IN THE COURT OF QUEEN'S BENCH OF NEW BRUNSWICK

TRIAL DIVISION

JUDICIAL DISTRICT OF FREDERICTON

BETWEEN:

HER MAJESTY THE QUEEN

- and -

ALLAN JOSEPH LEGERE

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

APPEARANCES:

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

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

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October 21 and 22, 1991.

VERNA PETERSON
COURT REPORTER

(COURT RESUMED ON OCTOBER 21, 1991, AT 9:30 a.m.)

(JURY CALLED - ALL PRESENT.)

(ACCUSED IN HOLDING CELL.)

THE COURT: Now, Dr. Bowen was being cross-examined?

MR. WALSH: Yes, My Lord, I'd recall Dr. Bowen for that purpose.

CROSS-EXAMINATION OF DR. JOHN BOWEN CONTINUED:

MR. FURLOTTE: O.K., Doctor, I believe we finished off Friday morning with comparing different probes with probe D16, at least comparing the autorads, and for the faintness of bands; is that correct?

A. That is correct.

Q. And while - during the comparison it was found that on different autorads there was a number of faint bands but maybe not quite as faint as the ones on D16?

A. Part of the distinction between calling the inconclusive on D16S85 was not only the fact that the bands were faint, it was the fact that some of the bands were indistinct, non-uniform, and thus I felt that I would not make a call based on those bands.

Q. Before I go on to the second gel that was run on those bands I have a few questions I'd like to clear up. I believe there was - you already mentioned that there was a fifth gel in this case where you attempted to see if an alleged father of Allan Legere, it might be possible that this person would have been Allan Legere's father?

A. That is correct.

Q. And without necessarily having to know his name did this person have a French name?

A. Yes, I believe so.

Q. And it was not Legere?

A. No, it was not.

Q. Now, were you in court when Dr. Waye testified?

A. Yes, I was.

Q. And just to touch again on it a moment as I go through his testimony what I believe - he compared gel to gel but he only compared the sizings, not the actual autorads themselves, is what I recollect was his testimony.

A. Dr. Waye did compare the autorads and the sizings.

Q. And the sizings?

A. That is correct.

Q. Between the two different gels?

A. That is correct.

Q. And before I get on to that, do you have your notes with you?

A. Yes, I do.

Q. When you were in court on the previous occasion you testified about the insoles that were given to you for testing?

A. That is correct.

Q. And that was given to you for - I believe you said to see if you could find hairs, not to get sweat samples out of?

A. That is correct.

Q. Your lab report of December 4, 1990 -

MR. WALSH: Has this got something to do, My Lord, with respect to the DNA?

MR. FURLOTTE: It's in respect to his DNA report, My Lord.

MR. WALSH: Because my understanding is Dr. Bowen - we exactly brought Dr. Bowen down on the last occasion so Mr. Furlotte could cross-examine him

on those particular aspects. Otherwise Dr. Bowen would not have had to have come until this time. Mr. Furlotte cross-examined him on those particular aspects and from what I can see here he wants another little go-around, and I don't think that's proper.

THE COURT: Well, what is there new about this, Mr. Furlotte? I do recall that Dr. Bowen was brought back specially so you could complete your cross-examination on his earlier testimony at that time.

MR. FURLOTTE: There was a question of continuity on the insoles that prior occasion and he showed in court a slip where he gave the insoles over, I believe, to Constable Charlebois in December of 1989, but it's just this one -

THE COURT: But this is related to DNA?

MR. FURLOTTE: This is related to DNA in the sense, My Lord, it's in relation to quality control and quality assurance.

THE COURT: Go ahead. If you get too far afield I'll perhaps stop you.

MR. FURLOTTE: That's fair, My Lord. Your report of December 4, 1990, does your report tell you that you still have the insoles in your possession?

A. Yes, it does.

Q. And that report December 4, 1990, says you still have the insoles in your possession but earlier you testified that you gave those insoles to Constable Charlebois in December of 1989?

A. No, I gave the insoles to Constable Charlebois on November 28th of 1989.

Q. November 28th of 1989?

A. That is correct.

Q. So you made a mistake somewhere?

A. This is a typographical error in the sense that I missed that exhibit transfer form when typing up the report. I also had in my possession tins of hair that I had removed from those exhibits.

Q. From what, the insoles?

A. From the insoles.

Q. So you did find hair on the insoles?

A. On one of them, yes, I did.

Q. As you found five hairs in the bread bag, or were you -

A. I never had possession of the bread bags, I had possession of the hairs removed from the bread bags.

Q. O.K., that's fine, and you couldn't obtain any DNA from any of those hairs?

A. There was insufficient DNA for analysis.

Q. Now, you also mentioned Friday that in TWGDAM one of the quality assurances was that there would be blind testing, blind proficiency testing?

A. One of the guidelines for quality assurance includes blind testing of each lab that performs DNA analysis. It's not blind testing of each individual, it's of the lab itself.

Q. And that was to represent the minimum quality assurance requirements for DNA RFLP analysis?

A. Each lab is supposed to be blind tested once a year.

Q. And that was considered to be a minimum requirement?

A. That was considered to be a minimum guideline.

Q. Which is not followed in the R.C.M.P. lab?

A. As I said, it is a program that we're developing.

It's very difficult to instantaneously have this sort of program put in place with any of the forensic labs in North America.

Q. And I believe you mentioned that in the OTA Report that there was one lab that was found to have made a mistake in a proficiency test on DNA analysis?

A. One lab performing the RFLP type analysis. A second lab made an error using the polymerase chain reaction.

Q. Does that mean three labs were checked and two of them were found to have made an error in DNA samples?

A. I believe so.

Q. And that was a trial out of 50 samples two firms each declared one false match?

A. I believe, yes, there were 50 samples.

Q. Maybe if we could read on Page 79, the OTA Report, this paragraph here, the bottom of the last paragraph.

A. "With respect to blind trials of forensic testing in the United States, CACLD organized trials using case simulated samples in 1987 and 1988. The three major commercial facilities then performing forensic DNA analyis participated in each trial."

Q. Go on, finish the paragraph.

A. "In the first trial out of 50 samples two firms each declared one false match" - with a reference number 60 - "that could have resulted in the conviction of an innocent person. The errors apparently are both from sampling handling problems" - again reference number 11. "The third company declared no false matches." - reference 60. In the second trial one company again

reported an incorrect match" - reference 13.

Q. So in those two blind proficiency tests it was found that there was three mistakes made?

A. Apparently, yes.

Q. Two by the same lab?

A. That is correct.

Q. Also on Page 78 under the typing of proficiency would you read this paragraph here?

A. "A 1978 study" - reference 73 - "found an appalling" - reference 68 - "number of participating laboratories reported erroneous results in testing blind samples with as many as 94 out of 132 laboratories participating obtained unacceptable blood typing results. Another critic reports that from 1978 through June, 1988, the numbers of errors for blood stain or physiological stain proficiency tests varied from seven per cent for one test to 77.7 per cent for another and that overall an average of 25 per cent of crime laboratories returning results made errors." - reference 38.

In one human blood test to evaluate genetic markers 15 of 69 participating laboratories 21.7 per cent made at least one error" - reference 38. "None of these tests invovled DNA typing."

Q. None of those tests involved DNA typing but we know that even tests that do involve DNA typing, proficiency tests shows errors?

A. Early proficiency tests done in 1987 and '88 that with the private companies there was a problem with sample mixing.

Q. So with these kind of statistics, labs making so many errors, why is it that especially the R.C.M.P. Lab doesn't feel it's necessary to follow the standards that they even set for themselves?

MR. WALSH: Objection.

THE COURT: Your objection, Mr. Walsh?

MR. FURLOTTE: What's your objection?

MR. WALSH: That isn't what Dr. Bowen, my understanding, testified to, that they don't feel it's necessary

to follow those. I think Dr. Bowen gave different testimony than that. That's something Mr. Furlotte would have liked him to say but he didn't.

MR. FURLOTTE: Well, most of the R.C.M.P. members of the Forensic Lab in Ottawa doing DNA testing belong to TWGDAM, the organization TWGDAM?

A. That is incorrect.

Q. You belong to it?

A. I belong to it and Dr. Ron Fourney belongs to it.

Q. Dr. Ron Fourney belongs to it, and basically you're the supervisor of the lab in Ottawa, DNA testing?

A. I am in charge of operations, yes.

Q. In charge of operations, and what's Dr. Fourney's position?

A. He is in charge of research and development.

Q. Research and development, so you're both members of TWGDAM?

A. That is correct.

A. And you don't find it necessary to follow your minimum guideline standards?

A. We do find it necessary. I mean I've been trying to establish the fact that we have engaged in open proficiency testing, outside agency proficiency testing, and are in the process of trying to set up blind proficiency tests.

Q. In this case, Mr. Legere's case, I believe you gave the preliminary report on November 10, 1989?

A. That is correct.

Q. And that preliminary report came after the first probing?

A. That is correct.

Q. Which was which one?

A. D2S44.

Q. D2S44, so after that first probing you gave a preliminary report on your finding?

A. That is correct.

Q. And you continued testing up until - I believe it was December, somewhere around December 5, 1989, up until you got to D16S85?

A. Sometime in December, 1989, yes.

Q. And you ceased testing then until November of 1990 on this D10S28?

A. I ceased testing that particular blot, yes.

Q. That particular blot, and you didn't give any report after the next three probes?

A. That is correct.

Q. Well, actually after the next four probes until we got to D16S85. After you hit D16S85 did you discuss your findings with anybody?

A. There were ongoing discussions with individuals such as Dr. John Waye during that process of examining the autorads up to that point, yes.

Q. Were there any concerns about your findings in D16S85?

A. None whatsoever.

Q. O.K., so I believe Dr. Waye also testified that that D16S85 was called inconclusive because of your explanation of the bands, they were a little faint and they weren't quite properly formed?

A. That is correct. He also mentioned that in his lab he would have made the call.

Q. He would have made the call because he was only something like maybe about 95% certain and in order to bring evidence against an accused person

you should be more certain than that?

A. I like to think that in his lab under the circumstances that he would be evaluating a sort of match he would probably try and reproduce it himself. The fact is that since this is a forensic case and we are applying it for forensic purposes I like to set a standard that I would like to be absolutely sure that indistinct bands are either reproducible or be able to get a slightly better result.

Q. So it's not prejudicial to an accused person?

A. Exactly.

Q. So by calling it inconclusive that's actually doing the accused a benefit?

A. Yes.

Q. Otherwise we'd have - if you were able to call that we'd either have a six-probe match here and a five-probe match for 1J?

A. I don't believe I would have ever called 1J; possibly 135.

Q. No, possibly 135, O.K. I'll get back to 135 on that autorad in a moment. First I want to go through a few notes here. O.K., Doctor, I believe your second report was dated November 2, 1990?

A. November 2, 1990?

Q. Yes.

A. I have one December -

Q. I believe it was a letter to the -

A. Oh, yes. There was a letter, yes. Yes, there was a letter on November 2nd of 1990.

Q. O.K., and would you read the letter?

A. This is a letter written to Superindent Zaccardelli, OIC, 'J' Division, Criminal Ops.

"Re: Murder of Anne Flam, Attempted Murder of Nina Flam, Murder of Donna Daughney, Murder of Linda Daughney.

Based on multiple probings it is possible to say that the DNA profiles obtained from the body swab from Linda Daughney, the body swab from Donna Daughney, and the vaginal swab from Nina Flam match the DNA profile obtained from the combined scalp and pubic hair standard from Legere. There was no exhibit material available from Anne Flam and therefore no analysis was conducted. A full report will be available by December 1, 1990."

Q. O.K., and that report was made before you had the test results of D10S28, D7Z2, and DYZ1; is that correct? Would you like the exhibit of - can you tell by the autorads?

A. Yes, it's the day before I had my first result with D10S28.

Q. Yes, that was the day before you had your result of D10S28. Now, from the time you finished up to D16S85 on December 5th of 1989 until November of 1990 when you made that report and before you had these results what other tests did you make so that you could give a decision on November - was it second -

A. Second.

Q. - second, of 1990, that you couldn't give in December of 1989?

A. There was no additional tests.

Q. There was no additional tests. Why didn't you give a report in December of 1989 once you finished D16S85?

A. No report was given because it's not customary to give a preliminary report at all. Essentially we only give a final report once the final analysis is completed and that includes using the monomorph and the 'Y' probe.

Q. O.K., but you gave a preliminary report here on November 10, 1989, you gave a preliminary report here on November 2, 1990, and after you had all them completed you gave another final report on December 4, 1990; is that right?

A. Again, the two preliminary reports were very preliminary and they were also at the insistence of the investigators.

Q. Now, I believe you mentioned you couldn't proceed after you did D16S85 in December of 1989, you subsided with testing until November of 1990 because you were changing your lab over?

A. That was one of the reasons.

Q. One of the reasons.

A. We underwent extensive renovations. I then became involved in the training of ten new individuals for DNA typing. I had other -

Q. Just stop a minute, couldn't you use the testing of Mr. Legere's cases here as part of the training process for other students, showing them how it's done?

A. No, case work is not used as part of a training process.

Q. O.K.

A. I had received further exhibits in the summer of 1990 which I processed prior to continuing with the processing of this particular blot, so I was working in other aspects of the case, I just did not happen to re-probe this blot until November of 1990, and that was contingent upon the completion of the database for D10S28. I knew it was forth-coming and I waited until the database was ready before I actually used it in case work.

Q. Now, in order to be conservative and to benefit the accused you ruled D16S85 inconclusive. Do you have your sizings with you that you made on D16S85?

A. Yes, I do.

Q. And although you drew it inconclusive you did give lane 3, Mr. Legere's sample, sizes?

A. That is correct.

Q. And you also gave lane 10, 1J, sizes?

A. That is correct.

Q. And you also gave lane 19, 135, sizes?

A. That is correct.

THE COURT: I don't think the jurors will find this - the jurors haven't got this information, this sheet?

MR. FURLOTTE: No, they do not have this information. Now, the sizes in lane 3, Mr. Legere's, you gave the top band 1,600 base pairs, correct?

A. That is correct.

Q. And in lane 19 you gave the top band, Mr. Legere's, 1,614 base pairs?

A. That is correct.

Q. Not Mr. Legere's band but the top band in lane 19, 1,614 base pairs?

A. That is correct.

Q. And the bottom band in Mr. Legere's lane, you gave it 1,015 base pairs?

A. That is correct.

Q. And in lane 19, the bottom band in that lane, you gave it 1,002 pairs?

A. That is correct.

Q. And you also applied a percentage as to how far the bands would have been out between lane 19 and lane 3?

A. That is correct.

Q. And the top band in lane 3 and 19 were out by plus .9 per cent?

A. Sounds about right, I don't know where it is.

Q. I have mine here if you want to - it's a copy of yours.

A. Oh. That is correct.

Q. And the bottom band was out by minus 1.3 per cent?

A. That is correct.

Q. Now, isn't that odd to have a difference in bands going in opposite directions?

A. Not at all.

Q. Now, in comparing bands from - you mentioned earlier from lane 3 to lane 19 it might be difficult to see if they are - if there's any difference between them because of you're going a farther space. If they're right close together you can tell whether or not they're level and identical but the farther apart they get the harder it would be to tell if they're -

A. It's more difficult to follow totally across the gel as opposed to lanes side by side, yes, but it can be done, always using the reference markers to visually align the bands.

Q. Now, I believe also in your direct testimony and confirmed by Dr. Waye that when you were comparing gel one to gel two you were looking for matches, exclusions; is that right?

A. Gel one to gel two, yes.

Q. And you found visible matches between all the probes that you've compared? You didn't compare D16S85 but the other ones you found visible matches between gel one and gel two?

A. That is correct.

Q. And they all fell within the match window?

A. That is correct.

Q. Now, if you compare gel one and gel two with D16S85, you've never done that?

A. I believe I may have.

Q. Did you get a visual match or did you get an exclusion?

A. I never called a visual match with those samples.

Q. That's right, you never called a visual match within the first gel?

A. That is correct.

Q. But if you compare between gels do you get a match or do you get an exclusion?

A. If -

Q. Let's not give Mr. Legere the benefit of the doubt here any longer, O.K.? If you're only 95% certain or other labs would call this a match but to be beneficial to Mr. Legere we're going to say, oh, we're not going to count this one, O.K., let's not do Mr. Legere any favours, let's give it to him, let's call it, let's not say this is inconclusive, D16S85, I don't want you to do him any favours -

THE COURT: The question is approaching a speech.

Q. O.K., now, if you want to compare the first gel with the second gel do you not get a visual exclusion?

A. No, you do not.

Q. Would you show us, please? Is that D16S85?

A. That is D16S85 or blot one, gel one, court exhibit P-161. This is court exhibit P-161(7).

Q. O.K., now would you get out autorad for D16 in the second gel? Now, how do you compare visual

matches between gels?

A. One uses the markers from one gel to the next to compare how they ran from gel to gel and uses that to give you an idea of how these samples ran compared from one gel to the next. Obviously doing a gel to gel comparison one has to rely more on the computer imagery to give you a size for that band to see if it falls within your match window.

Q. If these bands are the same size from one gel to another you should have equal distance between bands, should you not?

A. No, because what happens here is that when you run different gels the way the markers migrate is different, so I don't know - they should be comparable.

Q. They should be comparable. Would you transpose those to -

THE COURT: Mr. Furlotte, perhaps if you were to do as you did Friday and stand over this way and Dr. Bowen's voice would carry over to the jury.

A. O.K., I'll try and point out what we're comparing here. This is the marker lane from gel one, this is the marker lane from gel two, this is the result from gel two, and these faint results are from gel two - sorry, gel one. Now, we cannot compare by superimposing these two gels because look at the difference in the markers. Look at the way the markers have run, they have run differently so you cannot say that what you see with one particular gel is superimposable on another gel because each gel runs slightly differently and that's why we have marker lanes

in the gel to tell us how that particular gel ran and to give us a size for those particular fragments. If I ran this gel for three hours longer I would get a greater separation between the bands because that's the way the electrophoretic system works, so no two gels are identical and that is why we use markers in order to determine the size of the fragments within that gel, so you cannot perform this experiment because you can't even superimpose the two markers.

Q. Why not? You're going to run them for the same length of time, why doesn't everything travel at the same -

A. Everything travels at the same time with respect to the markers. The markers are the control -

Q. But if you can't control your markers how can you expect to control your evidence samples?

A. But the markers run according to the way that particular gel was run, samples ran in that gel, so it is an indication of the size of the fragments in that gel.

Q. So are you saying you can manipulate the sizes of your DNA fragments by according to as to how long you run the gel?

A. No, because what this does do, if you use a computer to scan the size of these bands they end up being the same size, or within the match window. The computer does not determine that, it's the markers and how they ran in that gel determine the size of the fragments, and the markers run in a similar fashion because they're in the same gel as the polymorphic fragments that we've run in the gel two, therefore they all run

the same way.

Q. So you're saying if I lined - I can't line it up in here.

THE COURT: You do it for him, Dr. Bowen.

A. I'm not quite sure what he's trying to do.

Q. O.K., I guess we can't show the jury in the - maybe we should have the lights on.

A. You want to try it on the light box?

Q. Maybe we could try it on the light box.

A. Fine.

Q. That would be lane 19?

A. That is correct.

Q. If you lined up the length of the two bands, top band level?

A. That is correct.

Q. Now, we see here the band in lane 19, 135, on the top?

A. Approximately, yes.

Q. Yes, and it is much higher than the lower band for Mr. Legere?

A. That is correct.

Q. And you say that's normal?

A. All one has to do is look at the comparison between the markers. The marker here is almost level and yet this one is much higher as it is in the other gel. Relative to the markers these bands are running true. However, the fact is we're dealing with a gel to gel comparison where the markers have run to a different extent because of the gel conditions, perhaps the buffer solution, the per cent agarose, the time of the run can all make various slight differences in the way one gel runs as opposed to another, but the

bands, the polymorphic bands, the fragments in the samples that we're comparing, run true as compared to the markers run on that particular gel.

Q. O.K., that's one argument. If that was true would you also not have the same amount of inconsistency in the bands of the other probes?

A. Depends on what area of the gel you're looking at. The amount of inconsistency is going to vary slightly throughout the gel. This is a very broad area where the resolution of the gel is quite good. and thus the extent that you run the gel, the differences that you'll see will be more apparent in the lower portion of the gel than it would be in the upper regions of the gel where the fact is that these molecular weights are much closer. It has to do with the size of the fragments that you're dealing with in the fact that how much you can detect a difference between the way these two gels ran. Remember it's a geometric separation, this is not linear, and the difference between here and here is 600 base pairs. The difference between here and here is 400 base pairs. That's a thousand base pairs, that's another thousand base pairs, that's another thousand base pairs.

Q. So it's going to make a difference in your computer sizings?

A. No, it will not, because the computer looks at the markers as they ran in that particular gel and uses that as the standard.

Q. So why do you get different computer sizings for the D16 between your first gel and your third gel out by 5.5%?

A. Because with the size of the bands that we've seen -

Q. Dealing with the same size bands, Doctor.

A. No, no, I'm talking about the physical size, the fuzziness of the bands, that fact that with that first exposure of D16S85 that I ran on the third gel the markers were overblown and the fragment sizes were overblown, meaning they were very large, it's much more difficult for the computer to find the centre of those bands. On reprobing that membrane with D16S85 using it under more suitable conditions where the markers were not overblown, the band fragments were not overblown, the computer was better able to give me a more precise size for those bands and in that case it fell within 5%.

Q. O.K., we'll leave this one here for now, and would you get the - oh, we don't have those in evidence. Do you have the autorads for the third gel?

A. Yes, I do.

Q. Maybe we could put those into evidence.

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

THE COURT: The third gel, that was -

MR. WALSH: Yes, perhaps an explanation from the doctor just to refresh everyone's memory as to what that applies to.

A. The third gel contained additional known samples purportedly from Mr. Legere, it contained a known sample from Father Smith and the questioned hair found on the body of Father Smith.

THE COURT: That would be Exhibit D-11.

Q. O.K., maybe we could compare that to -

MR. WALSH: What are we comparing here?

A. There's actually two autorads for this particular probing. One was performed on November 23rd of 1990, it's the first hybridization for locus D16S85. This is the one that I mentioned that the computer sizings, as Mr. Furlotte has pointed out, were slightly outside our match window. The second hybridization with the same probe done at a later date, March 15th of 1991, was done and this one indicated that the comparisons were within the match window. In fact, they were 5%.

Q. How can you get the difference?

A. Very simple, the computer can give you totally different numbers plus or minus 25% scanning the same autorad several times.

Q. O.K., but nevertheless the bands should be the same distance apart on both of them because once the bands are put onto the nylon membrane they never move?

A. That is correct, so the bands for this particular set of two autorads are superimposable because it's actually the same blot that we're reprobing.

Q. And speaking about the computer, I believe you can override the computer, too, to get whatever readings - if you don't like the reading you can override the computer and move it wherever you want?

A. It is possible to have some limited ability to move bands wherever you want. We do not use that particular override in case work.

Q. O.K., so maybe we'll put this one on. This first one would be Mr. Legere's lane?

A. Yes.

Q. Again, Doctor, this is lined up with the top band?

A. That is correct.

Q. Mr. Legere's is lined up with the top band in lane 19 which is Exhibit 135, the body swab from Linda Daughney?

A. That is correct.

Q. And the bottom band would appear to be much lower than the other mark?

A. That is correct.

Q. And this is a marker lane?

A. Mm-hmm.

Q. And this is a marker lane?

A. That is a marker lane, if you want to move the two markers -

Q. O.K.

A. - again you can see this marker lines up and this one is lower, so relative to the markers these bands are running in the same position. You have to compare the markers run on one particular blot as compared to another, so you cannot again superimpose one autorad on top of another if they came from different blots.

Q. O.K., if you look at the marker lane on the first gel, the bottom line seems to be right in line with the bottom marker lane?

