning process I have essentially complete certainty that the true value is smaller. I go through the calculations. I still get a value of 1 in 3.1 million.

Human beings can't distinguish between 1 in 3 million and 1 in 5 million. Those are just numbers. They're all very rare.

An example, I like to take the extremes here, if the FBI data base were used it would be a somewhat less common pattern so if we take the upper Canadian 1 in 3 million and the FBI as 1 in 9 million that's a factor of 3 difference. Well, that's comparable if you buy three lottery tickets your chances of winning are three times greater than if you buy one lottery ticket but all of these are only slightly greater than if you bought no lottery ticket at all. They're all very tiny numbers and variation in that range is meaningless. The important point is they're all small numbers. None of them, when the loci are combined, is on the order of 1 in 3, 1 in 10, 1 in 20.

Q. The manner in which Doctor Carmody has expressed the confidence interval associated with the statistics in this particular case, do you have an opinion as to the appropriateness of expressing it in that fashion?

A. In situations where I have testified before where the companies have used a floating bin approach I have not been happy with the numbers they reported because they did not report confidence intervals and so I have always in terms of numbers to which I will testify, I have always recalculated them using confidence intervals and taking the upper 95-99% confidence interval and used those. I'm sorry, that's a very long-winded way of saying yes I think it's appropriate. I think it's a very good indication of how certain you are that it really is a small number.

Q. Doctor, you have touched on this particular topic - perhaps you have touched on it as much as you want to, but I have a question here with respect to what is substructure? If you could explain that, please, in a little bit more detail and what relevance it would have to probability calculations, your opinion as to its existence and its effect for the purposes we're dealing with here. It's kind of a loaded question but I would wish if you could flush out this whole concept on substructure.

A. I am tempted to give a flippant answer that it's a red herring but I will try to be a little more specific.

No human population has true random mating for all components. I mentioned before, we know there is assortative mating by height. Tall people tend to marry tall people; short people tend to marry short people. We know there is definite assortative mating by level of education. People tend to meet their mates in late teens - early twenties. If you are at college you tend to meet a college student. If you are not in college you tend not to meet a college student.

From a genetic point of view though, one has to say is any of this relevant to the genetic systems, the DNA variation being transmitted on the chromosomes. And for it to be relevant these differences have to be associated with different frequencies of some sort of alleles. One can come up with hypothetical examples of one that I've used in teaching many times: red hair and spina bifida in Boston.

Boston has a very large Catholic population with two components, Irish Catholics and Italian Catholics. The Irish have the highest frequency in the world of spina bifida, a birth defect. They also have the highest frequency in the world of red hair. Even if the Irish and the Italians are mating at random the mere fact that they started from two populations, one with very high frequencies of both spina bifida and red hair; one with very low frequencies of spina bifida and red hair, it will be several generations before there is complete mixture of the genetic components for those two traits. So that if one finds a person with spina bifida in that population it is more likely that most of their ancestry is Irish as opposed to Italian, even if they have got an Italian surname because there's some Italian ancestry, and since most of their ancestry is Irish they have a higher probability of having red hair. So that's a hypothetical example. I know of no data but it's an illustration of the phenomenon which is real and exists in humans but its relevance to the forensic situation is that, one, you have to start with two populations that are reasonably discreet and differ dramatically for two characteristics that are being looked at, not just one. So what we know about the variation at these VNTR loci is that virtually the complete range of variation exists throughout Europe. There are minor frequency differences but not dramatic frequency differences. And the other complication is that these are now not two-state genetic loci, like red hair versus black hair or spina bifida versus normal, but there are many variables here. So that

the evidence is very strong in my opinion that such disequilibrium will not exist to any measurable degree. That's not to say it doesn't exist in the formal sense but it might require samples of a thousand or several thousand to demonstrate its existence because it will be at that numerical level of being insignificant with respect to applications in a forensic situation.

Q. You have indicated in Europe you have looked at different Caucasian populations, Doctor. I believe you did comment on that with respect to determining substructure and its existence and its effect?

A. A major part of the research in my laboratory is looking at population variation for the frequencies of RFLPs. As I said, we have studied over a hundred in our populations. None of these particular ones is in that hundred but we have used some of these in other studies. Our mapping studies. What we find is that all of the populations contain virtually all of the alleles. There are minor differences in the frequencies but across Europe there are not very large differences for any of the systems we have studied. All of the populations are highly variable and that's the other aspect of this, the high variability. Because if there is high variability it's very unlikely that two people will have the same pattern by chance. The coincidence factor. I mentioned the Amazon tribe where in fact no two people did have the same pattern even though they were closely related.

The frequencies will be different that one calculates because of these variations in allele frequencies but by and large they will all be small numbers. And I saw an affidavit by someone that talked about the difference between 1 in 50,000 and 1 in a 100,000. That's ridiculous. That sort of difference is not meaningful. And that is where one has to keep distinguishing between precision for an estimate of a pattern and deliberate overestimation to a degree that we may not know precisely how much our over-estimate is but we know it is a large overestimate for the purpose of biasing everything giving the maximum advantage to the defendant.