A. No, it seems to be slightly lower.

Q. Slightly lower?

A. Again this is why the comparison was not made. The fact is you're looking at a very fuzzy band. It's very difficult to position it, that's why it was called inconclusive. It does appear to be slightly lower than this particular marker point.

Q. Not as low as this one?

A. Again, relative to the markers and the way this particular gel ran it's in an identical position.

Q. And this is the sizing of Mr. Legere's bands in lane 3 in the first gel?

A. That is lane 3 of the first gel.

Q. And this would be Mr. Legere's lane on the third gel?

A. That is correct.

Q. We don't have any big blobby bands in Mr. Legere's lanes because there was never much DNA to begin with, so for the computer to find the centre it's not like trying to find the centre of this or some other - or this one here?

A. That is correct, but that is why this is the first probing where we found it to be outside the match window. You've just pointed out exactly why. The markers are overblown, it's difficult to find the centre of these bands and that's what the computer uses as reference points. Therefore it quite simply fell out of our match window whereas these ones the bands are much tighter in the markers, much easier for the computer to determine where the centre of those bands are, and it gave me a match that it was within our match window.

Q. But still, you take your top band here which is much easier to see in lane 19, the evidence of a body swab from Linda Daughney, it would appear to be right in line with the marker?

A. No, again I beg to differ, it's slightly below the marker.

Q. Well, if that is slightly below the marker this must be a lot below the marker?

A. But it's relative to the way the markers ran.

This gel ran more, so the more you run it the greater the difference is going to be.

Q. Between the marker and the band?

A. Yes, because it maintains the same relative position. If the markers are further apart as they are in this gel, then any sample that ran true to the markers is going to be slightly further. It all depends on the way the gel ran. You cannot superimpose one autorad on top of another from a different blot because the gels run slightly differently, and the markers are incorporated in the gel to tell you how that gel ran and how the samples in each of the lanes ran according to the markers.

Q. O.K., so what you're telling me is you have to rely - it's hard to go with the markers because it depends on how far the markers are apart. You're saying because these markers didn't run down long enough, then you would expect to see it right opposite the marker?

A. One would expect to see it slightly closer to the marker.

Q. But if you run the gel for a longer period of time everything's going to travel down farther to the bottom of the gel?

A. The markers will become more spaced out and the samples that are between them will become slightly -

Q. Become more spaced out, so in comparison you're saying that, well, if the gel is run longer you would expect the band to fall below the marker?

THE COURT: Excuse me just a second. I understand that in the holding cell they're having difficulty

hearing. It's perhaps a matter of where the microphones are located or - let me see, it's a little bit early for a break yet.

CLERK: They say it might be picking up a fan.

THE COURT: Picking up a fan? Could the fan be turned down a little?

CONSTABLE: It's down as far as it will go.

THE COURT: Is it? Pull the plug outside on the fan. Nothing else that can be done? Well, let's carry on. Perhaps if counsel and witness would raise their voices as much as they can that microphone would pick it up. All right, it should pick up better there now, it's been relocated.

MR. FURLOTTE: O.K., Doctor, I believe you were saying that if you run the gel longer and you get your bands further apart, then you would expect a band maybe on this gel, which is level with the marker. If it's run longer then you expect this not to stay parallel with the marker but to actually gain ground on it and get to the end of the gel quicker?

A. As I've said, it isn't quite level with the marker to begin with, it's slightly below the marker, and it will travel according to its size just as the marker does in this particular thing. Therefore, if you run the gel longer the separation, the visible separation, will be greater because you've actually been able to resolve this a little better with -

Q. O.K., Doctor, I'm putting this as - appears to be a straight edge. Maybe this one's straighter, I don't know. We'll line up the two markers and it seems to line up exactly with both markers, does

it not?

A. In the centre of the density is -

Q. O.K., but I'm not at the centre of the two markers, I'm at the bottom of the two markers and it seems to pick up the bottom of the band.

A. That's about the middle of the band.

Q. That's about the middle of the band?

A. If you're looking at the way the markers run, that is the way the markers run. That is the centre of the density. You cannot see anything in that lane. If you go down below the centre of the density, then you can see the top of that band appearing. Thus it has run faster, it's migrated more than the marker lane has. Therefore it's below -

Q. You interpret then - O.K., you're saying it's a little low. Let's, for instance, say it was even and you run your gel for a longer period of time, would that stay consistent with your marker or would it go below?

A. If it was the same size as the marker as you're trying to indicate, then it would run the same size as the marker all along, but I am saying, and I think it's apparent from this, that it is not the same size as the marker and thus it will migrate according to its size.

Q. Let's try the top one over here.

A. Again you're below the marker lane and you're beginning to see the top of that particular band. It is below the marker.

Q. O.K., that one looks to be a bit below, and you say this one is below also?

A. That is correct because you are now looking at

below the marker to find that band here. You're below the marker and you're about the centre of the density of that band.

Q. So it's a matter of interpretation, you would admit that, if it's below or even?

A. I would expect -

Q. You would interpret as being below?

A. I would expect anyone with experience in reading these autorads would agree with me.

Q. How about the bottom band?

A. The bottom band it's hard to say because as I say, and this is why I have not made this call, it's too fuzzy a band. I don't really know where that band is, could be up here, could be below here, could be the centre there, I don't know.

Q. Now, these marks here - see this mark here?

A. Yes.

Q. Now, I believe you scored that as two bands?

A. That is correct.

Q. And I believe from the sizings you have they are only 20 base pairs apart, the top band is 776 base pairs and the bottom band would be 756 base pairs. That's scored on December 3, 1990, whichever one - the December 3, 1990, one, which one is that? That would be this one.

A. That is correct. It was scored at a later date.

Q. It was scored at a later date, so these are only 20 base pairs apart?

A. That is correct.

Q. So even when you're only 20 base pairs apart you can see a distinguishable difference if they're right under and in the same lane?

A. Depends on the area of the gel. This is not a

very clear and distinguishable difference.

Q. O.K., 20 base pairs apart out of 756 and 776, what kind of percentage would that be?

A. I don't know the numbers, what was it?

Q. 756 and 776.

Q. It would be less than three per cent apart?

A. Oh, yes.

Q. Closer to two per cent apart - about two and a half, three per cent?

A. Somewhere in that range.

Q. So you can see a distinguishable difference between bands when they're only two and a half to three per cent apart? Is that correct?

A. It is possible, some areas of the gel, to distinguish that, yes. In this portion of the gel you couldn't get that distinction.

Q. And when you had the reading of the band between Mr. Legere's first gel and his third gel you have bands 5% apart. It was 5.5 but you did it over and got 5%?

A. That is correct.

Q. So there should be a distinguishable difference if they were in the same gel or right next to one another?

A. Not necessarily, no. Again, as I've said, these are very fuzzy bands. It's very difficult for the computer to find a centre of a band and distinguish where that band actually lies. I really place very little faith in the fact that those measurements happen to be 5% off. Basically that's part of the reason why I haven't called this particular locus. I am not happy with the shape and formation of those bands. Therefore I'm

not going to place that much weight on the fact that I can match those bands using a computer.

Q. O.K., now, I'm wondering, when you get this with D16, you get the difference in the size, the distance between the two bands, O.K., like we mentioned here, which it seems to be quite a difference between the size of the - oh, here we are - O.K., you seem to be quite a bit below. Now, the question I want answered, why don't you get that in the other probes when you transpose the other probes?

A. As I said, the visible difference between the bands in this region of the gel is going to be much more distinct because look at the difference in size, as I said. This here is a difference between 500 base pairs and 1,600 base pairs. Therefore this is a difference of 1,100 base pairs here, that's quite a difference. In this area of the gel the same difference in base pairs, this is approximately 1,000 base pairs here, it's a much smaller difference. It's non-linear. Therefore, in the bottom of the gel you can be able to distinguish this much greater than you would at the upper -

Q. Depending on the size of your bands you would get the distinguishable, you're saying?

A. Visually, yes.

Q. Visually. O.K., maybe we could put these away and we'll do the same thing for the D1S7 between gel one and gel three.

THE COURT: Could we have those marked by the Clerk? The two autorads for the third gel would be D-11.

CLERK: D-11(A) and D-11(B), My Lord?

THE COURT: O.K., or D-11(1) and D-11(2), we've been using them.

CLERK: Yes, My Lord.

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

THE COURT: I guess so, yes, we'll have a morning break now, please.

(BRIEF RECESS - RESUMED AT 11:15 a.m.)

(JURY CALLED - ALL PRESENT.)

(ACCUSED IN HOLDING CELL.)

CROSS-EXAMINATION OF DR. BOWEN CONTINUED:

Q. O.K., Dr. Bowen, maybe we'll try the same comparison between the first gel and the third gel with D1S7, which is a larger size fragment. Now, the other fragment sizes on D16 we were dealing with fragment sizes under 1,000 to 700 base pairs?

A. In that size range, yes.

Q. And this size range we're dealing here with fragment sizes 7,300 for the top band and 4,550 for the lower band, would that be about right? I'll show you my size fragments here.

A. That's right.

Q. For lane 3, 7,301 for the top band and 4,550?

A. That is correct.

Q. Now, this is lane 19 which is the body swab of Linda Daughney?

A. That is correct. That is blot one, the probing for D1S7 on chromosome one for lane 19, yes.

Q. And here in lane 4 would be for Mr. Legere, we'll take the lighter bands because it might be easier

to compare?

A. Sure.

Q. O.K., would those top bands be about level?

A. That is about correct, yes.

Q. And again the bottom band on the third gel would appear to be lower than the bottom band on the first gel?

A. It appears to be slightly lower, but again if you compare the markers the markers have run slightly different in that region, too. In fact, the marker here is slightly lower also. Unfortunately this particular exposure is slightly overblown in that region of the markers but it does show you the same effect. The markers did not run with the same separation that one sees here, there's a slight difference.

Q. But again we're in a higher region of the gel. Before we were talking - you were saying because you're in the lower region of the gel you're going to get that disparity?

A. You'd see a greater disparity at the lower regions of the gel, you still see some of that at the upper regions of the gel.

Q. It's about the same disparity, isn't it, at the top of the gel?

A. I don't know, I don't have the other one in front of me, but it seems to me this is slightly smaller.

Q. Slightly smaller. The other one we were dealing with bands between 700 base pairs and 1,000 base pairs and now we're dealing with bands between 4,500 base pairs and 7,000 base pairs?

A. That is correct.

MR. FURLOTTE: I believe one is an exhibit and maybe we could make the other one an exhibit?

THE COURT: Is this an exhibit now?

A. No, this is D1S7 of the third gel.

THE COURT: Oh, a probe on the third gel, yes, so this would be D-12, I guess, or would it be D-11(3).

A. Since we've combined all the autorads for a particular gel I guess to be consistent this should be 3.

THE COURT: D-11(3), yes.

Q. O.K., now, Doctor, maybe we could go on to comparison between the D4 in the first gel and D4 in the third gel, and I believe you stated this is your most sensitive polymorphic probe?

A. That is correct.

THE COURT: Well, now, can we mark that as an exhibit? You want to put this in, too?

MR. FURLOTTE: Yes, I would.

THE COURT: So this is the D4 probe, D4S139 probe on the third gel, and that would be Exhibit D-11(4).

MR. FURLOTTE: Again, Doctor, we're dealing with bands in the range of 4,500 up to around 5,700?

A. They were between 4,000 and 6,000 base pairs.

Q. So they're approximately 4,670 on the third gel, for Mr. Legere's lane 2 we have 4,670 base pairs ranging up to 5,830 base pairs?

A. That is correct, about the same range that we were just previously looking at with D1S7.

Q. And this would be lane 19, Linda Daughney?

A. That is correct, on gel one.

Q. And this would be also Mr. Legere's lane, the lighter bands?

A. That is correct, on gel three.

Q. Is that properly adjusted, Doctor, or do you want to change it?

A. That's suitable.

Q. And it looks here, Doctor, as if the bands are a closer match than on the other two, on the other two that we did for D16 and for D1 -

A. D1S7? Yes, it appears closer, yes.

Q. Yes, so this is a middle of the range approach because we're somewhere in between the size of the bands for D17 and for D16, would that be right?

A. No, I believe the upper band was - D1S7 is slightly higher and the lower band was lower than both these bands.

Q. Yes, the lower band would be about the same in this one here, D4 and the D1? One was 4,500, this is 4,600?

A. If that's correct, yes.

Q. And the only difference would be in the top band?

A. That is correct.

Q. Why wouldn't you have the same amount of discrepancy in this cross-reference of these two probes, the D4, as you would in the D1 or even the D16?

A. Well, if I remember correctly the D1 band was higher, it was around 7,600?

Q. Yes.

A. O.K., that one we matched the top band of each of the two lanes and found that the lower band was further discrepancy because you have a wider size range here than you were actually looking here. With these two you're looking at a closer size range between the two bands and thus one would not

be able to distinguish the difference that closely.

Q. So we're talking now about not just the amount of base pairs but we're also talking about the size range difference between the two base pairs?

A. No, because as I stated before, the way the markers run and the way the gel runs is geometric. Therefore one would not be able to distinguish a difference at the top part of the gel as well as at the bottom. You're looking at an area higher than this compared to an area lower than these two bins. Therefore one should be able to distinguish that difference more than two bands that are intermediate to that.

Q. So basically, Doctor, is there any way that you can compare band sizes from gel to gel aside from relying on the computer sizes?

A. Yes, there is. One can look at the markers. One has to be aware that the markers will migrate differently from gel to gel and gauge that difference when comparing one autorad to another. It takes experience, there's no doubt, but one can do that.

Q. Then the matter of interpretation, would you say it's very subjective?

A. I wouldn't say it's very subjective but there is some subjectivity to it, it requires experience in looking at the markers and gauging how the bands fall between those markers if one is trying to do a visual match from gel to gel. This of course is confirmed using the computer which is more objective.

Q. O.K., but we saw in the lower bands, I believe,

and even in the upper bands, how the bands did not even line up with the markers on each gel. One would be almost even with a marker, the other would be quite a bit below the marker?

A. But then one has to look at the difference between how the marker bands ran and compare that. It requires a little thought and care in determining how one would predict it would run in the same gel.

Q. The frequency levels that you gave in this case, you described them as - one in 5.2 million as what, being remote?

A. That is correct.

Q. And how did you describe the one in 310 million?

A. Extremely remote.

Q. Extremely remote. You didn't mention anything about the chances - one in 68, what you considered that to be?

A. I do not believe I was asked.

Q. No, nor did you give an opinion as to one in 7,400. How would you describe those?

A. I would say that they were consistent with being from the same individual.

Q. O.K., let's leave - not the consistent being from the same, just say consistent. You wouldn't give any probable or highly likely or any - you wouldn't care to qualify those numbers, would you?

A. No, they're based on one or two-probe matches, which is not improbable that two unrelated individuals could match at two loci.

Q. Now, are you just relying on the bands matching, or are you relying on the numbers also when you say remote and highly remote and consistent?

A. I rely on the number of loci that match plus the estimated frequency.

Q. Plus the estimated frequency?

A. It's a combination of both.

Q. On the monomorphic probe in the first gel, DYZ1, which is the sex probe, you found for the first time that there was male DNA in one of these lanes?

A. That is correct. The lane for item - the male fraction of item 109 which I believe was the vaginal swab reportedly from Linda Daughney.

Q. So you found some male DNA in that lane?

A. That is correct, a very small amount of male DNA.

Q. And when you did your separation - were you able to find any male DNA when you did the separation, into the next lane?

A. I believe the only patterns that I saw in that particular lane -

Q. O.K., that was the male fraction?

A. That was the male fraction, yes.

Q. There was no male DNA in lane 11, the 109F, was there?

A. That is correct.

Q. But when you did your separation between female epithelial cells and semen, supposedly, there did appear to be some male DNA that were transferred when you did the separation over into lane 109?

A. There did appear to be male DNA present in lane 109.

Q. And also in - I suppose it's lane 12, item 109, I should be saying, there were bands recorded for that lane?

A. That is correct.

Q. Which matched Donna Daughney's DNA?

A. I'm not sure if it's Linda or Donna. I would have thought Linda but I could be wrong.

Q. Exhibit P-160, the book.

A. You're right, it's Donna Daughney.

Q. Right, so when you run your autorads you found the same bands in lane 11, which was the female fraction of the vaginal swab reportedly from Donna Daughney?

A. That is correct.

Q. And in lane 12 which was supposedly the male fraction of vaginal swab reportedly from Donna Daughney you found the bands to be consistent with each other throughout your tests?

A. And consistent with Donna Daughney.

Q. And consistent with Donna Daughney?

A. That is correct, indicating carryover from the female fraction into the male fraction.

Q. Now, you say it indicated carryover; is there any way that you can tell that the male DNA in lane 12 was not identical to the female DNA in lane 11?

A. If we apply a little logic to what I saw in lane 12 the amount of male DNA present in that sample would not be sufficient to give a band pattern.

Q. Not even in your most sensitive probe, the D4?

A. That is correct.

Q. How do you know that?

A. Through experience.

Q. Through experience. Again it's a matter of interpretation of the density of the bands?

A. That is correct for the sex-typing probe, yes, the DYZ1, and the monomorphic locus.

Q. I believe in your direct testimony when you mentioned about the third gel you said that gel to gel comparisons are more difficult and you have to rely on visual matches but they're more difficult.

A. That is correct.

Q. And I believe you also said you rely matches more on the computers?

A. Yes, one uses the computer to certainly confirm that match, yes.

Q. And when the computer told you that on the third gel that you were outside your match window with Mr. Legere I believe you run it over again and got a different computer sizing the next time?

A. When the computer told me that on one band for one locus that I was outside the match window I did go back and rehybridize that membrane because I, having examined the autorad, understood that the markers were slightly overblown and the fact that the computer would have difficulty in sizing those particular markers and thus would possibly give me an erroneous result for that particular band. Therefore I did reprobe it and found that it was within the match window. It was not of any great concern that it was outside the match window to begin with because it's something we've observed within our database to begin with.

Q. When you start off the beginning of your tests does it depend on how high up in the gel you - let's say for instance this is your autorad. Would it depend how high up in the gel you would put your DNA as to how far down it's going to travel? All the lanes starting off at the same starting lane is what I'm saying, you start some

off a little sooner or later?

A. No, all gels are run with the sample wells in an identical position.

THE COURT: Aren't we being somewhat repetitive in these last few questions?

MR. FURLOTTE: No, I never asked that question before, My Lord. It's something I wanted clarification on.

THE COURT: No, I'm talking about the twelve questions before that.

MR. FURLOTTE: And, Doctor, the amount of DNA you had to work with in the evidence lanes and even on the first gel with Mr. Legere, they were just barely enough, it was stretching the limits of the technology?

A. They were approaching the limits of technology, as the fact that we were unable to obtain a result with many of the probes, yes.

MR. FURLOTTE: No further questions.

THE COURT: Thank you very much, Mr. Furlotte. Re-examination, Mr. Walsh?

REDIRECT EXAMINATION BY MR. WALSH:

Q. Dr. Bowen, Mr. Furlotte questioned you extensively with respect to blind proficiency testing. The guidelines that were developed by TWGDAM, you're a member of that actual group, are you not?

A. That is correct.

Q. And you have undergone open proficiency testing yourself?

A. That is correct.

Q. Each time you accept a case from a police force or agency or one of your R.C.M.P. detachments anywhere in this country, when you're doing the

actual tests where does that case have the potential for going?

A. To court.

Q. And the potential for going to court, what if any other potential does it have in terms of other people looking at your work?

A. For every case that is reported a second independent analyst has looked at the results and confirmed any matches or conclusions made for that particular test.

Q. What if any potential is there for outside experts looking at your reports?

A. In many cases outside experts, defence experts, do examine the results of all the tests made in a particular case and either confirm or disagree with the conclusions based on their experience.

Q. Are you aware of these potential reviews when you do a test that you've accepted?

A. No, I'm not. I'm aware of the second independent analyst within the R.C.M.P. because that is standard protocol as part of our quality assurance program.

Q. But are you aware that there is always the potential for defence experts looking at your work?

A. Yes, I am.

Q. And when an expert does review your work is he able to look at each step that you've carried out on the process?

A. Yes, every step is documented and available for second opinion.

Q. Mr. Furlotte took you through this Office of Technology Assessment Report, he had referred it

to Dr. Waye as well. He referred you to findings with respect to some labs. Were they police labs or private labs?

A. They were all private labs.

Q. Were any such conclusions drawn with respect to the FBI or the R.C.M.P.?

A. None to date, no.

MR. FURLOTTE: My Lord, I believe we might be misleading here since I don't - let's find out first if any blind proficiency tests were run of the R.C.M.P. or FBI.

MR. WALSH: Did you -

THE COURT: He's not speaking about blind proficiency tests now, he's speaking about the criticisms that were made of the errors made by the private labs, I think, isn't he?

MR. FURLOTTE: Well, My Lord, if the R.C.M.P. or FBI refuse to have them done, then I think the jury shouldn't be misled.

THE COURT: This has nothing to do with blind proficiency tests, do you?

MR. WALSH: Well, Mr. Furlotte does make a valid point. There is that - what he's talking about is blind proficiency testing and I was asking a question associated with whether or not the FBI or R.C.M.P. were commented on in this particular report.

THE COURT: Oh, well, they were done in blind proficiency testing, yes, I see.

MR. WALSH: Yes, the other ones. Mr. Furlotte does make a valid point but he did say something I would suggest is incorrect about the R.C.M.P. refusing to have them done. I don't believe -

THE COURT: All right, go ahead.

MR. WALSH: Is the R.C.M.P. refusing to have blind proficiency testing done, Doctor?

A. Not at all. In fact, I don't believe the OTA Report refers to blind proficiency testing. The labs in question knew they were proficiency tests. In fact, the R.C.M.P. has also engaged subsequent to that in outside agency proficiency tests, and in fact, we've performed three or four, you'll have to ask Dr. Fourney that, from outside agencies, and these have been evaluated.

Q. The private labs, so the jury understands, who began doing this work in North America first, the FBI and R.C.M.P. as a police lab, or in a private lab?

A. The first initial case work was performed by two private labs, Lifecodes and Cellmark.

Q. And these are labs that they make money doing these work for people, is that correct?

A. Yes, it's a commercial venture where they do paternity tests and forensic case work for commercial interests, and obviously monetary gain.

Q. And this OTA Report when it refers to those mistakes those labs made, those would have been in what years?

A. I believe it was 1987-1988, prior to the R.C.M.P. even opening their facility.

Q. Did you agree with everything those labs were doing back in them time frames?

A. No, I was quite aware that they had quality assurance problems in both those labs. They were not used to the custody of samples for the continuity of samples for case work analysis and it was a learning process for them.

Q. Did those labs have all the controls that the R.C.M.P. - back then did they have all the controls that the R.C.M.P. have now?

A. No, they do not.

Q. With respect to the OTA Report Mr. Furlotte referred you to -

MR. FURLOTTE: My Lord, maybe we could establish whether Dr. Bowen knows that on personal or hearsay evidence, what controls did private labs have.

MR. WALSH: Are you aware of some deficiencies the private labs had back then compared to what the R.C.M.P. have now?

A. Yes, I am, through Dr. Eisenberg who was formerly with Lifecodes.

Q. Mr. Furlotte referred you to the OTA Report and some of the findings they made associated with testing done on those private labs back at that time. Are you also aware, Doctor, whether or not the OTA Report made specific - after reviewing all of these things and reviewing the private labs and reviewing - what else did they review in this OTA Report?

A. They reviewed many things. They reviewed the basic biology of the technology, the quality assurance, and the statistical and population genetic aspects.

Q. Are you aware if after making that review whether or not they made any recommendations with respect to the underlying biology and/or the RFLP technique and whether it could be applied?

A. They recommended that it in fact is a reliable technology that can be used in forensics as it has been used in the clinical and research world for

many years.

Q. I'll show you Page 7 of the OTA Report, the bottom on the righthand column to the bottom on the other page. Would you read that just to yourself first and tell us whether or not that is the recommendation that you're referring to?

A. That is correct, it is the recommendation I was referring to.

Q. Would you read it to the Court and to the jury slowly, please, so they clearly understand the recommendation?

A. "Genetic and molecular principles underlying DNA identification are solid and can be applied to DNA isolated from forensic evidence. 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. 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 of applying the techniques per se are red herrings that do the courts and the public a disservice."

Q. Do you reject or accept that opinion?

A. I certainly accept that opinion.

Q. Mr. Furlotte asked you about the amount of sample that you had left after you completed these particular tests and you indicated that there was not a sufficient amount from the crime scenes to use doing this RFLP technique; is that correct?

A. That is correct.

Q. Is it or isn't it an unusual occurrence in a forensic lab to have minimal amounts of samples that you cannot -

A. It is not an unusual occurrence, in fact it happens in most cases that there is insufficient DNA for several analyses.

Q. You were referred by Mr. Furlotte to certain

sample lanes that had evidence of degradation; is that correct?

A. That is correct.

Q. Did you call any matches in any of those lanes?

A. No forensically significant matches, no.

Q. You testified - Mr. Furlotte had asked you a question, you testified that you've had no known standard available to you from Nina Flam; is that correct?

A. That is correct.

Q. How does the process of differential extraction assist you in this regard, if at all?

A. The process of differential extraction, as I've stated before, is an attempt to separate the female epithelial cells from the male sperm cells. In the female fraction one normally obtains female DNA which is presumably from the person who donated that swab. Thus one can distinguish a pattern found there as being from the victim and the pattern seen in the male fraction as being from the suspect or the accused or whatever.

Q. And you can use that as your standard?

A. One can use that as a standard, yes.

Q. Mr. Furlotte had you refer to the fact you didn't call 1I to 56A, 69A, even though there was a visual match?

A. That is correct.

Q. And you explained that. Would you just briefly just refresh the jury's memory why you did that, why you didn't call that?

A. That was with locus D17S79.

Q. That's correct.

A. And it was because the female fraction matched the

pattern seen in the male fraction for that particular swab. The fact that I never saw male or foreign DNA in the male fraction other than with our most sensitive probe led me to conclude that a conservative interpretation of that particular match would be that it came from the female.

Q. In whose favour would that - the decision that you made not to call that, in whose favour would that decision be?

A. The bias would be in favour of the accused.

Q. With respect to D16S85, and that's the one shown on the summary chart that has all the inconclusive calls, Mr. Furlotte questioned you extensively about these inconclusive calls at this probing. What was the underlying philosophy or policy of the R.C.M.P. Lab that led you to make those inconclusive calls?

A. The underlying philosophy of the R.C.M.P. Lab, as has been established, is a conservative approach in interpreting autorads and calling matches, and the fact is that these bands were not well-formed, poorly defined, non-uniform bands. Even though reproducible I did not call them as a match because they did not meet my criteria or standard for a good crisp band.

Q. If you hadn't have followed that conservative policy with respect to D16S85 at the match or between 56A and 69A in lane 19 in the item 135 what would that - if you had have actually called that a match what would that have done to the one in 310 million best estimate probability that you provided?

A. It would have made that best estimate definitely less common.

Q. Meaning?

A. That it would have been a more rare event.

Q. Instead of one in 310 million it would have been higher than 310 million? I know the term higher and lower - would it make it more rare or more common, the match?

A. It would make the match more rare.

Q. Just perhaps we can clarify this, I know it's between a scientist and a layman, higher and lower have different meanings. Will you explain when a scientist uses the term higher frequency or a lower frequency what you're actually -

THE COURT: Why can't we just settle that by saying you would have got a figure one in a billion instead of one in 310 million, or something in that order?

A. It would have been slightly more rare than one in a billion.

THE COURT: Now we're back where we started from.

A. Yes.

MR. WALSH: That's why I think this question might be important, My Lord, I know from my own experience. O.K., would you explain to the jury when science uses the term higher frequency or lower frequency how should your mind look at the numbers when you use those terms, using for example one in 5.2 million and one in 310 million as your comparison?

A. Why don't I use one in 68 as opposed to one in 310 million?

Q. O.K.

A. Actually that number means one divided by 68,

O.K., 68 is the denominator. Therefore that is actually a much larger number than one divided by 310 million, so the larger number of course is more common and this is more rare. I know it's difficult to understand that one is looking at the inverse of the particular number that we're looking at, so one in a billion is not a larger number because it's one divided by a billion which is actually a much smaller number, so it's preferable, I think, to avoid confusion to say more common or more rare.

Q. Now, with respect - Mr. Furlotte asked you questions with respect to the period of time that went by between the time that you had run your D16S85 probing and that time and the time that you ran the D10S28. What if any bearing would the time period between those two probings have on the validity of the test results that you found?

A. No bearing whatsoever.

Q. Mr. Furlotte referred you to two letters, the two preliminary reports that you gave before you made your final report.

A. That is correct.

Q. You gave one when you got your first probing at D2S44, is that correct?

A. That is correct.

Q. Who were you giving that to and why were you giving it?

A. That was given to a police investigator as an investigative aid so that they could focus in on one particular suspect, because at that time they had seven or eight suspects in hand and it's very difficult to investigate seven suspects as opposed

to one, so it was basically to help them focus their investigation.

Q. And with respect to the letter that you sent subsequent to that indicating you had done more probings, why did you send that particular letter?

A. That particular letter, if I remember correctly, was at the insistence of both the R.C.M.P. and the Crown Prosecutor's office because at that time they wanted to lay charges. I was not prepared to give a full report and thus I just gave at that point the information verbally or qualitatively in that particular letter.

Q. It was to explain where you were at at that time?

A. Essentially that's the basis of that letter, to explain where things stood at that time and to indicate - well, I guess it did not indicate that there were further things that had to be done.

Q. If you call one prob inconclusive like you did on the first gel is it scientifically acceptable then to compare gel to gel on something that you've called inconclusive?

A. It's generally not scientifically acceptable. If one is not willing to make a conclusion based on one gel, then to compare that inconclusion that - to something else is slightly unscientific.

Q. Mr. Purlotte had you superimpose some autorads on the overhead projector. Is that a scientifically acceptable comparison or experiment in the manner that was being asked you to do?

A. No, as I stated, the only way you can superimpose two autorads is if they came from the same blot. Each gel runs slightly differently and the markers themselves run differently and the DNA

samples run slightly differently. Therefore you cannot superimpose one autorad on top of another directly and make some sort of conclusion from that.

Q. Mr. Furlotte asked you about the qualitative statement that you made with respect to one in 5.2 million and one in 310 million and you had indicated qualitatively one in 5.2 million the probability of someone else contributing the sample was remote and in one in 310 it was extremely remote, and you indicated on questioning that you made those statements based on a combination of the numbers and the fact that there were four and five-probe matches; is that correct?

A. That is correct.

Q. Without generating the numbers -

MR. FURLOTTE: My Lord, I think we've dealt with all that on direct examination.

THE COURT: Well, we have been through quite a bit of that.

MR. WALSH: Fine, My Lord, I won't pursue that. I wanted to clarify a particular aspect when Mr. Furlotte raised that particular point I wanted just simply to clarify an aspect. I won't push the matter, I don't see any - there's no insistence on that if Mr. Furlotte is going to object.

THE COURT: Let's not push it, then.

MR. WALSH: Fine. The final thing is with respect to 109 and that was the vaginal swab purportedly to come from Donna Daughney, and you indicated that the sex-typing probe indicated male DNA in that particular substance, is that correct?

A. That is correct.

Q. And that is consistent with what?

A. Consistent with semen being present in the vaginal swab.

Q. And the semen consisted in the vaginal swab, the amount, compared to the amount of semen on the body of Donna Daughney, purported to come from the body of Donna Daughney, how did it compare?

A. There would have been much less male DNA in that particular sample.

Q. In the vagina or on the body?

A. In the vagina.

Q. More semen in the vagina than on the body - less semen in the vagina than on the body?

A. That is correct.

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

THE COURT: Thank you very much, Dr. Bowen. I think that's the end of you. Thank you for coming. You're not taking away any exhibits that you should be leaving?

A. I don't think so.

THE COURT: Probably glad to see the last of them.

MR. WALSH: Call Dr. Kenneth Kidd.

DR. KENNETH K. KIDD, called as a witness, being duly sworn, testified as follows:

DIRECT EXAMINATION BY MR. WALSH:

Q. Would you give the Court your name, please?

A. Kenneth K. Kidd.

Q. And your present occupation, position?

A. I'm Professor of Genetics, Psychiatry, and Biology at Yale University School of Medicine.

Q. And, My Lord, if I may with your permission take Dr. Kidd through his curriculum vitae?

THE COURT: Yes.

Q. Doctor, you have a Master's and Doctorate degrees from the University of Wisconsin, is that correct?

A. That's correct, in genetics.

Q. Your specializations were in immunogenetics and population genetics?

A. That's correct.

Q. Would you explain to the jury what immunogenetics is, please?

A. The study of blood groups, primarily at that time things like the ABO blood group in humans and other normal genetic variation that's identified by studying blood.

Q. And your other specialization was in population genetics?

A. That's correct.

Q. We touched on it with some of the other witnesses, Doctor, but if you would, please, if you would explain to the jury what the field of population genetics is?

A. The field varies quite broadly from very theoretical and mathematical analyses of structures of population, the effects of mating patterns, the effects of geographic isolation on what happens to

the genetics of a population; from that at one extreme to the other extreme of very empirical or applied observation of exactly what is seen in an actual population, and I've worked especially with respect to humans at both levels.

Q. You were a United States National Institutes of Health Postdoctoral Fellow with Dr. L. L. Cavalli-Sforza at the Institute of Genetics in the University of Pavia in Pavia, Italy, and you were later with him as a Research Associate at the Department of Genetics at Stanford University School of Medicine?

A. That's right, after I got my doctorate in genetics at the University of Wisconsin I applied for and was awarded a postdoctoral fellowship to go to Italy to study with Professor Cavalli-Sforza because he was considered one of the foremost human population geneticists at the time and that warranted the U.S. Government paying for one of its students to study abroad. While I was with him he was offered and accepted a professorship at Stanford University in California and moved to Stanford and I moved with him and stayed with him for a total of three years.

Q. And as you pointed out, your postdoctoral fellowship was in the field of human population genetics?

A. That's correct.

Q. You were also Assistant Professor of Anthropology and Pediatrics at Washington University and Washington University School of Medicine in St. Louis?

A. My first faculty position was at Wash. U. in St.

Louis. Because I was studying human genetic variation I can be considered in that sense an anthropologist and was part-time, half-time, in the Anthropology Department teaching undergraduate and graduate courses in human genetic variation and I was half-time in the medical school teaching general human genetics to the medical students at the medical school and participating in the clinical genetics program.

Q. In the medical school you would be dealing with medically-oriented human genetics?

A. That's correct.

Q. Would you explain to the jury what medically-oriented human genetics is?

A. Understanding and study of how different inherited genetic diseases are in fact inherited and how they're transmitted through families, so it involves a lot in those days - which is now twenty years ago - it involved a lot of genetic counselling, telling people who had had one child with an inherited genetic disease what was the risk of having another child with such a disease, telling people who were siblings of someone who had a genetic disease what their chance was of having a child themselves with such a disease. It's become much more molecular now and the work that I do in terms of inherited disease is more now trying to use molecular genetic techniques to actually identify the individuals who are carrying defective genes, or, in the case of one disorder I'm working on, to identify children very early in life who have a predisposition to certain kinds of cancer before they develop the cancer so that they

can be followed very carefully clinically and be treated early with appropriate lifesaving treatments before they develop the cancer.

Q. You went from there, Doctor, to become Assistant Professor of Human Genetics at the Yale University School of Medicine, is that correct?

A. That's correct. I was only at St. Louis a very short time. Yale started a new Department of Human Genetics the year I was in St. Louis and they wanted to hire a human population geneticist. They looked around and decided I was the one they wanted. I did not seek the job but once they identified me they made a very strong case and convinced me to move.

Q. And you went from Assistant Professor to Associate Professor and now you're a full Professor of Human Genetics, Psychiatry, and Biology, at that university?

A. That's correct.

Q. You were also a Visiting Associate Professor at Harvard Medical School and you were also a Visiting Scientist at the Biology Department of M.I.T., is that correct?

A. That's correct. In the very late 1970's and through 1980 it became obvious to me that the new molecular technologies for studying DNA and DNA polymorphism were going to be extremely important in all sorts of human genetic research. At that time there were only a dozen of these kinds of polymorphisms. Of the kinds that are entered into this case only a dozen were known, but I knew they were going to be important so I took my sabbatical year and went to Harvard and M.I.T. and

spent the year retraining myself to start up a molecular laboratory of my own which is now quite large.

Q. How large is - you run your own lab at Yale, I understand, Doctor?

A. That's correct.

Q. How large is your lab and what kind of people do you have in it?

A. Currently there are - I think it's sixteen people. It changes about once every month as new students arrive and postdocs leave to get their own faculty positions. I have five technicians who do a lot of the laboratory work. I have four people with Ph.D.'s who are involved in various levels of running the laboratory under me, either as staff research faculty within the university under my overall direction or as postdoctoral fellows just as I was with Cavalli-Sforza. After they get their Ph.D. some have come to me for additional specialized training, and then there are several graduate students.

Q. Do you have visiting scientists as well from other labs, other countries?

A. Yes, from - just this past week I had a visiting scientist from Israel who brought two of her graduate students to get a quick one-week course in my laboratory. I had a visiting scientist from Australia spend six months in my laboratory earlier this year, that sort of thing.

Q. You touched on it, Doctor, with respect to one of the areas that you were dealing with, but to understand what your lab does, what are the major areas of research interest of your lab?

A. My laboratory does many different things, but it has two very large themes that run through all of the projects. One of them is molecular methodology, not only very extensive typing. We've done probably over the last few years several hundred thousand typings of individuals for DNA polymorphisms, also development of new molecular methodologies, but the second theme that runs through it is a very strong statistical and data analysis component. My laboratory is one of the largest computer users in the whole medical school because some of the kinds of analyses we try to do in this research use a lot of statistics, require a lot of very sophisticated calculation, so that it's - I think my laboratory is one of the relatively very small number in the U. S. and Western Europe where in one laboratory both the statistical and population genetic expertise are very strong as well as the molecular.

Q. You have indicated that you were attempting to - you're dealing with an inherited form of cancer.

A. That's one of the particular projects we started on about ten years ago trying to find where the gene was. We have now located the gene. When I say we, it was a collaboration with Dr. Nancy Simpson at Queens University in Kingston, Ontario. We identified where the gene was, on which particular chromosome, happens to be on chromosome #10. We've narrowed it down to a small segment of that chromosome and now the work has become no longer statistical but almost entirely molecular as in the laboratory we're trying to actually clone the gene that causes this cancer so we can

study the DNA, find out what the gene does normally and abnormally and learn why the cancer results so we can figure out how to keep the cancer from occurring.

Q. The jury has heard about restriction fragment length polymorphism technique, RFLP; what if any use do you make of that technique in your lab?

A. When I said several hundred thousand DNA typings, those were all RFLP typings. We use them for constructing the general human linkage map, we've used them for identifying where this cancer gene is, they're the basis for all the number crunching on the computer that I mentioned earlier and we are also doing very extensive studies of human populations with RFLP's. We had a paper published in collaboration with Cavalli-Sforza, we're still collaborating with him quite closely. Even though it's been twenty years since I left his laboratory he's not only a friend but a scientific colleague. We published a paper in the proceedings of the National Academy of Science in February of this year in which we had studied one hundred different RFLP loci in a relatively small number of populations but populations distributed around the world, so we have a very large RFLP laboratory. I think my current collection of probes for loci that we are able to type in the laboratory is around 750 different RFLP's that we can type in the laboratory.

Q. And in addition to that you're doing human population studies, as you've indicated, from around the world?

A. That's correct.

Q. You're a member of a number of professional organizations and other professional activities, Doctor, I was going to take you through some of them. You're a member of the Genetics Society of America, is that correct?

A. That's correct.

Q. You're also a member of the American Genetic Association.

A. That's right.

Q. And you became a Council Member in 1990, is that correct?

A. That's correct, I'm in my second year of that three-year term.

Q. And what is the difference between being a member or being a Council Member?

A. Being a Council Member is being elected to the Board of Directors of the Society. There are twelve Council Members, four elected every year for three-year terms. We meet annually and help run the organization but there are several hundred members.

Q. You are also a member of the American Association for the Advancement of Science, you were a member from 1966 to 1981, and in 1982 you became a Fellow of that organization. What is a Fellow?

A. A Fellow is someone who is nominated and then elected by the Board of Directors of that association as someone who has been recognized as having made an outstanding contribution to the scientific community. It's limited to no more than ten per cent of the total membership.

Q. You're also a member of an organization called The Human Genome Organization, the acronym is HUGO?

A. That's correct. That's a relatively new organization formed to coordinate on an international basis the human genome project so that efforts are not duplicated, so that the research being done in countries all around the world is coordinated. It's an organization of scientists to try to advise the various national research funding organizations and to try to assure that really high quality science is done.

Q. The Human Genome Project, would you explain to the jury what that is?

A. The Human Genome Project means different things to different people. Depending upon who you talk to different aspects of it will be emphasized, but it is often - the analogy is often drawn that it's like trying to get a man on the moon in this decade. It is really a concerted effort to try to bring a variety of different scientific disciplines all to bear on really understanding the genetic composition of human beings. It's often stated that the goal in fifteen or so years is to have a complete sequence of the DNA. There are three billion bits of information in the human genome and to know what all of those are, what the complete sequence, is listed as one of the goals. In fact, there are a variety of other goals and the complete cloning and mapping of the genome is one of the steps along the way.

Q. You were also, Doctor, I understand, recently appointed to a committee on human genetic diversity, a committee of that organization. Could you explain who the members are and what you're trying to do in that committee?

A. O.K., I'm a member of two committees of HUGO. One is the Genome Mapping Committee which is a committee of about fifteen membes of HUGO trying to coordinate all of the various international scientific meetings, helping set dates, helping appoint organizers of the individual meetings, and that's because I have done a great deal in the past on gene mapping, but I have most recently been appointed to a much smaller committee on attempting to define a sub-project within the genome project to look at total genetic diversity or genetic variation in homo sapiens as a species. There are six of us on the committee, we are working to write a document to submit to international agencies as well as national agencies in many countries to define what needs to be done on a global scale. Our current estimates are that we should be studying about 300 to 500 different populations around the world and look at all of those populations at a large number of different genetic loci to try to really understand in a very minute way what the scope and nature of genetic variation is.

Q. And the six members, they're worldwide, is that correct? They belong to different countries?

A. That's correct. There are three from the United States. Cavalli-Sforza is Chairman of the committee. Mary Claire King, Professor of Genetics and Epidemiology at the University of California, Berkeley, is a member of the committee. I am the third member of the committee from the United States. There are three committee members from Europe. Dr. Julia Bodmer who has

specialized very much in the human histocompatibility system, the system that's involved in organ and blood transfusions, she is in London; Dr. Marcello Siniscalco, who was in the United States at the Memorial Sloan-Kettering Cancer Institute but is now back in Italy heading a new molecular biology institute that the Italian Government has established, and Dr. Svanto Paabo who is, I think, Swedish in origin, studied extensively for many years at Berkeley and is now a professor in Munich, Germany, is the sixth member.

Q. You are also, Doctor, a Charter Member of the Mammalian Genetics Study Section of the National Institute of Health?

A. That's correct. That was the U. S. Government's review panel for funding federal grants in human genetics research. That panel was started in 1979 or 1980, I don't remember. It is ongoing. I was a member of it when it was first started and served a four-year term as one of the twelve people who review all human genetics grant applications for the U. S. Federal Government.

Q. You're also a member, Doctor, of the Board of Directors of the American Board of Medical Genetics and you were also certified as a Ph.D. Medical Geneticist with the American Board of Medical Genetics?

A. That's correct. I mentioned earlier even when I was at Washington University in St. Louis I was involved in the clinical genetics program. I've continued to be involved in that at Yale. The American Board of Medical Genetics is a certification board that basically gives a seal of

approval and says this is a person who has qualifications in this. It's like a board certified neurosurgeon or a board certified pediatrician. I have been certified and I also served a period of time on the Board of Directors of that certification agency helping write the examinations that would be given to subsequent people.

Q. You're also on the Editorial Board of the Journal of Genetics, is that correct?

A. That's correct, and a few other journals.

Q. You also were a Special Consultant to the Howard Hughes Institute serving as a Scientific Director for the Human Gene Mapping Library and you were a co-organizer with Frank Ruddle of the Tenth International Human Gene Mapping Workshop?

A. That's correct.

Q. Would you tell us, please, what the Human Gene Mapping Library is or was and what if any practical application would it have to what we're doing here?

A. In my various roles associated with the Gene Mapping Workshop, this is a series of international meetings on the early stages of the Human Genome Project, it was a predecessor, if you will, of the current larger-scale project, I had many functions. One of them was chairman for two years of the DNA Committee, and all told a member of that committee for six years. The DNA Committee was responsible for keeping track of every bit of information that was known about DNA polymorphisms and for much of that time - you've probably already come across these various D numbers like

D10S28 - I was the one responsible for assigning those numbers to loci in order to keep track of them. The Human Gene Mapping Library started as a research project and became an international computer database in which all of this information was stored, and I helped design that computer database and then for a couple of years actually ran the whole operation which at its peak had seventeen staff members running the computer database. That was in addition to my research laboratory in the medical school. That database no longer exists, it was superseded and all of our information transferred to a new database using a new computer technology that is now operating out of the Welch Library at Johns Hopkins University.

Q. Doctor, I note from your C. V. that you have approximately 260 scientific publications of which you are either sole author or co-author.

A. That's right, I'm co-author of most of them because it's very rare these days that one scientist can do a lot of research and now I find my role is much more in directing the graduate students and postdocs in their research, so I'm included as an author because sometimes they're my ideas, sometimes they're the student's, but I work with them on all of the research.

MR. WALSH: My Lord, at this time I would probably - I'm finishing up very quickly with Dr. Kidd on the C. V. I see it's twenty-five to one. One of the things I'm going to ask Dr. Kidd is to give a couple of definitions to the jury on certain aspects so we'll probably be another ten minutes. If you want to break we can finish up pretty

quickly right after lunch on this.

THE COURT: I think that would be a good idea, perhaps, and we'll do that, then, and you shouldn't talk to anyone about this case until all your testimony is finished.

DR. KIDD: Right, I understand that.

THE COURT: So we'll go to lunch until two o'clock.

(JURY WITHDRAWS.)

(COURT ADJOURNS. RESUMES AT 2:00 p.m.)

(JURY CALLED - ALL PRESENT. ACCUSED IN CELL.)

DIRECT EXAMINATION OF DR. KENNETH KIDD CONTINUES:

Q. Doctor, when we left off we had touched on your publications and of the last hundred or so publications it's my understanding that about 80 or 90 per cent of those dealt with DNA or human population genetics?

A. Yes, I believe that's correct. Some of the others deal with database design.

Q. You have been - what I can understand from your background you've been working in the field of human population genetics for approximately the last 25 years?

A. Just about that. I started my first study of populations on the island of Bougainville in about 1967, so that's getting close to 25 years.

Q. You've touched on this aspect as well, and that is statistics. Could you just briefly explain the relationship of statistics to the field of population genetics and human population genetics in particular?