MR. WALSH: My Lord what is your preference? I can continue --

THE COURT: Well, I think we'll stop there. We have made a good start in the evidence of Doctor Kidd.

MR. WALSH: I don't expect, My Lord, I will be going too much further in the morning before we actually hit the case specific evidence so we have progressed quite satisfactorily from my point of view in terms of my projections.

THE COURT: Yes. The normal course, Dr. Kidd is still on the witness stand and wouldn't be permitted to talk to anyone about the case until all your evidence is completed under our rules but we have made special dispensation here, I think, permitting you to talk about the case specific evidence, but Mr. Walsh has given an undertaking that if you have made errors in your evidence so far he can't tell you - coach you to try to correct those tomorrow.

A. My errors are my own.

THE COURT: He probably won't recognize them if you have made any.

MR. WALSH: You save me the point of saying that as well My Lord.

THE COURT: So we'll recess until 9:30.

(COURT ADJOURNS TO 9:30 A.M. MAY 16, 1991.)

IN THE COURT OF QUEEN'S BENCH OF NEW BRUNSWICK

TRIAL DIVISION

JUDICIAL DISTRICT OF FREDERICTON

B E T W E E N:

HER MAJESTY, THE QUEEN

- and -

ALLAN JOSEPH LEGERE

AFFIDAVIT

1. THAT I am a stenographer duly appointed under the Recording of Evidence by Sound Recording Machine Act.

2. THAT this transcript is a true and correct transcription of the record of these proceedings made under Section 2 and certified pursuant to Section 3 of the Act. (Pages 1 to 56 and 111 to end.

3. THAT a true copy of the certificate made pursuant to Section 3(1) of the Act and accompanying the record at the time of its transcription is appended hereto as Schedule "A" to this affidavit.

SWORN TO at the City of Fredericton in the Province of New Brunswick this 27th day of May, A.D., 1991.

BEFORE ME:

Verna M. Peterson
A COMMISSIONER OF OATHS
MY COMMISSION EXPIRES
DECEMBER 31, 1994

Dolores M. Brewer

SCHEDULE "A"

RECORDING OF EVIDENCE BY SOUND RECORDING MACHINE ACT

FILE:

CERTIFICATE

I, Dolores Brewer of Fredericton, New Brunswick certify that the sound recording tapes labelled:

HER MAJESTY, THE QUEEN

- and -

ALLAN JOSEPH LEGERE;

initialled by me and enclosed in this envelope are the record of the evidence (or a portion thereof) recorded on a sound recording machine pursuant to Section 2 of the Recording of Evidence by Sound Recording Machine Act at the Voir Dire hearing (Jury Trial) held in the above proceeding on the 14th & 15th day(s) of May, A.D., 1991 at Fredericton, New Brunswick, and that I was the person in charge of the sound recording machine at the time the evidence and proceedings were recorded.

DATED at Fredericton, New Brunswick this 15th day of May, A.D., 1991.

Dolores M. Brewer

IN THE COURT OF QUEEN'S BENCH OF NEW BRUNSWICK

TRIAL DIVISION

JUDICIAL DISTRICT OF FREDERICTON

BETWEEN:

HER MAJESTY THE QUEEN

- and -

ALLAN JOSEPH LEGERE

AFFIDAVIT

1. THAT I am a stenographer duly appointed under the Recording of Evidence By Sound Recording Machine Act.

2. THAT this transcript is a true and correct transcription of the record of these proceedings made under Section 2 and certified pursuant to Section 3 of the Act. Pages 57 to 110, inclusive.

3. THAT a true copy of the certificate made pursuant to Section 3(1) of the Act and accompanying the record at the time of its transcription is appended hereto as Schedule "A" to this affidavit.

SWORN TO at the City of Fredericton in the Province of New Brunswick this 24th day of May, 19 91.

BEFORE ME:

A COMMISSIONER OF OATHS

SCHEDULE "A"

RECORDING OF EVIDENCE BY SOUND RECORDING MACHINE ACT

CERTIFICATE

I, Verna Peterson, of Fredericton, New Brunswick, certify that the sound recording tapes labelled #1 and #2, J. D., R. v. Allan J. Legere, May 14/91, initialled by me and enclosed in this envelope are the record of the evidence (or a portion thereof) recorded on a sound recording machine pursuant to Section 2 of the Recording of Evidence by Sound Recording Machine Act at the voir dire hearing held in the above proceeding on the 14th day of May, 1991, at Fredericton, New Brunswick, and that I was the person in charge of the sound recording machine at the time the evidence and proceedings were recorded.

DATED AT FREDERICTON, N. B., the 14th day of May , 1991.

Verna Peterson