A. We are always dealing with large numbers and attempting to make estimates of what's really going on in populations based on looking at a sample or a small number of individuals, sometimes a larger number, sometimes a small number, and statistics is what is involved in trying to understand and analyze those data, determine how confident we are in the estimates we make, try to measure our level of uncertainty. Mathematical statistics is also very involved in most aspects of population genetics in that we're always trying to apply mathematical formulae to the observations we have relating a lot of different factors, how long people live, how many people there are, a variety of other things, to explain the frequencies we observe in the population.

Q. What is demography and what if any relationship would that have to the field of human population genetics?

A. Demography is the study of many of those variables that I was just mentioning. The average life span by sex, everybody knows women on average live longer than men. It differs by a large amount in undeveloped countries versus a country like Canada where there's much better health care, a variety of things like movement and marriage patterns, how far distant from where you were born was your spouse born, things that have changed over the last few hundred years as movement is now much greater than it was a few hundred years ago. These and many other things that you can easily imagine, birth rates, the average number of offspring produced per female who is in the

reproductive years, all of these are part of demography and they all impact on what we would make as predictions for what we would find for these DNA variants or any normal variation, what we call a polymorphism, something that has many forms in the population. How frequent each of those forms is, how many there are, are all determined by these demographic parameters.

Q. And what experience do you have in the area of human demography?

A. When I was still a postdoc with Cavalli-Sforza I was studying theoretical and mathematical demography and gave lectures at Stanford in graduate courses on those aspects of demography and clearly over the years I've had to study and incorporate the values in many of the examinations I've done of specific populations. My primary research is not to determine those variables but rather I have to use what other people have studied, people who have done life tables like the insurance actuaries who know how long on average people live. People who have looked at migration, I use their data in attempting to understand my data.

Q. I understand, Doctor, that you have given expert testimony in courts before on the forensic application of RFLP typing and the human population genetics issues associated therewith; is that correct?

A. That's correct.

Q. You have testified in the State of New York, on three occasions in the State of Virginia, in the State of Colorado, twice in the State of

California, in Vermont and in Ohio; is that correct?

A. That's correct, and also once in Arizona.

Q. In Arizona. Have you ever consulted for the defence in relation to any cases?

A. Yes, I've consulted for the defence on two separate occasions - I'm sorry, three, three separate occasions.

Q. And have you been asked to testify in other cases in Canada?

A. I have received requests but by and large I get many requests to testify, I turn down virtually all of them, and the one other request I've had from Canada I turned down.

Q. The time you spend in court, is that impacting on the research you do in your lab? Is that having an impact or an effect?

A. Yes, a very negative impact.

Q. You don't have as much time?

A. I don't have as much time. Testifying in court is an inconvenience but I do it because I think it's important that some scientists do testify.

Q. And last week I understand, Doctor, you were a symposium speaker at the Eighth International Congress of Human Genetics in Washington, D.C., is that correct?

A. Right, I spoke in a symposium on DNA variation and forensics.

MR. WALSH: My Lord, at this time I'm going to ask that Dr. Kidd be declared an expert in the field of molecular genetics, DNA technology and testing procedures, and human population genetics.

THE COURT: Any questions you want to put to the witness,

Mr. Furlotte?

MR. FURLOTTE: The Crown is asking that you be declared an expert witness in the area of human population genetics. Could you describe how that would differ from just other population genetics?

A. As I mentioned earlier, population genetics has a broad range from the almost purely mathematical and theoretical to the very applied specific to a given organism, and depending upon the nature of the organism the specific questions will be much different. In drosophila genetics and population genetics the individual fly lives only a short period of time, flies only a certain amount of distance. Those sorts of things impact on the structure of those populations and hence the questions that are relevant and addressed, and I've spent more than twenty years studying human populations and the particular questions and types of data that are available for human populations, so that I would say the main distinction would be the expertise in knowing the relevant questions, the relevant kinds of data, and knowing a great deal about human history, human migrations, and other studies of human data.

MR. FURLOTTE: But as to whether or not the mathematical formulas would apply to human populations or other types of populations it's the same basic principles?

A. Most of the principles are the same. There are some very specific formulae and procedures one would use in human population genetics that one would not use in drosophila population genetics because slightly different questions are relevant.

MR. FURLOTTE: And would that have any significant value for forensic purposes?

A. What's relevant for forensic purposes is human population genetics, the nature of human populations, not the nature of drosophila populations.

MR. FURLOTTE: Would the RFLP's be measured the same way?

A. If one is talking about the purely molecular technology, yes, it's very much the same. A lot of work is being done in mouse with RFLP's and virtually the identical technology is being applied to study mice, both the laboratory mice and wild populations of mice, that are being used for humans. The individual loci are different, of course, because the DNA sequence is different. It's a different species.

MR. FURLOTTE: For forming population database of population genetics databases for either human populations or other types of populations would there be any significant difference?

A. Well, I'm not quite sure what you're getting at. Certainly anybody with general knowledge of population genetics would be able to state the general principles that have to be applied in a database, but I would certainly construct a database very differently for mice where you can have tremendous differences from one side of the barn to the other side of the barn because they never move very far away from where they're born to have their offspring. I would construct a database very differently for wild mice than I would for human populations.

MR. FURLOTTE: O.K., when you use the example you construct a database differently for mice on one

side of the barn and the other side of the barn because they don't - is that because there's not random mating between them or -

A. That's right, because it's known that mice have in the wild an extraordinarily subdivided population in complete distinction from the situation in humans.

MR. FURLOTTE: So basically it would be less random than humans, is that what you're saying, or -

A. I'm not saying how I would construct the database, I'm saying it would be very different, I'd have to give it a lot of thought, but one has to take into account the nature of the organism that you're studying to know what kind of a database should be constructed.

MR. FURLOTTE: But you would use a similar binning system?

A. One could. That's not -

MR. FURLOTTE: But does one?

A. Nobody's done it.

MR. FURLOTTE: For mice?

A. For mice.

MR. FURLOTTE: What about for other forms of populations, animal or vegetable?

A. Certainly forensics doesn't generally apply in those situations and databases are being constructed for research purposes but they're constructed very differently for research purposes than they are for forensic purposes, so I think the question is irrelevant.

MR. FURLOTTE: O.K., I've read something in the paper and whether it's rightly or wrongly where the police agencies are actually using DNA to identify

different types of animals and where they may have come from in the wild for just offences against the Wildlife Act to identify fish, even.

A. Yes, that's correct. Almost always those are very species-specific differences that they are looking at, not polymorphisms within a species, and it's very easy to tell the DNA of a dog from the DNA of a cat from the DNA of a human from a moose and a fish.

MR. FURLOTTE: So you don't need a database for that particular distinction?

A. No.

MR. FURLOTTE: Other than human population genetics what other types of life forms would the scientific community form databases for which are similar to the human?

A. I think none if you are talking about the kind of database that is being used for forensic purposes but databases are being formed for several different types of organisms that are rare and endangered, but they're being done for a different purpose, they're using different kinds of technologies. I suppose some of them are using the VNTR's, but almost certainly they would not use binning. They're interested in different questions.

MR. FURLOTTE: O.K., maybe for an example, Doctor, I believe there's a Dr. Carmody is going to testify on behalf of the Crown also as a population geneticist.

A. Yes.

MR. FURLOTTE: What can you offer the Court that he can't?

A. What can I offer that he can't? I can offer an independent opinion.

MR. FURLOTTE: O.K.

A. I can offer an opinion that is based on having done in my laboratory several hundred thousand DNA polymorphism typings of humans which he has not done.

MR. FURLOTTE: But you haven't done that in your laboratory for forensic purposes?

A. No, I have not done it in my laboratory for forensic purposes though the types of questions we always have to examine when we are evaluating our results are exactly the same kinds of questions that arise in forensics. There are many situations where in a medical genetic counselling system I have to ask is this DNA sample from the child of the two people that I have these other DNA samples on or was I sent mislabelled tubes. That's a question analogous to paternity, it's clearly an identity question. We get tubes sent to us that are mislabelled, we have to identify that by looking at the DNA results and saying, something's wrong, so we're always trying to match bands to find out if they're the same or different because we're looking for new forms of variation, so the basic molecular and laboratory types of things we do is very similar to what's involved in any forensic evaluation.

MR. FURLOTTE: O.K., back to the question. Could you give an example of what you can offer the Court which Dr. Carmody can't as a human population geneticist? What does Dr. Carmody - what area is he involved in?

A. I'm not going to speak to his credentials, I don't know them that well. I'd prefer that he or someone else address that. I know him, I know he is well trained in population genetics. What I am able to offer, I think, is exactly what I just said, an independent opinion based on many years of work specifically with human population genetics, and most recently with molecular genetics studies of human populations, and it is simply that expertise that I have and it differs in many ways from the expertise he has.

MR. FURLOTTE: O.K., maybe I can just ask this simple question, is there any reason why Dr. Carmody's opinion would be less valuable than your own besides -

THE COURT: Well, I think that's unfair to ask this witness to answer a question like that.

MR. FURLOTTE: No, but speaking of your general scientific experience, not necessarily on your individual capabilities.

THE COURT: I think he's answered that question already, or he's explained why he doesn't want to answer it.

MR. FURLOTTE: I must have missed the answer, My Lord.

A. With your permission I will -

THE COURT: Yes, go ahead, elaborate.

A. There are certainly many areas where I think his opinion would be just as valid as mine. There are undoubtedly areas where he has more personal experience and personal expertise than I have. I can think of one area where I think I would have more personal expertise than he has, and that's in some of the specific studies of specific

populations where I have or my laboratory has done the studies. To the degree that he knows the data he is competent to comment on it, but I probably more than almost anybody else in the world know the data very well because my laboratory generated them.

MR. FURLOTTE: That's fair, Doctor. I have no further questions at this time.

THE COURT: Have you any re-examination?

MR. WALSH: No, My Lord.

THE COURT: You injected a new term, drosophila populations, into our vocabulary. By that I understand non-human populations, is that the purport of that word?

A. Drosophila is the little fruit fly that has been the subject of genetic research for almost 90 years.

THE COURT: These fruit flies keep cropping up in our case here. Do you people have a love for them?

A. They turn out to be a marvellous research organism because you can raise hundreds of them in a little bitty milk bottle and they've got genes and they can be studied easily, and a lot of the early understanding of genetics actually came from studying fruit flies, and I spent five years of my early career studying fruit flies.

THE COURT: May I just ask you this, does the term drosophila populations, does that extend to non-living as opposed to non-human; in other words, vegetables and plants?

A. No, no, no, it refers just to this one particular species that's called drosophila melanogaster. I was using that simply as an example. One can do

mouse population genetics, one can do the population genetics of wild potatoes in the Andes Mountains, and indeed some people are looking at the molecular DNA variation in wild potatoes in order to understand how domestic potatoes evolved and in order to find genes for disease resistance and such things.

THE COURT: Well, the jury and I will be very careful how we use this term drosophila in future. Go ahead, Mr. Walsh.

MR. WALSH: My Lord, the motion on the declaration to have him declared?

THE COURT: Yes, I'm totally satisfied that the witness has established an expertise in the fields of molecular genetics, DNA technology and testing procedures, and in human population genetics. Those are the fields in which you requested and he's been adequately established in each of those fields.

MR. WALSH: Thank you. Dr. Kidd, I'll first direct some questions in the area of the RFLP typing technology that arise at the autorads, the interpretation of the autorads, before we get into the population genetics. Are you aware of the RFLP typing system that's presently in place or in place at the R.C.M.P. DNA lab in Ottawa?

A. Yes, I am.

Q. And how did you become aware of this particular system?

A. Through a series of personal interchanges primarily. I first met some of the people from the laboratory at meetings hosted by the FBI in Quantico, Virginia. I have subsequently visited

the R.C.M.P. labs on two separate occasions, have looked at the facilities, have discussed the specific methodologies, and have actually gone through their laboratory protocol notebooks.

Q. And what if any reputation does the R.C.M.P. DNA Forensic Lab in Ottawa have in the scientific community?

A. It has an excellent reputation. Those people who know of it are impressed by the quality of the work that has been done there.

Q. And what if any opinion do you have as to the R.C.M.P.'s RFLP system's ability to produce reliable and reproducible results?

A. I have complete confidence in it.

Q. Doctor, this morning you mentioned the Gene Mapping Library and you referred to the designations on some of the probes shown there. Are you familiar with the probes used in this case, D2S44, D1S7, D4S139, D17S79, D16S85, D10S28, D722, and DYZ1?

A. Yes, I am, to varying degrees for the different loci. Some of them I have actually used in my laboratory, others I have not used personally but I have seen results and read papers describing them and certainly know of them.

Q. In fact, were you responsible for the designation numbers on those probes?

A. On most of them. Some of them were assigned very early, before I got that responsibility, but for most of them.

Q. And your opinion as to the validity of using these particular kinds of probes for forensic DNA work?

A. I think they are completely valid.

Q. Are you familiar with the enzyme Hae III?

A. Yes.

Q. And its relationship to the use of these probes?

A. Yes, I am.

Q. What if any opinion do you have with respect to the use of the enzyme Hae III in conjunction with these particular probes?

A. It is the standard enzyme used for revealing the variation at these loci. It is a standard commercially available enzyme, one of several dozen. It has special properties that make it appropriate for use in these systems in terms of where it cuts relative to these loci. It's a robust and high quality enzyme so that it's not finicky, it's relatively easy to use in the laboratory.

Q. We have evidence, Doctor, with respect to D722, and it's been identified as a monomorphic marker that is applied after the highly polymorphic probes are applied. What if any opinion do you have as to the use of the monomorphic marker in the R.C.M.P.'s forensic system?

A. I think it's an important control to include in the tests. It's a good marker because it is slightly repetitive so it's easy to test after everything else has been tested. With every subsequent test a little bit of the DNA is lost, it becomes a little harder to do the next test, so this is a very good marker to do at the end because it's a very strong marker.

Q. And your opinion as to the use of - there is evidence here that the probe DYZ1 is used, it's been called the sex typing probe. What if any

opinion do you have as to the use of that probe in the R.C.M.P.'s forensic system?

A. It is a probe for DNA that's specific to the Y chromosome which is what makes a male a male, so that it will detect the presence of a Y chromosome and except for very rare medical situations, the sort I know from clinical experience but in a normal population do not occur, it will distinguish between DNA from a male and DNA from a female.

Q. And do you think that is an important probe to have in this system?

A. Yes, it's a very good control again to - especially in the situation where you're trying to look at sperm from a vaginal swab where there may be some female DNA present.

Q. Your opinion, Doctor - we have evidence that there's a male and female controls are run in their tests. What is your opinion as to the use of a male and female control in the R.C.M.P.'s forensic system?

A. It's always necessary to run controls in experiments to make sure that everything is working the way it's supposed to, so by having a known male sample that makes sure that the Y probe, the DY probe, is working, because it should give a signal and having a female control makes sure that it does not give a signal in a female which might happen if you used the wrong probe, so it's an internal control that the work has been done properly and that everything is working.

Q. Doctor, there's evidence on this trial that the R.C.M.P. uses a visual match and they confirm that

using a monomorphic marker and they back that up with the computer quantification using a 5.2 per cent matching window. Are you familiar with that kind of interpretation?

A. Yes.

Q. And what if any opinion do you have with respect to that?

A. I think it is a good procedure to follow, I think it's the appropriate one to follow. The human eye and the brain that's behind the eyes are extremely good pattern recognition systems and so a visual match, if they really line up the eye is just about as good as anything possible to say yeah, they really line up. Having the computer sizing as a back-up is, however, an important safeguard that there's not something strange that occasionally might cause you to misjudge something, so it really is a safeguard against an occasional bias or misinterpretation by the human eye, but clearly if things aren't the same the human eye can see that and it's not necessary to go in and measure them and say are they within 5.2 per cent, they're different, so I think that's an appropriate way to do the examination.

Q. How appropriate is the 5.2 per cent match window to the R.C.M.P. system?

A. My understanding is that that is based on their experience. One can run exactly the same DNA sample many times and measure it independently with different people measuring it run on different days and you will get some variation in the actual size estimate. It's not always going to be the same. Five different people could take

a tape measure and attempt to measure the length of that wall in front of the jury box and you would get five slightly different answers. That sort of variation is inherent in any sort of measurement and the R.C.M.P. lab has done those tests, has said this is the amount of variation we find in the system. In fact it's an overestimate, they usually have far less, but they're being careful and they say that anything beyond that is really too far out to be considered the same, so it's based on their measurement under their technique. If things were done by a slightly different technique, then it might be appropriate to have a slightly different match criteria.

Q. There's been evidence that the FBI's match window was five per cent. Is that what you're talking about?

A. Exactly. They use a slightly different technique and they've chosen a slightly narrower match window. They're both valid, they're both appropriate for the different approaches.

Q. What is a false positive in relation to what we're dealing with here, Doctor? What would you consider a false positive to be?

A. There are two different ways that people have used the term false positive, so I want to be very clear that if a match occurs there are two explanations for it. One - well, sorry, let me back up. A match occurs. There are two possible situations. It is a true match in the sense that the bands really do have the same size. There are then two explanations for why that might have occurred. One, two different people have bands

that are the same size, or the DNA sample in the two lanes came from the same person and therefore it of course has the same size. I would not call that first situation a false positive. That is a coincidence that two people have the same sized band, and that's what, as I'm sure we will get into, all of the statistics is about. What I would call a false positive is the situation where two DNA samples really have different patterns but because of some error or some problems or difficulties in the analysis they are measured as being the same. That I would call a true false positive and that is the sort of situation that I think with this technology is virtually impossible. The kinds of errors that can be made, and errors can be made, my laboratory has probably made every single one possible at one time or another, that's the nature of research, but those errors have two consequences. Either there's nothing you can see on the autorad because the DNA was destroyed, or the bands really show up in the wrong place, so that you don't get bands moving to be the same. You would possibly get bands that might be the same either disappearing entirely or moving someplace else and what that would be is a false negative or no result, so the kinds of laboratory errors that can occur are partly controlled for in the R.C.M.P. controls that we went through a little while ago. If those work you know most of the technique worked well.

The other kinds of errors that you would find result in simply no signal whatsoever, no conclusion, or in an inconclusive result, so that I

think a false positive is not something that is going to occur.

Q. Doctor, we'll move to the population genetics aspect, and you've touched on it just a few minutes ago. If a scientist concludes that a certain pattern of bands are indistinguishable, that is, they match, what significance should that have or what significance is there to the fact that band patterns match as Dr. Bowen has said with respect to this case?

A. If the patterns match there are two possible explanations as I mentioned just a moment ago. Either you've observed a coincidence that samples from two different people look the same by this technology or you have DNA from the same individual that was run in the two different lanes. The DNA from the crime scene and the DNA from the defendant really came from the same person or the DNA from the crime scene came from another person who by chance has the same DNA profile as the defendant, those are the two questions or the two possible explanations that have to be decided between.

Q. And where does the statistical aspect come in? What if anything must a scientist do to answer that particular question, whether or not there is in fact a coincidence?

A. The statistics comes into whether or not there's a coincidence. As a scientist one can never say absolutely there was no coincidence. What one can try to do is obtain some estimate of how likely that was, and that is done by looking at a population database and determining what the frequencies

of the types of patterns we're looking at, what those frequencies are in the population at large, in order to estimate how likely a coincidence really is.

Q. And population database, what considerations should go into the selection of a sample population? That is in essence what a database is, a sample of the population?

A. A database is a sample of the larger population. You can't go out and test, if you're interested in a Caucasian in Canada - sorry, I don't know the size of the Canadian population, but however many million people it is that are Caucasians in Canada you can't go out and test all of them, so you choose a random or representative sample.

Q. O.K., would you explain the relevant considerations in doing that?

A. One would want people who are not closely related. One would choose them at random with respect to their DNA type so that you don't want to know what the DNA type is in advance, you want to choose them so you can estimate what it is. You would ideally want people from several different parts of the country and you would want a sample that is large enough that the statistical uncertainty was very small. Clearly a sample of ten is far too small, there's a great deal of uncertainty extrapolating from ten people to several million, but just as the political surveys - I assume you have political polls in Canada the way we do in the United States though I have to say it's our problem that I don't hear much Canadian news, it tends not to be broadcast in the States. They

will do a sample of 800 adults and say, this is the frequency who think he should be confirmed versus he shouldn't be confirmed, to use a recent example, and this survey has an error margin of plus or minus three per cent. That plus or minus three per cent is based on the uncertainty by having a sample of about 800 people extrapolating to the total voting or adult population in the country. If you ask ten people you'd have to have an error around that of plus or minus 20 per cent or more in terms of the uncertainty of how accurately that sample reflects the total population.

Q. And in relation to these kinds of DNA polymorphism when you're looking at the allelic frequency at these particular polymorphisms what in your opinion is valid concerns or -

A. The larger the sample the more accurate, but for application in forensic situations, so long as the degree of uncertainty is taken into consideration anything above a few hundred, three or four hundred, is going to give a reasonably accurate projection or extrapolation or estimate for the total population.

Q. And what about ethnic diversity within your population?

A. I've spent at least twenty-some odd years studying ethnic diversity all around the world. It depends on what type of ethnic diversity. On the island of Bougainville off the coast of New Guinea there are in this one island that's only a hundred miles long and twenty miles wide there are 29 mutually unintelligible languages spoken, and these 29

little pockets, there is tremendous ethnic diversity in that little range. There is more diversity there than one sees all across Europe so that - and the languages are more different than German is from French is from Italian, so that one has to think of ethnic diversity in relationship to what part of the globe and what population. Clearly, within Caucasians there is not a lot of diversity, there is not a lot of difference between a Swede and an Italian in terms of the frequencies of these kinds of markers or of any of the polymorphisms.

If one were trying to compare, as we have to think of in the U.S. more than you in Canada, we have a very sizeable black population which has a large part of its ancestry from Africa, not from Europe, and there difference between blacks and Caucasians is known to be larger and one needs to look at them separately in that case. Here in Canada you have a sizeable native Amerindian population and there one might expect the frequencies to be different and so one would tend to look at Amerindians separate from Caucasians. Similarly you have a growing population of new immigrants from Asia and they would have to be considered separately from Caucasians but -

Q. Within the Caucasian population -

A. Within Caucasians there is not a tremendous diversity and so one does not need to think about having a large number of separate databases for different ethnic subdivisions within Caucasians.

Q. Are you aware of the R.C.M.P. Caucasian database, what it comprises and how it was obtained?

A. Yes.

Q. And have you seen some of the work that Dr. Carmody has done statistically with these databases?

A. Yes, I have.

Q. And have you seen the demography associated with the provinces and the various per cent populations?

A. Yes, I have.

Q. And do you have an opinion, Doctor, as to how representative the R.C.M.P. Caucasian database is of the Canadian Caucasian population as a whole and the New Brunswick Caucasian population in particular as it pertains to the DNA areas that are being studied?

A. I think it is a very good representation of the Canadian population as a whole. It contains a sizeable number of individuals who are from New Brunswick and I think it's also - since there is no evidence that individuals from New Brunswick are any different than individuals from any other province I think it's also a very good representation of the New Brunswick population as well.

Q. What if any concerns do you have with respect to the R.C.M.P. Caucasian database since no small communities have been sampled?

A. There's no particular reason to sample a small community. Small communities just represent a few people but they're no different than if you took the people living in one city block in a big town. There are a few possible exceptions to that. I'm studying a large Mennonite communite in Alberta and Saskatchewan. This is a community

that has been isolated in terms of reproduction because of their religious beliefs for many generations and yet when - that theoretically raises a possiblity of concern but when one looks at their DNA they have lots of genetic variation and one really sees they're no different than any other Western European population.

Q. What if any necessity is there, in your opinion, Doctor, to sample the population where the crime was committed and to use that as a database? For example, if a crime was committed in Burton, New Brunswick, what if any opinion would you have as to actually taking a sample population from that area?

A. Certainly one could but it's not necessary, in my opinion, to do that. One is making estimates of these patterns, the estimates uniformly come out that any single pattern is very rare, and one would not expect - and in fact there's lots of evidence that in one town it's not suddenly going to become a common pattern.

Q. And you've indicated you've studied isolated populations from around the world?

A. Yes.

Q. I take it you're referring to extreme examples of areas that are very to themselves, so to speak?

A. I mentioned the studies on the island of Bougainville that I first got involved in over twenty years ago and now we're going back and doing some studies at the DNA level and in fact have data on some of these same systems for one of the small tribal groups on Bougainville. We're also studying Amerindian tribes and have looked at what

is probably the most extreme example of a human genetic isolate that I know of, a single tribe in the Amazon Basin that has over the last couple of decades been reduced by illness and other things to one village. The whole language is only spoken by the people in this one village. Everybody born in the last ten to fifteen years are all descended as fourth or fifth generation descendants from one single chief and one or more of his three wives, so it's basically one big family, and I think a total of maybe 175 individuals, total of whom we sampled 54, and even in that which has to be - it's certainly the most extreme example I know of isolation and genetic differentiation, being different from everybody else. Even in that population there was considerable variation at many loci. There was only one locus that had a drastic reduction in the number of alleles but every one of these loci still showed genetic variation and every individual had a unique DNA pattern.

Q. You could differentiate between even those individuals?

A. That's right, everybody had a unique pattern.

Q. And that's the most extreme example you know of?

A. That's correct.

Q. The evidence at this trial, Doctor, with respect to the method in which the R.C.M.P. calculate frequencies, there's evidence that they use the fixed bin method to calculate the frequency for a particular band. They used the Hardy-Weinberg equation to determine the frequency of two bands at a particular location together, and they used

the product rule to calculate the frequency for each probe. Are you familiar with that method of calculation in forensics?

A. Yes, I'm very familiar with it.

Q. And what is your opinion with respect to the use of that method of calculation?

A. It is a method that is deliberately designed to overestimate the frequency of a given pattern in the population. This is a deliberate attempt to bias the calculations in favour of the defendant. One is not actually calculating the frequency of a given band or allele, one is using instead the frequency of all of those alleles that fall within a given bin, so one is calculating the frequency of in total a collection of hundreds of distinguishable patterns and collectively lumping them and saying all of these are roughly similar to the pattern we observed, but it's a frequency that's far in excess of what the true frequency of that pattern would likely be. I think that's absolutely appropriate. I've mentioned before we have to be concerned about our uncertainty in making these estimates when we extrapolate from our sample to what we would expect in the whole population, and one of the ways in a forensic application is to make sure you'd use a number that's bigger than a true number because a bigger number is in favour of the defendant, it means - if you get a very high probability of a given pattern it means the pattern is common in the population and so a coincidence is likely. If this is - the pattern is a probability of one in ten and you have to judge is this a coincidence or

is it the same DNA and one out of ten people has this pattern, well, a coincidence is pretty likely. That's not going to be a rare event and one would say, yeah, it could very well be a coincidence, so that's why the bias is helping the defendant and in a forensic case that is an appropriate thing to do.

Q. Doctor, have you had an occasion to study the autorads in relation to this particular case, the ones that have been generated by Dr. Bowen?

A. Yes, I studied them when I was here for pre-trial hearings a few months ago. I have not had a chance to look at them today.

Q. And when you did study them when you were here a few months ago did you have occasion to make any calls in relation to those autorads?

A. I studied the autorads completely blind to the previous interpretations that Dr. Bowen had made and I differed from him in that I would have called a match in, I think, one situation where he called the result inconclusive. In all of the cases where he called a result I absolutely agreed with him so -

Q. The only disagreement was in one case he called something inconclusive and you would have called it a match?

A. And I thought it was a match.

Q. In whose favour would Dr. Bowen's call be as opposed to your call?

A. In the defendant's favour. I might add that that was an appropriate conservatism. I understood why he had said it was inconclusive. It was, if you will, the weakest of the matches, but I still

would have said I considered it a match.

Q. Did you have occasion to review the sizings, that is, the computer quantifications, as to the match window, where they fell within the match window back at that time?

A. Yes, I did.

Q. And how was your opinion after you viewed the sizings? Did it differ any than when you looked at the visual matches?

A. No. No, I did not do a computer sizing or a graphical interpretation of the sizing but I've done a lot of estimates from just visual and his were - the sizings were very much what I would expect them to have been.

Q. Did you have occasion, Doctor, to review the statistical probability of the best estimate or the point estimate he's referred to that he gave to each of the matches that he called?

A. Yes.

Q. O.K., first of all, Doctor, I'm going to refer you to Exhibit P-162. Are you familiar with those particular calls that Dr. Bowen made?

A. Yes, I am.

Q. Are you in agreement or do you disagree with the calls that he made in that particular summary?

THE COURT: Excuse me just one moment, Doctor. I'll rely on you, Mr. Walsh, to indicate a time when we might have a mid-afternoon recess. Your lectures are normally one hour?

A. I have been known to talk much longer.

THE COURT: I don't know how long you're going to be in direct examination with the witness, I gather for some time yet. Will you choose an appropriate

moment? We're almost halfway through the afternoon.

MR. WALSH: Yes, My Lord, I just wanted to get through this little aspect and then I think that we could have a break. I was just trying to break it at a logical point, that's all.

THE COURT: O.K., you do that.

MR. WALSH: Doctor, if -

A. I mentioned earlier that I'd done an independent evaluation and every place where there is something in here is where I had also called a match and completely agreed. It was for one of these but I don't remember which one for D16S85 that I had said yes, it was clear enough that I thought it was a match, and he considered it inconclusive, but that was the only point at which I disagree.

Q. And the probability, the best estimate frequencies that he gave to each of those matches, have you seen those estimates before?

A. Yes, I have seen them.

Q. And your opinion with respect to those estimates?

A. Those are the conservative estimates for the patterns that would have fallen into the same bins as these, so they are estimates of the frequency of these patterns and they are conservative. What these estimates do not take into account is the actual confidence interval for the frequency of each bin at each locus, which is a function of the database size, how good an estimate each one is, so there is some inherent uncertainty around those numbers but those are the best estimates for the patterns.

Q. Are you aware of anyone associated with this case who has for the R.C.M.P. prepared confidence intervals around those numbers?

A. Yes, Dr. Carmody has.

Q. I see, and have you reviewed those particular confidence intervals that he's applied?

A. Yes, I have.

Q. O.K., we'll get into those after the break. I'm just going to ask you a couple of questions, Doctor, and then we'll move into a break. Before we go into these numbers any farther, and when you deal with the confidence intervals after the break I'm going to ask you, apart from identical twins and without even putting a probability figure - just ignore those probability figures for the time being - to a match, have you in your experience ever seen a four or five probe match between different individuals with these highly polymorphic probes?

A. No, I have never seen it, and that includes these very isolated populations such as the Amazon tribe I was talking about where, really, everybody is very closely related, and that's where you would expect the highest chance of seeing two different people with the same pattern, and I have not seen it.

MR. WALSH: My Lord, if we have a break now at this time it would be appropriate.

THE COURT: All right.

(BRIEF RECESS - RESUMED AT 3:40 p.m.)

(JURY CALLED - ALL PRESENT. ACCUSED IN CELL.)

DIRECT EXAMINATION OF DR. KIDD CONTINUES:

MR. WALSH: Doctor, just before we broke we - you had mentioned something about confidence intervals, I believe, if I'm not mistaken, around the figures that have been generated with respect to this particular case?

A. Yes.

Q. Would you explain to the jury, please, what is meant by a confidence interval?

A. I mentioned earlier that when we extrapolate from a sample to what we believe is really happening in the total population there is an element of uncertainty. We make an estimate in our sample of a frequency and that is our estimate of what the frequency is in the total population, but it's almost certainly never exactly the same, it is somewhat off, a little bit bigger or a little bit smaller. The confidence interval is defined as an interval above or below our estimate in which we have a certain level of confidence that the true value lies, so that if we say we have the 67 per cent confidence interval, some value below to some value above our initial estimate, that means that 67 per cent of the time or two-thirds of the time the true value in the total population will be within this range of our estimate, and clearly a more accurate estimate is one that has very tight confidence intervals. If you've got a very inaccurate or poor estimate it will have very large confidence intervals. In general, to be very secure, the confidence intervals that have

been used on some of these frequencies have been the 99 per cent confidence intervals, meaning 99 times out of 100 we are confident that the true value is no smaller than the smallest value and no larger than the larger value; in other words, it is within this confidence interval.

Q. And with respect to the work Dr. Carmody did do you know what if any - the per cent confidence interval that he used in relation to the four and five probe match in this particular case?

A. He calculated the 99 per cent confidence interval.

Q. When you say 99 per cent is that 99 per cent on or is it 99-point something?

A. It's actually a little bigger than 99 per cent, 99.6, I think it is, but we generally shorten it so that it's - anyway, it's more than 99 per cent of the time we would expect the true value to be within this range.

Q. And are you familiar with the estimates that Dr. Carmody - the confidence estimates that he made around the four probe match of one in 5.2 million and the five probe match of the best estimate of one in 310 million?

A. Yes, I am.

Q. And what were these calculations? What was the confidence interval he assigned to those numbers?

A. The confidence interval for the four locus match ranged from one in 3.1 million to one in 17 million, so the one in 3.1 million was the largest, the most likely. The one in 17 million was the least likely. One in 5.2 is the single best estimate but we believe that the true value is somewhere between one in 3.1 and one in 17

million. For the five locus match which was here one in 310 million, the most common it could be is one in 175 million, whereas it could be as rare as one in 1.3 billion.

Q. What if any opinion do you have with respect to the validity of those confidence intervals around those best estimates?

A. I have complete confidence in their validity. This is very much the way I like to look at these sorts of questions. I have sometimes done a - what I would call a quick and dirty, something that's easier to do with pencil and paper than the elaborate calculations he did. I tried that on this and I came up for the five locus match with my more extreme estimate of one in 66 million being the most likely it could be. His are better estimates of the true 99 per cent confidence intervals. These are - it's that largest number that's the most relevant. That's the one that is most in favour of the defendant and so the numbers would be one in 3.1 million or one in 175 million, and I think even more important than these actual estimates it's this upper confidence interval that is more relevant because we've got virtual certainty that the true value is really smaller than this. This is not the estimate but this is an upper bound of the estimate. We know the estimate is really smaller than this.

Q. Meaning rarer than that?

A. Rarer.

Q. Are you aware of any comparisons that Dr. Carmody made between the estimates that were generated in this particular case by the R.C.M.P. Caucasian

database, what if any comparisons he made using this data and putting it through Caucasian databases in other places in North America?

A. Yes, and -

MR. FURLOTTE: My Lord, I know with expert witnesses they're entitled to hearsay evidence but I wonder if they can push it beyond the limits of just their knowledge of their field and relating it to case specific evidence. I do not believe this type of evidence is admissible.

MR. WALSH: I don't understand why not, My Lord. He's giving an opinion evidence, an expert opinion evidence. This is within his field of human population genetics, I think that was adequately established. He's simply looked at the data of another scientist applicable to this case, he's taken that data and he's being asked to provide opinions with respect to it. I obviously am required - before there is independent proof to the jury of those confidence intervals I'm obviously required to call Dr. Carmody to provide that, but it certainly would not - it would be no different if I called Dr. Carmody to give those and then called Dr. Kidd to comment on them. In this way it facilitates the proceedings and it's something that I understand from the law is certainly allowed.

THE COURT: Yes, well, you're asking for a comparison between the use of this R.C.M.P. Caucasian database and -

MR. WALSH: - other databases, other Caucasian databases in North America.

THE COURT: Used by FBI, presumably, you're talking

about?

MR. WALSH: Yes, there's a number of places. Dr. Carmody has done that particular work, Dr. Kidd has seen this particular work. I'm asking asking him to relate what Dr. Carmody's conclusions were and asking for his opinion on them. They don't form evidence until such time as Dr. Carmody actually testifies with respect to it. I would support my position by reference to the Lavallee decision of the Supreme Court of Canada, and I believe that the majority decision would - they set out the steps involved and the majority decision would support my position.

THE COURT: It seems to me that this has a bearing on the applicability of the R.C.M.P. Caucasian database and I would - I can't see any objection to the question, Mr. Furlotte.

MR. FURLOTTE: Well, My Lord, as I understand thus far, I'm not aware of this witness actually checking the bin frequencies of any other databases. He's relying strictly on the calculations calculated by Dr. Carmody when Dr. Carmody compared the other databases, the frequency in the other databases with, say, Mr. Legere's profile.

THE COURT: Yes, but surely as a population geneticist of his repute he must have been exposed to other Caucasian population databases and he hasn't prepared them himself but -

MR. FURLOTTE: Well, let's find that out. I do not believe he was exposed to, say, the Montreal database or the Minnesota database.

MR. WALSH: No, but the point I'm making, My Lord, is that - the question is whether you wish this

legal argument to take place before the jury.

THE COURT: Oh, well, I'm satisfied the question is in order so I don't really want to pursue it farther than that.

MR. WALSH: O.K., the point I'm attempting to make so you understand where I'm coming from, Dr. Carmody is the one who actually generated those statistics, he's the one that's going to have to prove those statistics. I'm going to ask Dr. Kidd -

THE COURT: Statistics for the -

MR. WALSH: - the confidence intervals that -

THE COURT: In the R.C.M.P. database?

MR. WALSH: And in the taking this data and running it through other databases. What I'm asking Dr. Kidd, what if anything do those numbers mean to him based on his experience with respect to Caucasian populations worldwide or in North America, what they reflect.

THE COURT: Yes, go ahead.

MR. WALSH: Dr. Kidd, are you familiar with confidence intervals that Dr. Carmody has generated with respect to other Caucasian databases in North America using the data that's been derived in this case?

A. He did not show me confidence intervals generated for the other databases, he showed me the equivalent of these frequency estimates generated using the bins for this case and applying the frequencies of other databases, so that it is a measure of the amount of variation one could get in these estimates if one used a different database rather than the one that the R.C.M.P. used, and yes, I am familiar with them, I have discussed how he

calculated them, I have seen the numbers and I can discuss them, if you wish.

Q. With Your Lordship's permission.

THE COURT: Yes.

Q. With respect to the four locus match, the four probe match, excuse me, that was generated in this particular case of one in 5.2 million being the best estimate, would you go through the various other databases that you know Dr. Carmody has did work in and give us the comparison, please?

A. There are three for which all five - I'm sorry, for which all four of those loci are present, three others. One is from Montreal, one from Minnesota, and one is the U.S. FBI Caucasian database. The frequency estimate with the R.C.M.P. database is one in 5.2 million. For Montreal it is smaller, it is one in 6.1 million. For the Minnesota database it is one in 8.4 million, and for the FBI database it is smaller still, it is one in 9.9 million. Now, while I say those are smaller I would argue they all differ by less than a factor of two, which when one is dealing with such extremely small numbers is basically a meaningless difference. These are all varying between one in five million and one in ten million, and that is virtually no variation whatsoever.

Q. And with respect to the five probe match?

A. Again the other three estimates are all smaller. Instead of one in 310 million for the Montreal database it is one in 356 million, for the Minnesota database one in 402 million, and for the FBI database one in 698 million. Again, approximately

a two-fold difference varying from one in 300 million to one in 700 million, not a large difference when one considers something in this range.

Q. How do these numbers that you've just given for the other databases - how do those provide, if any, example of the use of the confidence interval around these numbers?

A. Well, for the five loci the bottom limit of the confidence interval was one in 1.3 billion, and the smallest of these was one in 698 million, so it was much within the outer confidence interval, all certainly within this range. In the other case the confidence interval went as low as one in 17 million and the smallest was one in 9.9 million, again well within the confidence interval, so when I talk about the uncertainty of what the true value is is that one in 5.2 million, it's almost certainly not exactly that. I'm confident at the 99.6 per cent level it's between one in 3.1 and one in 17 million. All of these other estimates fell within that range, which is what I would expect. They are different estimates based on different sets of data but all sets of data that show variation within the range that you always find when you look at different samples.

Q. What if anything does the comparison that Dr. Carmody made - what does that tell you about the Caucasian populations that you've studied in North America and worldwide?

A. They are reasonably homogeneous with respect to their frequencies at these loci, and specifically in North America where I've done most of my work. I'm only beginning to do more detailed work on

populations still in Europe. On Caucasians in North America they are reasonably homogeneous.

Q. A word got inserted in your answer that I don't think we've heard yet and that's homogeneous. Could you explain what you mean by that?

A. Oh, similar, not differing that much. Caucasians from the east coast of the United States are not that different from Caucasians in the Canadian plains or Caucasians in Vancouver or Caucasians in Texas. Social customs may differ but the genetics doesn't differ that much.

Q. Doctor, do you know or are you aware of any evidence with respect in this case from a Dr. William Shields?

A. I am aware of his testimony in the pre-trial hearings.

Q. And did you have occasion to read the transcripts associated with that testimony?

A. Yes.

Q. Are you aware of his opinions regarding sub-structure?

A. As reflected in that transcript, yes.

Q. And could you for the jury, please, explain what those opinions are and what your comment is, if anything, on those opinions?

A. I will have to qualify it. He can give his opinions far better than I can give his opinions but I can certainly say what I understand they are.

MR. FURLOTTE: My Lord, again I'm going to - and I don't know, but I'm just wondering if this is proper questioning of witnesses which the defence has not callled yet. We had a voir dire to see if this

evidence would be admissible. Now, I have not called any evidence yet at trial.

MR. WALSH: Perhaps, My Lord, if we're going to get into this argument we should do so in the absence of the jury.

THE COURT: Yes, I think perhaps we'll have the jury go out for a few minutes.

(JURY WITHDRAWS.)

THE COURT: Well, why do you say, Mr. Walsh, that it should be allowed, and then I'll ask Mr. Furlotte to state his objections.

MR. WALSH: Well, my understanding is that the Crown can't lay in the bushes, so to speak, and rebuttal evidence, as Your Lordship is aware, in this country is restricted to issues that the Crown could not reasonably anticipate and it's necessary to call rebuttal evidence on that. I'm aware of Dr. Shields's opinions. I didn't have Dr. Shields's opinions in transcript form, obviously, before Dr. Kidd testified, so he was not able to comment other than an affidavit. I'm aware of Dr. Shields's opinions, apparently Dr. Shields is going to be providing evidence in this particular trial. Dr. Kidd is familiar with the evidence that Dr. Shields gave at the voir dire and I'm asking his opinions on them. The problem that it would pose for the Crown is that if I was not permitted to elicit those particular opinions now I would in essence be required to wait until the defence evidence was called and then call in rebuttal. The problem, obviously, with someone

with Dr. Kidd's busy schedule is I probably wouldn't - that would not be available to me. I would from a practical point of view not have the benefit of Dr. Kidd's evidence with respect to Dr. Shields's opinions. It doesn't cause as much -

THE COURT: A bigger difficulty from your point of view that I might very well say to you at that point you could reasonably foresee what Dr. Shields was going to testify to and why didn't you ask Dr. Kidd when you had him on the stand before. Would I not do that, Mr. Furlotte?

MR. WALSH: I'm sorry, My Lord, I misunderstood.

THE COURT: I say a bigger obstacle than the availability of Dr. Kidd might be that I might say to you if you were applying for leave to recall him in rebuttal - would I not then say to you, you should have foreseen that Dr. Shields was going to testify, as he has done, as a defence witness, and you should have asked Dr. Kidd about these things.

MR. WALSH: That was one of the fears I lived with at the voir dire.

THE COURT: But isn't that, Mr. Furlotte, a legitimate -

MR. FURLOTTE: Yes, I have no objections to Mr. Walsh asking this witness or any of his Crown witnesses what's their opinion on the type of evidence that he expects Dr. Shields to come in and testify to. My objection is that he is attacking Dr. Shields personally through this witness and saying that his evidence differs from definitely Dr. Shields and this is the evidence Dr. Shields is going to give and my opinion differs from Dr. Shields. I object to him doing it in that manner. Let him

direct his evidence to his opinion for sub-structure -

THE COURT: But hasn't the witness rather made clear that he - as a matter of fact, when Mr. Walsh posed the original question I was about to intervene and say well, look - I was going to say Dr. Shields will have to give his own explanation or expound his own theories and this witness can only say what he understands them to be, but the witness before I had an opportunity to do that said exactly what I was going to say and anticipated what I was going to say, but how else can it be done. I'm trying to figure out a better way of doing it. It's not being put on a personal basis, it's -

MR. FURLOTTE: What happens, My Lord, if for some reason - and for the purpose of a voir dire I intend to call Dr. Shields - what happens if for some reason, either medical or otherwise, Dr. Shields is not able to testify? Then the jury is going to feel that, well, I didn't call Dr. Shields because Dr. Kidd or the other witnesses shot down his testimony before I even had the opportunity to get him into court and therefore by not calling Dr. Shields I'm submitting, throwing in the towel, and that would be a definitely wrong impression and the possibility is there.

THE COURT: What would be the probabilities of that, allowing for a - I don't think we can reduce that to probabilities, the event of his illness or sickness, but I feel that Mr. Walsh is quite correct in anticipating that evidence and in putting these questions now and having the views of this witness elicited on those questions, but

can you suggest a better method of doing it than to say, now, if Dr. Shields testifies in a certain way what would be your comment on that? We have the benefit of knowing what Dr. Shields said when he was here before.

MR. FURLOTTE: There's no problem with Mr. Walsh referring to the type of evidence - or let's say the type of arguments that Dr. Shields will be presenting in court, and he can have this witness address those types of arguments against sub-structure or for substructure as Dr. Shields is going to testify to. He can put that to this witness without even mentioning Dr. Shields' name or even the case specific evidence.

THE COURT: Well, then he's going to have to stand up in argument, or someone is, and say look, those questions, those hypothetical views that we knocked down, were precisely the views that Dr. Shields is giving now on his testimony. Isn't that - that's what's going to have to happen.

MR. FURLOTTE: That's what's going to have to happen. I can cross-examine this witness on those hypo-theticals, again without mentioning Dr. Shields's name.

THE COURT: Well, can you devise any method, Mr. Walsh, short of what you're doing? I see Mr. Furlotte's point here. You know, you're -

MR. WALSH: But what he's being asked to comment on, My Lord, is not a fact. He's asked to comment on an opinion given by a scientist with respect to his interpretation of data, and I'm asking with respect to - I'm asking Dr. Kidd to comment on his understanding of Dr. Shields's opinions with

respect to certain aspect.

THE COURT: Well, really, I see no great objection to your saying Dr. Shields has - and you may have to phrase the hypothesis through the witness's own evidence, but from your saying Dr. Shields has testified earlier that so-and-so and so-and-so, which I think fairly represent his views on a certain aspect of this thing, now will you comment on that, do you agree or disagree. I don't see how we can do it in any other way short of that. You're going to have the advantage here, Mr. Furlotte, of having Dr. Shields testify second and -

MR. FURLOTTE: Well, My Lord, I guess it's the same analogy I've used as if we had a voir dire if the Crown was going to try to admit a statement given by an accused person and they had a voir dire and the accused took the stand in the voir dire to testify against the voluntariness of a statement and then the judge ruled it in. Then we'd get in trial and the Crown would be able to cross-examine the witness as to the testimony that the accused gave during the voir dire as to testimony he gave. Come trial I probably would not put the accused on the stand, so if we use the same analogy, if he can't cross-examine a witness as to the testimony the accused gave as a witness, then surely he can't cross-examine a witness as to any witness who may have taken the stand during a voir dire.

THE COURT: Yes, but Dr. Shields - these views of his have been expounded on the voir dire in the summer. Surely he's not going to change his views and comments on these things.

MR. FURLOTTE: Gee, I hope not.

THE COURT: No, he isn't, and - or at least one would not expect him to, and presumably he'll be expounding some -

MR. FURLOTTE: No, I don't expect him to change his testimony.

THE COURT: And presumably he'll be expounding some of the same views he did then.

MR. FURLOTTE: I don't mind the Crown shooting down Dr. Shields, either credibility or shooting down his evidence at trial under cross-examination, but before the witness ever testifies for them to attack his evidence, maybe his character, I don't know, maybe his credentials, maybe his expertise, I don't know exactly what's going to come out of this witness's mouth. I know at the voir dire he testified as to an affidavit that Dr. Shields gave in another case that was right before him. Whether he's going to properly interpret Dr. Shields's testimony from the voir dire I don't know. Dr. Shields having now understood the criticisms against his testimony in a previous case may explain his testimony a little different today or next week than he did at the voir dire and it's -

THE COURT: Dr. Shields may, yes.

MR. FURLOTTE: Dr. Shields, and it's just strictly not fair to Dr. Shields and it's not fair to the accused because, you know, you've got the Crown witness attacking defence evidence before it's even into evidence.

MR. WALSH: My Lord, I don't understand his logic. If we take it to this degree - assume for a moment

Dr. Shields testified and somehow his opinions varied from the voir dire, between the voir dire and the trial. I would have a right under law to show the discrepancy as Mr. Furlotte attempted to do, for example, with Dr. Waye, is to show him the transcript of the voir dire and ask him to comment with respect to the statement he made at the voir dire and how it now differs or doesn't differ between the statement he's making at the trial. I would have the right to do that, and I would also have the right if he raised something that I was completely taken unaware of, the right to rebut that evidence with a Crown witness. In Dr. Kidd's situation I am aware of evidence that a defence expert gave, I expect he's going to give the same evidence at trial. If he doesn't, then I'm going to have the right to delve into the voir dire. I've asked for Dr. Kidd's opinions, he's giving his interpretation of Dr. Dr. Shields. If that interpretation of what Dr. Shields is saying is wrong, then Dr. Shields will have a chance to say so. I don't - from a practical point of view I don't know how else we could possibly deal in a reasonably intelligent fashion with evidence I know is going to come, and I can't from a practical point keep him -

THE COURT: Just to stop there, Mr. Walsh, I think that you have to anticipate at this stage that Dr. Shields will probably testify, that he will give the same views that he did before, and I think you've got to - if you want to knock those views down or have contrary views put into evidence I think you've got to do it now on the examination

of this witness or your subsequent witnesses, and so I think you've got to proceed in the way that you're doing it. I can't see any alternative to that.

MR. FURLOTTE: O.K., My Lord, just for the record, then, I'd still like to voice my objection and from a practical point of view I can see Mr. Walsh's position because he doesn't want to have to bring Dr. Kidd back for rebuttal evidence, or any of his expert witnesses. From a legal point of view it's all hearsay evidence that Dr. Kidd is going to be giving.

THE COURT: It's not hearsay evidence in the - these are opinions, these are scientific views, scientific opinions, and -

MR. FURLOTTE: No, this is case specific evidence we're talking about here and -

THE COURT: Well, all right, go ahead anyway. I've ruled on it, the objection is noted.

(JURY CALLED - ALL PRESENT. ACCUSED IN CELL.)

MR. WALSH: Dr. Kidd, I had asked you some questions with respect to whether you're aware of the opinions of Dr. William Shields that were given in relation to this particular matter. The qualification you added was that what you're going to give is your interpretation of his opinions, of what his opinions are; is that correct?

A. Yes.

Q. Would you give me your interpretation of what his opinions are with respect to substructure?

A. I understand that he is quite concerned that there

is extensive substructure within the Caucasian population and that that substructure makes it difficult to impossible to make in any way a valid estimate of the probability of a chance match or estimates of the sorts of frequencies of a particular pattern in the population.

Q. And in this particular testimony were you aware of data that he presented in support of that position?

A. It was a very long transcript -

Q. Any data in particular that you remember?

A. At the moment I am drawing a blank on specific data that he presented.

Q. Did you in fact read the whole transcript associated with the data that he presented?

A. I read the whole transcript but I did not have the benefit of the items of evidence that were often referred to in the transcript and I believe that some of the data that were being discussed were actually documents like these that are evidence.

Q. Do you have an opinion with respect to what you believe to be Dr. Shields's interpretation or opinion in regard to substructure?

A. I certainly have an opinion, and my opinion is that of course one can always look very closely and find small amounts of substructure in virtually any population. The question of relevance is whether or not there is sufficient substructure and sufficient relevant genetic difference associated with that substructure to cause there to be any need to revise those figures and those are two different things. There can be

very extensive substructure but if none of the components differ in their allele frequency it has no effect on these estimates. One can talk about substructure in terms of people who live in Manitoba versus people who live in Saskatchewan. That is a kind of substructure, it's based purely on where you live at the moment and basically has little relationship to flow of genes or who married who or what the gene frequencies are. The kind of substructure that might be relevant to having different gene frequencies is if you had within Saskatchewan a group of people who were all from one part of Europe, were marrying only among themselves, and a group of people from a very different part of Europe marrying only among themselves, and the frequencies of these various markers differ substantially in those two groups of people. Then that would constitute meaningful genetic substructure. Virtually all of what I know about human population genetics says that what substructure does exist is of a relatively minor sort and at least within most Caucasians is irrelevant to this point because the frequencies don't differ that much in any case. North American Caucasians are all descended from populations in Europe and some in the Middle East where Europeans derived from.

If one looks at gene frequencies across Europe one doesn't see a highly substructured population. Yes, Italians are a little more like other Italians than they are like Swedes, but Germans are sort of intermediate and Swiss are sort of intermediate. If you think of it as

colouring the map, it's not like you colour Germany green and France red and Italy blue and Sweden yellow where each of those countries is really genetically highly distinct. What you see, and in fact Cavalli-Sforza did this sort of analysis and it was the cover of Science Magazine about twelve years ago, if you look at all the loci together and then represent the sum of those data by colours what you see is a gradual colour change all the way across Europe from Ireland and Scotland being sort of reddish lavender through shades of blue, purple, into bluish lavender down at the Middle East. It's a much smoother change. Of course, if you look at the extremes there are gene frequency differences, but they're differences in frequencies, they're not differences that are black and white. It's a relatively smooth gradation and when you get to the North American population you find that people in the U. S. more than in Canada are really mixed very much in terms of where their ancestors came from. In Canada there's a much greater contribution of English and French as the two major groups but they're not very different from each other even in Europe. After all, the Normans conquered England in 1066 and there was a lot of flow that way of genes. There have been migrations among human populations for thousands of years. All of Europe was settled out of the Middle East within the last six to ten thousand years, so these are not popula- that are remarkably different to start with, and we simply do not see the kind of subdivision and substructuring in Caucasians that's relevant to

this issue.

Now, Dr. Shields used as proof of substructuring in his testimony here and in other testimony that I am aware of in other courts, he used my study of the Amazon Indians, but that's a study of tribes that speak different languages that are known to be highly inbred, that are known to be greatly isolated. I studied them because they are so different from Europeans and North American Caucasians. They bear no relationship on substructuring within Caucasians. Of course, substructuring does exist in the Amazon Basin and yet even there in Salzano's book of about ten years ago where they summarized literally over a hundred studies of something like nearly two hundred populations in the Amazon Basin, different tribes in the Amazon Basin, they concluded that there was so much gene flow that even though you could see this structure it was a very transitory thing and had no long term significance and that in terms of long term genetic change the whole Amazon Basin was acting as a unit.

Q. Are you aware of any opinions of Dr. Shields, or again your interpretation of any opinions of Dr. Shields, with respect to statistical versus forensic difference in relation to the numbers, and first of all I expect you're going to have to explain that to the jury.

A. Well, it is clearly a semantic issue of what you mean when you use a given word, and I take the opinion, and I gave it before in talking about these confidence intervals and talking about a two-fold difference that really a factor of two

when one is dealing with very small numbers, one is twice as large as the other but they're both less than one in a million. I take the opinion that yes, it can be a real difference, it can be a statistically meaningful difference, but that in forensic terms it has essentially no meaning when the difference is that little.

The analogy I would use would be buying a lottery ticket. If ten million lottery tickets are sold and you buy one your chance of winning is one in ten million. If you buy two lottery tickets you have doubled your chances of winning but it's still one in five million. If you buy ten lottery tickets you've got ten times the chance of winning but it's still only one in a million. Now, if I've got a ten times greater chance of winning I'm not going to quit my job and go try to buy a million-dollar house on the basis of that, it's still a very small number, and in fact I would argue that buying one lottery ticket with a chance of one in ten million is almost no different than buying no lottery ticket, and that's the philosophy I use. I don't buy lottery tickets and my chance of winning is almost as good as if I did buy a lottery ticket. So that this is an area where statistics and drawing fine scientific distinctions between whether two numbers are really different is something that is different from common sense and how one operates. Clearly, buying ten lottery tickets you do in reality have ten times greater chance of winning than if you buy only one, but your operational conclusions from that, the way you evaluate that, is not much

different in those two situations, it is still very unlikely that you're going to win, and especially in some of these forensic applications it is possible to get numbers like one in 310 million. That is a number smaller than the total number of Caucasians in North America, I think counting both Canada and the U.S. When numbers get that small it really means it's very unlikely that there is more than one person in that whole population with that type, and beyond that, as the numbers get smaller, the smallest interval got down to one in 1.3 billion, that has no meaning with respect to the North American Caucasian population, it makes no more - no more significant than one in 310 million. They both say it is very unlikely there is more than one person with this DNA type in all of North American.

MR. WALSH: My Lord, it's 4:30. I expect I would not be very much longer with Dr. Kidd. I can defer my direct examination to the morning or we can try and finish it up.

DR. KIDD: May I interject?

MR. WALSH: Yes.

DR. KIDD: My preference, since I would like to be able to leave tomorrow evening, would be if it at all possible to proceed.

THE COURT: Yes. We have been observing a practice here of trying to get the jury away by 4:30 because a lot of them have quite a long way to travel to get home, but I appreciate what you mean and Mr. Furlotte Friday, I think,said he'd probably see you out of here by Tuesday. How much longer are you likely to take?

MR. WALSH: I would think I can finish it up in fifteen minutes, My Lord.

THE COURT: Do you think that you can get Dr. Kidd out of here by tomorrow evening?

MR. FURLOTTE: Oh, I'd like to get rid of him as soon as possible.

THE COURT: You're going to be away by noon tomorrow.

MR. WALSH: I don't think it will have any bearing on tomorrow whether we do it tonight or tomorrow morning.

MR. FURLOTTE: I don't think so, really.

MR. WALSH: I think we're within the confidence limits of that.

THE COURT: Well, we may prove him wrong. We'll adjourn now, anyway, and you can continue in the morning with the direct testimony and we'll have you out of here tomorrow afternoon sometime. That does it all right for you, does it? I mean tomorrow if you're away by suppertime?

DR. KIDD: Yes, the plane is 5:15.

THE COURT: Oh, 5:15, your plane is, so the jury - we'll see you in the morning at 9:30, please.

(ADUOURNED TO OCTOBER 22/91 - RESUMED AT 9:30.)

(JURY CALLED - ALL PRESENT. ACCUSED IN CELL.)

THE COURT: Now, Mr. Walsh, you were going on with Dr. Kidd.

DIRECT EXAMINATION OF DR. KIDD CONTINUES:

Q. Dr. Kidd, yesterday we spoke about Caucasians. What is included within the term Caucasian in terms of - generally, in terms of ethnic ancestry? What comes within that term?

A. The term is derived from the Caucasus Mountains that are located just east of the Black Sea. Populations throughout Europe into the western part of the mainland of Asia where Russians are south into what we call the Middle East and across the southern part of Asia into India. The exact borders are fuzzy because humans aren't divided entirely into neat categories, there are populations like the Lapps in northern Sweden and Norway that are somewhat Asiatic, somewhat Caucasian. There are populations in India that are on the border that have a lot of Asiatic characteristics. There were invasions of Europe by Attila the Hun who - and who came out of Asia, by Genghis Khan who came from Mongolia, and invading armies even if they're all male leave genes behind in the populations they invade, so there's been a lot of admixture and one can't necessarily classify a specific population, particularly in the borders of Asia, as being Caucasian or Oriental. Similarly, as one gets through the Middle East down into North Africa there are populations that are largely intermediate between the sub-Saharan Africans and modern Caucasians, but generally what one thinks of as Caucasian is European, the Middle East out of which Europe was settled, and the very western part of Asia.

Q. Would that include, for example, the Irish and the Dutch, the Scottish?

A. Certainly, Irish, Dutch, Scottish -

Q. French?

A. French, Italian, Portuguese, Spanish, Lebanese.

Q. So your opinions with respect to Caucasian

populations would take into consideration those kinds of ethnic backgrounds?

A. Yes.

Q. The term background band sharing, it's a new term and we would not have heard that before, can you tell us something about background band sharing and what if any opinions are you aware of with respect to background band sharing and Dr. William Shields?

A. The concept of background band sharing is important in forensics with the type of multi-locus DNA fingerprint that is used in England. This is a technology that is somewhat different from what has been presented here. Here in this case for each one of these various loci you are looking at the bands that are contributed by that particular genetic locus, and you generally see two bands, sometimes only one band if there are two chromosomes are identical, in any given individual. The technique that is used in forensics in England and in some other places involves looking simultaneously at the bands from many different loci, and you cannot identify which locus a given band comes from, so there is the chance when you see two bands out of maybe 30 or 50 bands on an autorad when you see two bands that match one may come from one locus and the other may come from the other locus, from a different locus, so it's not a match in the sense that they are the same size allele at the same locus, it's a chance match because you're looking at many things simultaneously, and so one has to take into account this chance event that you would find a match by

chance when it may be a match in the sense that two bands line up but not a match in the sense that they represent a sharing of genetic material that's identical between these two samples. That's the origin. It has to be taken into account as the background and then a forensic test would require more bands being shared than you would expect by chance.

Q. Now, that applies to multi-locus probes?

A. And that's in the multi-locus probing. The situation in which it has been interjected in the voir dire hearings by Dr. Shields is looking at the forensic samples in this case from other individuals, not Mr. Legere but other - the victims and other initial suspects who were tested for these markers, and there are several instances according to him, I myself did not look back at the autorads to see if I agree, but I don't question his evaluation, where you find two bands between unrelated individuals that do a line. At a particular locus one of the two bands in one person is the same size, indistinguishable, as one of the two bands from another person. Now, the other allele or bands are different between the two people, so there's no question about these being the same samples, but he interpreted this high frequency, he claims high frequency, with which two unrelated people happen to share one band as indicative of this population being a small isolate with a high inbreeding coefficient relative to the general population and that would indicate that the frequency estimates being made from the general Caucasian population might not

apply to this community. Maybe there really is not as I said yesterday my interpretation of these that there's probably no more than one person in all of North America with this type that really in this small community there might be three or four people with this type. In fact, I think the way he went about his calculations is wrong. He concluded that this was a very rare event for two people to share a band.

It is not, in my opinion, and I think can be shown mathematically it is not a rare event. It's a very rare event for two people to share all the bands at all the loci, but if you're looking at just one or two bands out of 10 or 12, that happens fairly frequently. I have seen it before in other - among the few forensic cases where I've testified and evaluated the data, two victims who were unrelated happened to share a band at one of the loci. They were clearly different because all of the other bands were different. It's analogous to what is well known in probability classes and is always used in freshman probability and it's often used in the Sunday Times magazines as one of these brain twisters, what's called the birthday problem. You think it's very unlikely that two people would share the same birthday, and indeed if you pick April 21st it's very unlikely, you have to have roughly 365 people before there's a chance that one of those people - a high chance that one of those people was born on April 21st, but if you ask the question differently and you say, what's the chance that two people have the same birthday, then it can be any one of the 365

or, if you count leap years, 366 days, and then it becomes much more likely, such that if you've got a room with 50 people in it it's very likely - I don't remember the exact number but I think it's more than one out of two times that you would have two people with the same birthday. We're not saying two people with April 21st, it could be January 5th or February 12th, you don't know, but it's very likely that somewhere among those multiple pair-wise comparisons that can be made two people will have the same birthday. Seems sort of counter-intuitive but when you think you get 50 people you've got lots of possibilities, you're not just - it's not just 50 comparisons, it's every pair-wise comparison you can make, and it's all 365 days, so there are lots of possibilities for matching, and that's the sort of situation, and I know that Dr. Carmody did some simple calculations, turns out to be for this kind of situation mathematically a little complex, but even some simple calculations that are conservative approximations you would expect - out of about nine people that were on those autorads you'd expect three or four instances at least of one band occurring in common between two people, assuming no inbreeding, all unrelated, and what I know about the history of this region of Canada, which I'm not an expert but as I understand it this is not a community that's been isolated for generations, there are people moving in and people moving out, it's been settled by people from many different ethnic backgrounds, predominantly English, but not by just a small number, by a large number, I guess English and French, so I

don't see that there's any indication of excess inbreeding and this band sharing that was found is not in any way indicative of excess inbreeding or isolation of this population.

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

THE COURT: Thank you very much, Mr. Walsh, and now, Mr. Furlotte, cross-examination?

CROSS-EXAMINATION BY MR. FURLOTTE:

Q. Dr. Kidd, I believe in your experiences you mentioned that you did the study of blood groups by studying blood and doing the genetic aspect of it?

A. I looked at blood groups as a graduate student. I have not myself done blood typing since my graduate student days but I've analyzed data collected by many collaborators on blood groups.

Q. How would you compare doing blood typing to doing DNA typing for forensic purposes?

A. DNA typing I think is a much cleaner and simpler methodology. It's less subject to ambiguities and difficulties in interpretation. A lot of the blood typing which is very well accepted and standard really has a significant level of error and requires very high levels of expertise to interpret the various agglutination reactions or the hemolytic reaction. The starch gel work that's done on enzymes, red cell enzymes and serum proteins, that starch gel work is very analogous to the electrophoresis that's used in DNA but you often end up with less clear patterns when one has to do an enzyme stain. Some of the

acrylamide techniques, isoelectric focussing techniques, are much better and are more analogous to the DNA, but one of the problems with the classical serology and typing is that there are really about eight or nine completely different technologies involved that require different types of expertise. For HLA it's generally a cell death assay that is used, so a variety of things. With the DNA it's basically one technology that's used for all of the different systems and so I think in that sense it is simpler and easier to interpret and the kinds of laboratory errors that can occur will with DNA usually result in no interpretable result whereas the kinds of errors that can occur in the other systems I think may often result in a false positive. Certainly in ABO typing there are lots of examples of getting a false positive because of bacterial contamination or something and that just does not happen with DNA.

Q. It's a different system altogether for typing blood and then typing DNA profiles?

A. That's correct.

Q. And how would the categorization, say, the binning system in conducting DNA profiles and setting up your data bases - how would that compare with blood testing?

A. It is reasonably different in the sense that one is always dealing with qualitative differences in blood typing. It's Type A or Type B or Type AB or Type O. These are discrete categories into which the results are classified whereas with DNA with these particular systems you have a virtually

continuous series of allelic forms so you can't absolutely classify the difference - there really are distinctly different DNA sequences out there, but one that is 3,585 base pairs long is not measurably different from one that is 3,590 base pairs long. Our measurement, five base pairs out of 3,500, we can't distinguish, so we have to come up with some other way. We can tell 3,500 from 3,700, that's no problem, so the binning approach is one way of generalizing a classification. There are others, some of the other companies use floating bins as opposed to fixed bins, but it's simply a requirement of the technology that is different from the classical blood groups.

Q. So basically, Doctor, in your RFLP's some of the DNA fragment lengths are - you can distinguish them by measurements and others you can't?

A. That's correct.

Q. They may show up as appearing the same on an autorad but nevertheless be different fragment lengths?

A. That's correct, there is an element of similarity about that with some of the blood groups. It's a problem that geneticists have dealt with for many decades, and that is hierarchies of allele classification. Blood type A is really a composite, those alleles we call A alleles are really a composite of A1 and A2 which with another more sophisticated test can be distinguished, they often are not, so sometimes we consider the pool together, sometimes they're subdivided, so in that sense geneticists have always known that what we call an allele as a distinct category is only a

function of our existing technology and ability to make that classification. We may learn more later that would allow us to subdivide it.

Q. Now, I understand you visited the R.C.M.P. lab on two occasions?

A. That's correct.

Q. And do you recall when those occasions would have been?

A. I am sorry, I don't recall the exact dates. It was one year ago and something slightly more than a year ago, about a year and a half ago, I believe, but I do a lot of travelling and I'm very busy and I simply don't remember.

Q. O.K., that would be in their new lab, though, would it?

A. Yes, that's correct.

Q. You didn't have the occasion to visit their old lab to see how that was set up or -

A. That's correct. The remodelling had been completed when I visited the laboratory.

Q. Now, Doctor, I believe you mentioned that you find the time you're spending in court has a negative impact on your studies?

A. That's correct.

Q. And I believe you testified you have testified quite a few times in courts throughout the United States?

A. I've testified, I think it's about ten times. For the last year I have been declining all requests. I get probably two or three requests a week and if I wanted to I could probably triple my annual income by accepting those requests but I'm a research scientist, I made that decision decades

ago that my goal in life was not to become wealthy.

Q. So you find it inconvenient to come to court and conduct your personal interests?

A. That's correct.

Q. Now, you mentioned you could triple your income. I assume you're being paid for your professional services to come to court, then?

A. That's correct. Since I'm not home to repair the roof and fix the leaking pipe in the bathroom I have to hire a plumber and a workman to do it.

Q. How much do you charge for your professional services?

THE COURT: Well, I'm not sure this is - the doctor can say if he wants to, I'm not sure it's a relevant or a proper question. You want to what, establish that he's a prostitute or what degree of prostitute he is or -

MR. FURLOTTE: Maybe I want to establish that he may not be completely biassed and independent depending on how much he's being paid for the answers he's going to give.

THE COURT: Well, Doctor, I'll let you answer or not as you decide, or reply as you wish. You're not under any compulsion to disclose what you may be paid as a professional fee for attendance in court.

A. I will say what I am charging now which is more than I am being paid for this, but I agreed to testify in this court three years ago, or approximately then. I am currently charging $2,000.00 a day for my testimony, and I have many people willing to pay that and I decline because I am not

interested in making that much money.

Q. Now, you mentioned you consulted with defence, lawyers for defence?

A. That's correct.

Q. Have any of the defence lawyers ever been able to afford your services?

A. Yes, they have.

Q. And you've testified for defence, defendants?

A. I have not testified for the defence. They chose not to put me on the stand. I gave them my evaluation of the DNA evidence. I pointed out to them all of its weaknesses but I also pointed out to them that if I were to testify I would have to testify that there was a match and that I did not think it was an erroneous match.

Q. So I assume you charged for preparation time also besides your daily court fees?

THE COURT: Well, I don't think we should get farther into this business of charging at all. The witness is obviously retained on a professional basis.

Q. Doctor, I believe you testified that the match window the R.C.M.P. uses, like other laboratories, is based upon their experience within their own system?

A. That's correct.

Q. And the match window for the R.C.M.P. is 5.2 per cent?

A. That's correct.

Q. And do you know what the match window for the FBI is?

A. I believe it is 5 per cent.

Q. And do you know whether or not some of the

forensic laboratories have a much smaller match window?

A. I believe other laboratories have used a smaller window. I do not know what all of them are.

Q. Some of them may be as small as one per cent?

A. I'm not aware of any that use one per cent.

Q. How about two per cent?

A. I don't remember the percentages of other laboratories. I know that Cellmark uses a discrimination interval which is based on actual distance on the autorad that translates into different percentages depending upon whether it's at the top of the autorad where there are very large fragments or at the bottom where there are small fragments, because DNA runs in a more loglinear fashion, not in a completely linear fashion.

Q. Did you check the R.C.M.P. database to see if it was reliable?

A. The only way I could check the R.C.M.P. database to see if it is reliable would be to personally evaluate every autorad, size every band of every individual and compare it with what they got. That is simply not reasonable. I know how the samples were obtained, I know how they do the measurements, and based on the way the samples were obtained and the way they do the measurements it is a reliable database. In fact, the word reliable is not strictly applicable in the case of a database, I'm not sure I know what you mean. It is a database, it was correctly constructed, and it has utility for certain purposes.

Q. O.K., I was just wondering, Doctor, I believe

there was one of your prior cases you testified in for - I believe Lifecodes Corporation did the DNA testing which you came to court and substantiated the results found by Lifecodes?

A. I have done that in, I think, four cases in which Lifecodes Corporation did the testing.

Q. And in one of those cases it was later found out that Lifecodes' method for compiling their database and calculating their statistics or frequencies was not reliable and they had to do their database over again?

A. No, I don't - I am not aware of that in any of the cases in which I testified.

Q. Are you aware of any case that you testified that Lifecodes was later found to have improperly constructed their database because of the difference in match window, or was it Cellmark?

A. I know that questions have been raised in various court situations about the way Lifecodes calculated some of its frequencies from the database. I am not aware that in any way their database was determined to be incorrect. The way some of the calculations were done were challenged but if proper confidence intervals were used around the measurements in extrapolation from the database I don't know that there was any fundamental problem with the database.

Q. Now, I believe in the R.C.M.P. techniques or system that there is measurement imprecision within the system?

A. There is measurement imprecision in every system that exists in human existence. It's the fundamental nature of the universe.

Q. And from what I understand this measurement imprecision, the degree of it, is attempting to be measured by the same system which of itself is imprecise; is that a fair assessment?

A. One of the ways of determining measurement imprecision within a system is to do repeat measures of what you know is the same thing and see how similar your results are on multiple examinations. As I mentioned before, we could measure the length of the jury box and everyone would get a slightly different measurement and it would depend on whether we used a metre stick or whether we used a tape measure with much finer measurements how close people would be. The best estimate would be the average of all of the measurements, but that variation would give us an estimate of the measurement imprecision using whatever means we had. Applying the measurement imprecision with a tape measure with fine measurements would not be appropriate to the measurement imprecision from a metre stick with no subdivisions.

Q. But if we all used the same measuring stick to measure the jury box we should all be within -

A. Probably all within a centimetre.

Q. Pretty close to 99.9 per cent?

A. Probably within a centimetre, and that's going to be within a very small percentage, yes.

Q. So with the 5.2 per cent match window you could be out by 5.2 per cent or 5.1 per cent and still consider it precise enough to call?

A. You're beginning to confuse two things that I would like to keep distinct. The R.C.M.P.

declares a match first on the basis of a visual match and then backs that up with this guideline based on their experience, so there can be situations where it will be within 5.2 per cent but will be declared not a visual match because of other aspects of the gel. One has two bands in one lane like that and two bands like this in the other lane. That fact that one is smaller and one is larger will result in it being called a mismatch or a non-match, even though they may be within the five per cent range.

Q. So long as there's a visual discrepancy. What happens if you're in a position where you can't tell if there's a visual discrepancy? Maybe the lanes are a little too far apart or maybe you're comparing gels to gels.

A. Then one relies on the measurement that one gets, that's correct.

Q. I believe before you came to court, not necessarily today, but at least before you came to court the first time in this case, you had looked at an affidavit prepared by Dr. Shields, William Shields, in another case, Vanderbogart?

A. That's correct.

Q. And in that case, Dr. Shields had compared Mr. Vanderbogart's DNA profile with two different databases the R.C.M.P. had compiled - well, actually, they had compiled a database basically from who, their agents, FBI agents? Do you know who - do you know how the FBI compiled their database?

A. I know that an early component of their database involved the study of more than 200 new agents in

training who had come from all over the country to the FBI Academy in Quantico. I know that they have collected additional samples since then but I have not examined their more recent database so I'm not sure of the nature of all of those samples.

Q. O.K., but I believe when Dr. Shields ran Mr. Vanderbogart's DNA profile through the FBI's old database he came up with figures of one in 51,744 and then when he ran it through their newer data-base the figures came out one in 102,934, and then when he ran it through the R.C.M.P. database the figures came out to one in 200,107. Is that about right? Do you remember?

A. I don't remember the specific figures. If that's what you say they are, I'll accept that.

Q. So you might feel a little more comfortable I'll show you the transcript of the prior hearing which was your direct evidence.

A. O.K.

Q. And I believe you find that that again has no meaningful difference between databases?

A. I do not find that a meaningful difference. That is a four-fold difference maximum. In all cases they are numbers that are relatively small, not miniscule, but in the range of one in 100,000 and one in 50,000, one in 200,000. Those data would indicate that in any community of a couple of hundred thousand people one might find one to three people with that DNA profile and they all say that in a community of 200,000 there might be a few such people but not dozens, so in that sense they're all very similar, and they are probably

not statistically different given the uncertainty in the frequency estimates for any one of those. In one allele estimated at one per cent in one database versus two per cent in another database that will not be different yet that is a factor of two that gets multiplied through into that final number, so the difference between one in 200,000 and one in 100,000 could be simply one number estimated at one per cent in one database and two per cent in another database, so that's a very small difference that when it's multiplied through results in a 100,000 versus 200,000 difference in the denominator.

Q. O.K., now, you said there might not be a statistical difference.

A. A statistically significant difference.

Q. Might not be?

A. Might not be.

Q. What if there is?

A. If there is I would be somewhat surprised but if the databases are large enough it is possible that that might be statistically meaningful in the sense that in reality the data collected for Canada really do reflect a fundamental - a difference from the data collected in the United States, that this is not just chance but there is a real difference, but again I would look at what that real difference is and how you would interpret it. A real difference of this particular band size occurring in one per cent of Canadians versus two per cent of the people in the United States isn't really a very big difference. It may be real but it's not much different from buying one lottery

ticket versus two lottery tickets. To use the analogy I was talking about yesterday, so that there is a great tendency and a lot of testimony in courts in the United States about these very small differences and whether or not they are statistically significant. I would argue that that's not the major issue. The major issue is whether the numbers are really small, in which case a chance coincidence is very rare and unlikely, and that then becomes one element in the evidence in a case. The DNA data by and large should not be used as the sole element of evidence.

Q. O.K., I believe you stated the difference between one per cent and two per cent may or may not be statistically significantly different?

A. That's correct, it depends on the sample size.

Q. But no meaningful difference?

A. For forensics I would argue it is not a meaningful difference.

Q. How much of a difference would be necessary for it to be meaningful in a forensic sense?

A. That's not a question for me to decide, it's going to depend on the individual case, but clearly if the difference were a total figure of one in ten versus one in 100,000, that's a big difference. One in ten there's a big chance of coincidence. One in 100,000 there isn't. Those are judgments that have to be made in conjunction with all the other evidence in a case in my opinion, I'm not an expert in law. When a difference becomes meaningful is something that is going to be very case specific. In this particular case all of the

various numbers are exceedingly small and I would argue that there is no meaningful difference. They all indicate this is a very unlikely DNA pattern in all of North America in the Caucasian population.

Q. So now when you - scientifically it's possible to calculate whether or not there is a statistical difference, a meaningful or a meaningful statistical difference? Scientifically there's a way to calculate that, is there not?

A. There are accepted conventions of statistical significance that are agreed upon and they are usually at the one per cent level that says there is less than one chance in a hundred, so statistical significance is based on we consider it real if there is less than one chance in a hundred it could have happened by chance alone. We're talking about one chance in a million here that is far away. Scientifists use that as a guidepost for statistical significance, so even if we say it is statistically significant it may still have happened by chance alone. We can never prove that what we see did not happen by chance alone but we can say it's a very unlikely event, and the common border or guidepost there is one per cent.

Q. O.K., but back in relation to two different populations, say the FBI's database and the R.C.M.P. database, when you're looking at the difference in bin frequencies and you find there is a statistical significant difference between bin frequencies -

A. Is or is not?

Q. O.K. - pardon?

A. Did you say is or is not?

Q. That there is.

A. That there is.

Q. O.K., you know how to calculate whether or not there is a statistical significant difference in bin frequencies?

A. Yes, there are formulae that can be applied.

Q. There's formulas to follow that you can scientifically figure that out?

A. That's correct.

Q. Is there any scientific way you can figure out whether or not there is a meaningful difference?

A. No, that is a judgment that has to be made.

Q. O.K., so the opinion that you give whenever you say there's no meaningful difference, then that's not a scientific opinion you're giving, that's just your personal opinion, is that right?

A. It is my personal opinion based upon a lot of scientific studies of human populations and knowing when I would make different kinds of judgment calls, so my years of looking at gene frequency variation in humans in populations around the world says when I look at frequencies estimated in different populations and it's one per cent in one population and two per cent in another, even if my samples are large enough that that is a statistically significant difference I will conclude that for the kinds of studies I do of human evolution and human diversity that it's not a meaningful difference, and I would extrapolate that into this situation.

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

THE COURT: Well, we've only been going for less than an hour.

MR. FURLOTTE: Oh, well, O.K., I can -

THE COURT: Well, I won't press it. How close are you - don't want you to get your second wind.

MR. FURLOTTE: Oh, I still have a long way to go on my first, don't worry about that one.

THE COURT: Oh. Well, how are things looking? I mean in the overall picture.

MR. FURLOTTE: Oh, I think we can accommodate the doctor today, as far as that goes.

THE COURT: All right. Well, let's take a recess now, then.

(BRIEF RECESS - RESUMED AT 11:00 a.m.)

(JURY CALLED - ALL PRESENT. ACCUSED IN CELL.)

CROSS-EXAMINATION OF DR. KIDD CONTINUES:

Q. O.K., Doctor, I believe the electrophoresis methods in DNA typing that you do in your lab, you do it on discrete alleles?

A. Most of our work is done on discrete alleles but we use VNTR's as well; not as frequently, but we do use them.

Q. Basically you don't experience the same problems that the forensic labs experience?

A. Oh, no, we experience exactly the same problems and that's one of the reasons we don't use them quite as much for most of our research. We need to make absolute calls of exactly which allele it is in a given person, it may make the difference between whether we think they're susceptible to cancer or not, and the VNTR systems often don't

allow that kind of resolution so we have those problems, we experience them. For some of our population studies they are not as good as discrete allele systems because there again we need to know specifically what form of the allele it is. In some cases we've gone to other methodologies that do tell us but for the same systems but using a different methodology.

Q. You don't use a match window in your lab, do you?

A. We certainly haven't defined one as such but in practice we definitely have the equivalent of a match window because a technician in evaluating an autorad if the bands are too far apart will say something's wrong, we expect them to be the same, they don't look the same and so we go back and re-do things. We have the luxury that we can retest many times, we can investigate things. In forensics there's often a very limited supply of the DNA and one basically does it only once, but if it's very high quality and interpretable that one time one doesn't need to go back.

Q. But you're dealing with qualitative differences in your lab much more than, say, in forensic labs you're not dealing with much differences?

A. To repeat what I just said, most of our research is done with qualitative differences and we are not using these markers as much as forensic labs are.

Q. Because mostly you're dealing with - in analyzing your gels or your autorads you're dealing with distinguishing between bands of thousands of base pairs apart?

A. Not thousands but at least hundreds in the

majority of cases, but not in all cases. We do have the problems of having to distinguish amongst very similar bands.

Q. And again as you say, if you're not sure of a test you can run your tests over again?

A. That's correct.

Q. And you can run your tests over again to prove that the first one was valid as a sort of verification procedure?

A. We can do that, that's correct. It is not commonly done, it's usually not necessary because one nice thing about this technology is that simple inspection of the autorad will generally reveal most of the things that can go wrong, so one can generally tell just by looking at the result whether there is any serious problem or not.

Q. But the forensic application or the testing of quasi-continuous allele systems, would you say that that is more technically demanding than, say, the medicine aspect in your lab?

A. By and large, yes, it is more technically demanding.

Q. And would you say that the proponents of the forensic application of DNA technology are in using quasi-continuous allele systems taking DNA electrophoresis methods about as far as they can go?

A. There is an implication of what you're saying. They are taking the electrophoresis methods about as far as they can go and they have developed things like binning, either a floating bin or a fixed bin approach, to compensate for the fact

that they are approaching the limits of resolution, so in that sense it's not pushing the limits to use the bins. The electrophoresis itself is at about its limits of resolution, yes.

Q. O.K., before we get into the fixed bin approach used by the FBI and the R.C.M.P. and substructures and such, you mentioned the multi-locus probe used in England?

A. Yes.

Q. How it's different from the system used by the R.C.M.P.?

A. Correct.

Q. And I believe you mentioned there's anywheres from 30 to 50 bands to be compared on those multi-locus probes?

A. There can be that many. I have not looked at that many autorads. Usually fewer than that are clearly visible and easily studyable.

Q. And in England they used the multi-locus probe for DNA identification. They have no need of a data-base, do they?

A. They certainly do have a database of sorts as a basis for their estimating the background band sharing, but total identity is considered extremely rare and unlikely and I don't believe they have the same sorts of problems they have in Canada and the U.S. with respect to databases. I hasten to add that I have never been involved in the specific forensic applications as they're used in England, I have no experience in that and really know very little about the English legal system's approach to this problem.

Q. If the forensic labs in North America use ten

probes for identification rather than three, four or five, there probably wouldn't be any need of a database here either, would there? If you can match 20 bands, anywheres between 20 and 30 bands, there would be no need for a database?

A. If you can match 10 or 20 bands. However, when one starts to do these studies it's very possible to get a result for only one locus and not get results for any of the others for a variety of technical reasons, and in that sort of situation the data on that one locus is still perfectly valid. It may actually give better resolution than the ABO blood group locus in terms of limiting the pool of potential individuals who left the semen sample or whatever, and then one would need a database for each of those loci, but if you got a full 20 bands matching there is absolutely no need, in my opinion, to have a database because the probability of that happening is far less than the reciprocal of the total number of people on the earth, or in fact the total number of humans who have ever lived, so that at that level every person would be unique.

Q. O.K., would that be because once you're up in that high a level with, say, 20 bands matching, it wouldn't matter if there was a brother out there or a family member or a cousin or regardless to how high a degree of inbreeding any community had it would cover all aspects?

A. Except for -

Q. - identical twins.

A. - identical twins, I would say 20 bands would cover all aspects.

Q. So basically, Doctor, the general dispute between police forces and defence lawyers and other scientists who are defending against your position is that the police agencies do not run enough probes for identification, that's one of their arguments?

A. That may be. I disagree with that.

Q. And their second argument would be that as a result of difference between ethnic groups that there's likely also that same degree of difference within the Caucasians?

A. And I think that's an absolutely fallacious argument for which there is extensive data arguing the other way. As I mentioned earlier, I know that Dr. Shields has used the study that my wife and I did of Amerindians in several courts around the country, around the U. S., arguing that that study proves there is substructure in the white Caucasian population of the United States, and that's just nonsense. It's arguing -

Q. Well, that's not his argument. To be fair, Doctor, that's not his argument, is it?

A. Well, that's the way it's been relayed to me because I have not read those transcripts.

Q. Isn't his argument that it's because there's sufficient substructure within the Amerindians is that therefore there's no proof that there isn't that same degree of substructure within Caucasians; isn't that his basic argument?

A. Well, that's equally nonsense.

Q. That's equally nonsense, in your opinion?

A. Yes, in my opinion.

Q. There are many scientists within your field of expertise who disagree with you besides Dr.

Shields?

A. I am not aware of that. I know of many scientists who definitely agree with me. I know of people who have misinterpreted the data we got, who have treated the Karitiana as though they were like Poles in their evaluation of it and saying - which is certainly not the case. The Karetiana are basically one family, one tiny, tiny group of people, and as I said, the extreme I know of in the human race for a tiny isolated inbred group, and they were studied for that reason, to look at the extremes, and there with six of these loci every one was polymorphic. One had only a small amount of variation but every one showed variation among individuals and every individual we sampled had a unique DNA pattern, and some of those individuals are more closely related than full siblings.

Q. And how many did you test, was it 54?

A. We studied 54 out of the population and the total population is less than 200, I don't remember the exact number.

Q. O.K., I believe somebody mentioned that the odds of siblings sharing five probes was something like one in just a little over a thousand, would that be about appropriate?

A. Yes, that's correct.

Q. So if you checked 54 people it wouldn't be surprising that you didn't find any two people who matched at, say, five probes?

A. But just a moment, that's for a system like in Caucasians where it's highly polymorphic. This is clearly now an isolate where we're looking at the

extreme. I agree it's not surprising that we didn't find any, it simply confirms the point that there is a lot of genetic variation even in these isolates which are far more extreme than any possible subdivisions within the Caucasian population.

Q. But there's a lot of genetic variation between two brothers.

A. Yes, again which supports my point that DNA patterns individually are extremely uncommon, even among close relatives.

Q. Another area of dispute is - in your scientific community, as to whether or not you can use the Hardy-Weinberg formula and the product rule to obtain your calculations of probabilities, is that right?

A. There has been a lot of argument about that point, that's correct.

Q. And when it comes to - there's been a lot of court cases arguing those points?

A. There have been a lot of court cases. The arguments have been that it has not been proven that you could - that these populations or database samples were in Hardy-Weinberg. People challenge that they were based on misinterpretation of data. So far all of the rigorous examinations that I know of, of the FBI database, of the Lifecodes database, have shown that these are in Hardy-Weinberg ratios.

Q. All the tests have shown that they are?

A. All of the rigorous tests that I am aware of have shown that. Some have been done by Bruce Weir and some by Neil Risch. I think they found one locus

out of several in the U. S. black FBI database, one locus out of the five they looked at in that database was at the borderline of statistical significance but all of the others were in quite close agreement with what would be expected for Hardy-Weinberg proportions.

Q. Are you aware of the tests, the experiments, in the paper that was entitled, "Fixed bin analysis for statistical evaluation of continuous distributions of allelic data from VNTR loci for use in forensic comparisons", done by Bruce Budowle and co-authored by Dr. John Waye and Dr. Ron Fourney?

A. I read that paper some time ago. I don't remember all of its contents.

Q. Basically their study was - the study that they conducted found that it was not in Hardy-Weinberg equilibrium?

A. I do not remember how they did it or what assumptions.

Q. I have a copy of the draft of 1990 which has already been read to Dr. Waye when he was on the stand. On Page 24 it says: "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". It says: "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. 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". It states: "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 significant stratified populations what would be the implications for forensic purposes".

And at Page 29 they state: "Ultimately it would be desirable to define alleles discretely, to be correctly genotyping, not just phenotying, VNTR profiles and to reduce measurement imprecision, then it would be legitimate to apply the Hardy-Weinberg equilibrium". Are you aware of that study?

A. I am aware of that. That does not say they found they were not in Hardy-Weinberg equilibrium. It simply says that the existing methodologies are not appropriate for testing that question given the problems with these data. It is not appropriate in a simplistic application. The work that Neil Risch and Bernie Devlin did which was published in "Science", work that Bruce Budowle has done and I believe is in press, have attempted other statistical methods to compensate for some of the measurement imprecision and they have found that there is no evidence for any significant deviation from Hardy-Weinberg equilibrium. One

can never in science prove the null hypothesis. One can never prove it is strictly in Hardy-Weinberg equilibrium, one can only test whether or not we have done a big enough sample to detect differences. We cannot detect large differences or even moderate sized differences in the samples that have been done. We could detect them, we have not seen them. The samples and the studies that have been done could not detect tiny differences, and of course there are probably tiny differences, that's why all of this is considered estimation. Hardy-Weinberg is the abstract, perfect condition where all male gametes and all female gametes go into one giant pool and combine at random and produce new offspring the way clams and oysters reproduce. Humans don't do that so it's clearly not quite going to meet all of the perfect conditions of Hardy-Weinberg but it's been for literally hundreds of loci. We studied one hundred loci ourselves in the paper that we published in proceedings of the National Academy of Science last February, one hundred loci in five different human populations, and we found no significant deviation from Hardy-Weinberg, and this is a situation where if you've looked at that many loci scattered all over the different chromosomes you can pretty well say there is no major structural problem in those populations that would give deviations, so -

Q. Are there any scientists that disagree with you?

A. I think there are very few who would disagree with me. I am sure there are some. One can always find a scientist to disagree with almost any

point. There are some people who claim themselves as scientists who still believe in the Biblical creation story in spite of extraordinary amounts of evidence to the contrary.

Q. O.K., whether or not it's valid to use the Hardy-Weinberg formula and the product rule to get your high frequency or your low frequencies, as you said, that's in dispute within your general scientific community?

A. No, I would not say it is in dispute within the general scientific community. There are some scientists who are disputing it. Some of them are making a profession of going around to court rooms to dispute it. Some of those people are not what I would call part of the scientific community that has the expertise to really look at these questions, and many of them have based their challenges on fallacious interpretation of the data. A couple of years ago many people were challenging Hardy-Weinberg on the basis of too many homozygotes, individuals with only a single band at a locus. In fact, that was a misinterpretation, those were single band patterns but a large percentage of them were because the other band was in fact too small to show up on the gel, so there really were two bands, it's just one was not seen, it was a technical artifact.

Q. It would run off the end of the gel?

A. It had run off the end of the gel. In other cases there are measurement problems. If you have two bands that are very close to each other, in this technology they will tend to merge because each band has width. These are not perfectly thin

lines drawn with a sharp pencil and so it will look like one band where in fact it's really two separate bands that are just very similar, and statistical analyses have shown that that results in the appearance of homozygosity that is in fact not there, so many of the challenges have resulted from overly simplistic interpretation of the data reaching incorrect - making incorrect assumptions about the data and conseguently making an incorrect conclusion. Many people now believe that these are in perfect Hardy-Weinberg proportions or as near perfect as one can ever hope to find in humans, and so I would not say this is a major dispute in the scientific community.

Q. O.K., maybe you could for the benefit of the jury explain what Hardy-Weinberg equilibrium is?

A. Hardy-Weinberg equilibrium is a very fancy name for a very simple concept. It was first set out in a simple algebraic formula by the English mathematician, Hardy, on a napkin at a luncheon meeting in 1905. It was independently written out by the German scientist, Weinberg, in about the same time, but it wasn't recognized in the English-speaking world that he had done it until many years later, so it's called after the two people who wrote it out, and it simply says if you have a population of humans or of any organism that is bisexual and mating occurs at random, at random with respect to the alleles at a particular locus, that then if you look at a large sample you will find a relationship between the genotypes, the genetic types of individuals who all have two copies of every gene. You'll find a particular

mathematical relationship between the types of genotypes and the frequencies of individual alleles that go into those genotypes, and for two alleles where the frequency of one is P and the frequency of the other is Q it's P squared plus 2 PQ plus Q squared which is the binomial theorem that probability theory has been written about for decades, if not more than a century.

Q. Now, you mentioned that was in what year?

A. 1905.

Q. Were they aware of alleles, discrete and quasi-continuous allele systems, in 1905?

A. Yes.

Q. Were they able to test them in 1905?

A. Some of them, yes.

Q. And which ones were those?

A. Well, there were certainly various mutants that were being discussed in cattle, in rabbits, in various plants, 1905 was before work started on the fruit fly, a variety of different systems, and I would - it's been a few years since I really boned up on the history of genetics so I'm not sure what was already known by 1905, but certainly Mendel's Laws were rediscovered in 1900, so all of his discrete traits, round seeds, wrinkled seeds, tall plants, short plants, in peas were well understood in 1905.

Q. But at that time they were applying it to discrete alleles?

A. They were applying it to discrete alleles and -

Q. And there was no such thing as measurement imprecisions?

A. Oh, yes, there was measurement imprecision.

Q. Oh, yes, but to be able to apply it you would not be able to have measurement imprecision?

A. Well, it's very interesting. The ABO blood group system was discovered to be a three-allele system based on the application of Hardy-Weinberg principles, because ABO blood typing was so imprecise in the 1910's that you couldn't do a family study to determine how it was inherited. The frequency of errors was so high that you couldn't be sure that a Type A child had at least one parent with Type A but by looking at a large population of unrelated individuals they were able to determine that it was not two separate genetic systems, the A system and the B system, but it was one genetic system with three alleles, and that was done in 1917 by mathematical geneticists looking at the serologic data which was extraordinarily imprecise at that time.

Q. O.K., in the Hardy-Weinberg formula that was based because of the two-allele system originally?

A. It was originally written out but it absolutely generalizes to even an infinite number of alleles. It's a binomial expansion of any number of terms, it becomes a multinomial, it's well-known in mathematics, has lots of properties and eventually approximates a continuous normal distribution, so in fact measurement imprecision and the application of Hardy-Weinberg have been around for a long time. I mean there's another example of the red cell acid phosphatase locus where one has enzyme activity levels that a given allele has a whole range of activities but can be also detected as a qualitative trait using electrophoresis, so

it can be measured either as a continuous trait enzyme activity or as a discrete trait by electrophoresis, and in those case Hardy-Weinberg applies and some excellent work by Harris in the mid-1960's is in all the classic genetics textbooks.

Q. O.K., could you explain to the jury what linkage equilibrium is?

A. Linkage equilibrium is also known as gametic phase equilibrium. It basically says what allele is in a gamete at one locus is not correlated in the population with what allele is in the gamete at another locus.

Q. Could you explain what not correlation is?

A. Not correlated means in simple terms conveys no information. If you have a gamete that has the gene for blue eyes that tells you nothing about what that gamete contains at the locus for the ABO blood group system. It could be A, it could be B, it could be O, you have no information, compared to a gamete with the gene for brown eyes. That gamete could have A or B or O at the other locus, and the frequencies of A, B and O are identical whether you have a gamete with blue eyes or whether you have a gamete for brown eyes, and extrapolated to these systems it would say if you have a gamete at, let's take D2S44, a gamete that gives rise to a certain size band, a large band, what that gamete contains for D4S139, all of the different D4S139 alleles have the same chance of occurring as if you had a gamete that at D2S44 had a very small allele, so that knowing what you get at one locus really does not predict what you would get at another locus, so there's no

correlation or association in the population between these systems, and it is that absence of a correlation that allows you to multiply the probabilities. It's like having two decks of cards. What cards you draw from the first deck really doesn't tell you anything about what card you're going to draw from the second deck, assuming that they're two normal decks of whichever type, let's say a bridge deck, 52 cards, no association between the two, that is linkage equilibrium or gametic phase equilibrium. One is concerned about it because when you end up getting genes that are very close to each other on the same chromosome, then you find deviations from that, but in general genes have to be very close to each other or you have to have a highly structured population with big differences in the allele frequencies in the two different populations, so it would be like if you have Irish and Italians and you're not sure which but those are the two groups you're looking at, if you pull out a gamete for blue eyes it's very likely that gamete will contain the gene for blond hair or red hair whereas if you pull out a gamete for brown eyes it's very likely that gamete will contain a gene for dark hair because you've got Irish who as a group have both blue eyes and red or blond hair and Italians who as a group predominantly have dark eyes and dark hair, so that's when you've got an association, when you've got that kind of structured population, and indeed, you'd have it if you looked in some populations for those traits. By and large you do not see that

for these kinds of DNA markers.

Q. O.K., so as I understand it, your linkage equilibrium, if you're checking the distribution for one probe, say on D1, then you assume it's purely by chance however your assessment has been done, your -

A. That's correct.

Q. And for there to be continued linkage equilibrium the second probe you're doing, it must also be by chance?

A. I'm not sure I understand your question. If there is to be linkage equilibrium, then the distribution on all the probes is random and uncorrelated.

Q. O.K., so it's much like our - I don't know how your lotteries go in the States but in Canada we have the Lotto 6/49. I believe they put 49 numbered balls in a big wheel and they spin it and whichever ones come out at a time, that's coming out by chance, there's nothing controlling which one's going to come out.

A. That's correct.

Q. And everyone has an equal chance of dropping out, supposedly?

A. Well, it depends. If they do serial sampling the probability of the first one coming out is going to be somewhat different than the probabilities for the second one, but -

Q. Yes, the first one would be one in 49 -

A. And the second one would be one in 48 among the remaining 48.

Q. And one in 48 until we get to the six numbers, then -

A. That's right, but if you do independent sampling

the Connecticut Lottery has three numbers and so there are three of these ping-pong ball air blowing machines, each with ten balls in it, zero to nine, and so every number that comes up has equal probability. It can be zero through nine in the first, zero through nine in the second, or zero through nine in the third. Those are then completely independent and uncorrelated.

Q. O.K., so that's basically what you'd call linkage equilibrium?

A. Right. Right.

Q. That analogy?

A. Each of those ping-pong ball machines could be like one locus here, but with hundreds of balls in each one.

Q. So maybe where we have, say, a sample of linkage disequilibrium within our loci it would be maybe where there's a lot of band sharing within a population, maybe 50 per cent of the population would share this fragment length on loci D1 and then maybe in D2 50 per cent would share a distinct band in D2?

A. No, you're talking about apples and oranges.

Q. O.K., would you explain it?

A. Because there could be a population with a very reduced number of bands - hypothetical, I - haven't - it's not the Canadian population - where there is a reduced number of bands and a high frequency of band sharing, but as long as the band at D1 was completely independent what band people got, maybe there are only five balls in there for D1, but as long as it's a separate machine, then there's no correlation between the

band you get at D1 and the band you get at D10.

Q. And would there be a correlation between siblings?

A. I'm sorry, what?

Q. Would there be a correlation between siblings? Would there be linkage disequilibrium within siblings?

A. No, because each of these is on a separate chromosome and we know that what is transmitted to siblings, different chromosomes are transmitted completely independently to siblings, so the parent has two alleles at one locus and two alleles at the second locus, and all four combinations are equally likely among the children.

Q. All right, but when you compare these two siblings to the general population -

A. Oh, sure, there can only be - at any one locus among the siblings there can only be four bands at one locus because the father only has two and the mother only has two, so whatever those four are at that locus, those are the only ones that can occur in the children.

Q. O.K., so if you were comparing the two siblings to the general population you'd say that there was linkage disequilibrium in the two siblings?

A. No.

Q. No?

A. No, because they're siblings. I wouldn't do that test.

Q. O.K., but their band sharing would not be by chance, it's determined by their parents? You only have four choices where the general population you might have 27 choices?

A. That's correct.

Q. What would be an example I suppose of linkage for the different loci? What would you have to find to prove linkage disequilibrium?

A. It is very difficult to prove linkage disequilibrium for a system such as this but one could go about it by looking at one locus, taking all individuals who had a band in a certain size range, say a large size band at D2S44, and then looking at whether or not the alleles they had at D1S7 were any different as a distribution, the frequencies of the different alleles were any different from another group of people who had a different sized allele at D2S44, were their D1S7 alleles any different between those two subgroups of people, and that's the kind of study that would have to be done to show that there was this gametic phase disequilibrium. In the studies that have been done of the R.C.M.P. database, taking these various categories one does not see any difference. I did such a study many years ago on an early version of the Lifecodes database, it's been done on the FBI database, one does not see those sorts of differences. To say none exists is again - I cannot prove that the sun will come up tomorrow. One can never probe the null hypothesis, one can only say I've made observations, everything is consistent, I see no big deviations from my understanding of what's going on so I accept this as a working hypothesis.

Q. But the sample populations that you've studied is a very small population compared to population size that you would need to do an adequate study?

A. No, adequate is based on to what level of

deviation do you wish to test your hypothesis. I have looked at enough to say there is no large deviation, I have not looked at enough to say there is no small deviation, but the beauty of this system is that it is so powerful and all of the confidence limits that are placed around these numbers and the use of bins in all the frequencies which are all overestimates I am convinced will more than compensate for any small deviation that might still be there. Of course, if I were to look at the Amazon tribes that I am studying, of course I would see linkage disequilibrium within the Amazon Basin because I know these tribes have different frequencies, I know they are highly structured small groups, but I also know that's not the structure of the North American or European Caucasian population.

Q. O.K., and the small Amazon tribes, you were able to come to the conclusion that there is linkage disequilibrium?

A. No.

Q. No?

A. I have not looked at it. I do not consider it a particularly relevant scientific question for what I am studying in those populations.

Q. But just based on the bin frequencies you can conclude that it wouldn't be proper to use a data-base for one tribe when the accused belongs to a different tribe, or if you were trying - being an accused or somebody you were just trying to identify?

A. I would say based on my looking at the frequencies I would be much happier if the crime were

committed by an Amazon Indian to have more data than I have now, and certainly if the crime were committed by a Karitiana I would not use a Mayan or Surui data base. On the other hand, I don't expect there to be any two Karetiana with the same DNA pattern, so if I got a match I wouldn't be terribly concerned about the probabilities. I could actually go in and type all 150 Karitiana. I can't do all however million Canadians there are.

Q. So in the Amazon if you didn't do a sample data-base from each different tribe, had you just went and treated them all as one general population, it wouldn't be fair to them, would it, to use the general population database for those people?

A. I'm not sure what fair is in this case. One can ask many different questions and if I don't know what tribe the criminal came from or what tribe, even, the accused came from because maybe he's somebody who moved into the city and his four grandparents came from four different tribes, then the best database would be a general database of Amazon tribes pooling the data from all of the different tribes, and that would be probably the fairest. Again I would probably want to in that situation, because I know there is some reduction in variability at some of these loci, some of them only have three or four alleles within a tribe, I would probably want to do a couple of more loci because the individual loci aren't quite as good, but it would be very easy to construct a database and to assure oneself that the probabilities were low enough that one was approaching very, very low

chance that any two people had the same probability.

Q. O.K., Doctor, you mentioned that you don't know what fair is but the position is representing Mr. Legere I want the expert testimony to be as fair as possible to Mr. Legere. That would be understandable, right, so the evidence as I understand as the R.C.M.P. are bringing in is the likelihood of somebody other than Mr. Legere being a male Caucasian, and these are the figures; would that be right?

A. We cannot ever know precisely what the likelihood is of someone else having the same pattern as Mr. Legere without typing everyone around. We can make estimates and these are the estimates that have been made based on the Canadian population for these loci. We can also place around those estimates some indication of our confidence, of how accurate we think these estimates are, and those are the confidence intervals that I mentioned in my testimony yesterday, and even going overboard with the quick and dirty method that I've used to combine confidence intervals across loci, one that's not mathematically or statistically correct but is simple and more favourable, more fair to the defendant, I come up with an upper limit of one in 66 million, so I know the true frequency is somewhere below there.

Q. If we don't know that the person who did the alleged crimes is black, Chinese, Indian, or whatever ethnic group you can think of, is it fair just to assume that the attacker was Caucasian?

A. This gets into philosophy of what questions one is

really asking. In the abstract, and I'm more familiar with the situation in the United States, if there is a crime committed and we do not know the ethnic group of the criminal and we cannot assume that the criminal, the perpetrator, is the same as the defendant, presumed innocent until otherwise, and there are two questions that we can ask, how common is this pattern of the criminal in the population, and then we have to say, how common is it in blacks, how common is it in Hispanics, how common is it in Orientals, how common is it in Caucasians, and one can do the calculation, and in fact the FBI - where we have these significant minorities the FBI reports and says, this pattern we estimate to have a frequency of this in the Black population, this frequency in the Hispanics, and this frequency in the Caucasian, and they are different, they are different frequencies. One can also ask, here is an accused; looked at the other way, how common is this person's DNA pattern, might there be somebody else out there. My experience has been that the largest probability is usually obtained using the database for the ethnic group that the suspect belongs to, that's the one that's most favourable to the suspect, and then you're asking, how many other people are there out there like the suspect, and those are the numbers that have come up here. I don't know what the frequency of these patterns is among Canadian Blacks, Canadian Orientals, Canadian Native Americans. My expectation is that it's probably less common than this. Certainly we found when we compared this pattern with the

U. S. Caucasian database it's a less common pattern; not by a significant difference but it is numerically less.

Q. O.K., you stated that if you run the accused's DNA profile through all the different databases for the different ethnic groups the one most favourable to him would be the one he belonged to, Caucasian?

A. That's been my experience when I have seen those tests done.

Q. So if an accused person is run through a database for a subgroup to which he does not truly belong, then he will be prejudiced by it, be it a subgroup, a different ethnic group, or a different subgroup within the Caucasian?

A. No, he will be biassed by it only if that subgroup has different frequencies that are meaningful, and that's what some of the argument is about these various subgroups of Canadians and the results that I have seen indicate there is no evidence and I do not believe that there are -

Q. And that's one of Dr. Shields's arguments, is it not?

THE COURT: Excuse me just a minute, the witness didn't have a chance - you were starting to say, I don't believe -

A. I don't believe there are meaningful differences in gene frequencies among the different ethnic groups within Caucasians. I have to qualify that - for these loci. One can always find individual loci for which there are differences. I've mentioned blue eyes and blond hair and clearly ethnic groups differ for that.

Q. But I believe you stated that if you were going to run an accused person's DNA profile through different databases for different ethnic groups, Whites, Blacks, Indians, that he is better off - it would be more favourable for him if he was run through his own rather than the other ones? Your experience, that's what you said.

A. Across these large groups, large subdivisions of the human race, yes, that has been my experience.

Q. Now, one of the statements that you commented on that Dr. Shields had made previous in his affidavit that you had already commented on, certain aspects of it, one of his statements in Dr. Shields' affidavit in the Vanderbogart case, he stated, "If two populations differ in allele frequencies, then choosing the wrong sample for comparison is expected to produce a result biassed against the defendant; i.e., the estimated probabilities are predicted to be incorrectly lower when an individual is tested against a subpopulation other than his own", and do you recall what your comment was on that last hearing?

A. My comment was that that is not correct, that the bias can go in either direction depending upon the actual frequencies involved. There is no way to say that it will always go in one direction. A person - assuming subdivisions with real differences in frequency, if the person comes from one population but happens to have two alleles that are infrequent in that population but much more frequent in another population, and that's a possibility, then you will get a higher probability using the other population than you will the

one the person comes from. There is no guarantee that the person will always have alleles that are more common in his sub-population than they are in any other sub-population.

Q. Let me read Dr. Shields's statement again. He says, "If two populations differ in allele frequencies, then choosing the wrong sample for comparison is expected" - not must or will always, it says, "is expected to produce a result biassed against the defendant", and I understand when you said that if a person was tested against a population database other than in his own ethnic group, then he would be expected to be biassed against.

A. If one uses expected in the sense of mathematical expectation, which is a fancy way of saying on average, that's probably then a correct statement, but - I'm sorry, what -

Q. No, go ahead.

A. But it's not a rule and my - as I remember my initial interpretation of that statement it was more that this was to be what you would expect in the English language sense to find, this would be the normal observation as opposed to what on average might happen.

Q. O.K., but at the prior hearing in this case you said that that was an absolutely incorrect statement, is that right?

A. O.K., that's what I said.

Q. And today you agree with him, is that right?

A. I would like to see the original affidavit and look at that statement in its context. My interpretation at the time of the statement was as I've just said and I feel that that was absolutely

incorrect. If one looks at mathematical expectation on average then I might agree with him. I believe, however - no, I don't remember what sentences were around that quote.

Q. Dr. Shields's testimony was basically in Mr. Legere's case, and you've already referred to it, that the high degree of band sharing he found in the Newcastle area, his basic argument is that because of that band sharing there's likely a very substantial substructure group that is substantially different from the general population in Canada?

A. That was my understanding of what he said, yes.

Q. And if Mr. Legere's profile is run through the general population database for Canada or the R.C.M.P., then he is going to be severely prejudiced against or biassed?

A. No.

Q. That's Dr. Shields's opinion, I'm saying, and you disagree with that?

A. Oh, that is Dr. Shields' - as I remember, that was Dr. Shields' opinion, but there are two different elements there, inbreeding as opposed to - involving band sharing because of recent common ancestry versus substructure and differences of allele freguencies, and Dr. Shields I believe was referring to this, mostly in terms of substructure and different allele frequencies, and that was the basis for his conclusion.

Q. The likelihood of sharing a band between myself and somebody who is unrelated to me is, on a general basis without having to go through a population database - would be anywheres from one

in 50 to one in 70 or greater?

A. If you're talking about one locus or multiple loci, you have to define that -

Q. One locus.

A. - and you are talking about you and one individual person specified in advance -

Q. Well, just pick anybody at random, myself -

A. O.K., but not knowing already what their bands are.

Q. Oh, no, definitely not. Not knowing what their bands are, just if I picked anybody out in the crowd here and I said, what's the chance of my sharing one band at any locus.

A. It's probably on the order of one in ten, one in twenty. It's analogous to the birthday problem, I'd have to go through calculations, it depends on match, it's not a simple calculation, but since it could be any band at that locus it's really fairly high.

Q. Could it be one in 50, one in 70?

A. Depends on the locus and how much variation there is. Certainly, it's going to be different for every one of these loci. If you look at D17S79 it may be as high as one in ten.

Q. Right, but I'm saying without doing a frequency calculation amongst the general population, the general -

A. No, I'm sorry, it can't be done without doing some frequency calculations among the general population. That's the basis for saying what these probabilities are.

Q. What's the probability of a sibling sharing a band, one band not both bands, but one band on

the same loci?

A. Fifty per cent.

Q. So that's one chance in two?

A. Actually it's higher than that.

Q. It's one in four, isn't it?

A. No.

Q. No?

A. No, it's one in two. It's actually somewhat higher - actually, one band unspecified at one locus, assuming the two parents have four different bands, it's actually 75 per cent. It's one minus one in four. They're completely different one time out of four, and so they share at least one band three-quarters of the time.

Q. And it would be much greater for two unrelated people - much less of a chance, I mean?

A. Yes, much less of a chance.

Q. Doctor, in your experience so far in court and over the dispute as to whether or not the forensic methods are reliable in calculating the frequencies, there have been many different scientists in your field that have come to court and testified against the reliability of this method; is that right?

A. There have been several, yes.

Q. And there has been from your experience more different scientists testifying against the reliability of DNA testing than there has been for?

A. I have in the past been presented with lists of names that were three times as long for people who have testified for the defence against this with a short list of names of people who have

testified for it. I am not aware of all of the people who have ever testified. I do know that I would strenuously object to the credentials of many of the people that had been included in that list for the defence and I do know that the list I was presented with omitted several people of very high repute who had testified for the prosecution. I don't know how many have testified, I don't know that this is an issue of numbers.

Q. But in your experience the police forces have a difficult time in getting experts like yourself to come in and testify as to pro-DNA?

MR. WALSH: Objection, I don't understand the relevance of that particular question. I don't know how that question is relevant to the particular matters we're dealing with here. There's so many variables that would go into that that I -

THE COURT: I wouldn't expect the witness to know the answer to it, really. He's not employed by police forces. He has expressed his own reluctance earlier for what appear to be very valid reasons for not wanting to get involved as a professional court witness in DNA cases, because it would encroach on the time that he wants to devote to cancer research, but he says that as a scientist he feels obligated to - in this case primarily, to fulfill an undertaking that he gave three years ago, but what would he know about the difficulties that police may encounter in getting witnesses in other cases. He knows that he has turned down requests that he appear himself, but I don't think that's a valid question, Mr. Furlotte. I might say that his rate of remuneration is now running

at a rate less than fifty cents per question and answer.

MR. FURLOTTE: Maybe that's what they're worth, My Lord. Doctor, the matters in dispute before this Court are also in dispute within the scientific community? Would that be fair to say?

A. I would not phrase it the way you have phrased it. There is tremendous dispute within the scientific community - not tremendous, there is some dispute within the scientific community about how accurately one can make these frequency estimates. I think there is no dispute within the scientific community that every single DNA pattern is rare. I think there is no dispute within the scientific community that every individual has a unique DNA pattern if we look at enough markers, excepting identical twins. I think there is no dispute within the scientific community that this DNA technology can give reliable and reproducible results if done by qualified scientists. Most of the dispute within the scientific community, and there it's being raised by I would say a relatively small number of individuals, is about the precise numbers, and I have stated many times I am not terribly concerned about the precise numbers because I think it is not a relevant issue in forensics. It becomes analogous to arguing how many angels can dance on the head of a pin. As long as you know that there can be lots of angels on the head of a pin it doesn't matter too much how many there are.

Q. So for there being no forensic meaningful difference whether the bottom line is one in a

thousand or one in a hundred thousand that would be sufficient for you, is that right?

A. I think if a jury is presented with the confidence intervals that one has that that data can be weighed in conjunction with other evidence. If the DNA confidence intervals range from one in ten to one in a hundred, then a coincidence is likely but it's nonetheless consistent with that person's pattern. That's one component of evidence. If the confidence intervals range from one in 66 million to one in 1.6 billion, then that would indicate that there are very few individuals in all of North America with that type, and that's the consideration that the jury would make, so what - it does make a difference whether the answer is one in a hundred or one in a billion, but as long as one knows what the confidence intervals are around a given estimate, makes those conservatively taking into account our measurement error, taking into account the sampling error in constructing the database, I think the data that we have now are quite admissible in court and pardon me, I don't know about the Canadian system, but it would in the U. S. system be a matter of the weight of the evidence, not whether the evidence is valid or admittable.

Q. That's what we're discussing here, Doctor, the weight of the evidence, right?

A. And in my opinion the numbers speak for themselves. I cannot know precisely the frequency. I can make corrections, others can. The R.C.M.P. have built in corrections into their system and the single best estimate is presented here but

the confidence intervals have been discussed and will be discussed more by Dr. Carmody giving a measure of our uncertainty and how great that uncertainty is, and the greatest level of uncertainty is still that this is a very rare pattern.

Q. You have mentioned a word to take this into consideration with other evidence, right?

A. Yes.

Q. And it's the position of the forensic fields and experts doing these cases that there should be other evidence besides DNA evidence?

MR. WALSH: My Lord, that's getting into a legal question, not a scientific question as much as what we're delving into here is this is one aspect of a case that's being presented, one evidentiary aspect of a case. It's for this Court and yourself to address the jury as to how this evidence is to be applied to the rest of the evidence in the case.

THE COURT: Yes, I don't think this is a fair question for this witness, Mr. Furlotte.

MR. FURLOTTE: Well, My Lord -

THE COURT: You're asking can you rely on DNA evidence alone, and the witness has already said scientists or in the scientific community they can't be absolutely certain about any answer they give, and as Mr. Walsh points out, this is a circumstance to be taken into regard by the jury and it's up to the jury to attach the weight to it they will, but it's not up to this witness or any other witness to say, look, I would or we would convict on the basis of DNA evidence alone. That's what you're getting to, I think, isn't it?

I don't think it's up to a witness to say that.

MR. FURLOTTE: The only thing, My Lord, it's a question here of reliability, and if they don't rely upon it enough themselves for the sole evidence to convict somebody, then why should they ask a jury? That's my position.

MR. WALSH: The question we're dealing with here is a simple question of a particular piece of evidence that's being introduced in a particular trial. That's the sole question. It's got nothing to do with what Mr. Furlotte wants to ask witnesses about guilt or innocence. We're dealing with the simple area of a piece of evidence and he's strayed way outside that area.

THE COURT: Well, I'm afraid, Mr. Furlotte, you're asking this witness really to comment something that falls within the legal sphere.

MR. FURLOTTE: Doctor, you said like in the scientific - which is not in dispute, is that every pattern is rare; correct?

A. Every pattern for which multiple loci have been investigated, clearly not every single locus pattern, I make that clear.

Q. So what is in dispute is basically the question of how rare?

A. That's correct.

Q. And one in 100, I believe, would be considered rare in some circumstances?

A. It is for every individual to evaluate that. The word rare will have different meanings for different individuals. In medical genetics a genetic disease that occurs in one in a hundred is considered a common genetic disease. A genetic

disease that occurs one in ten thousand is a rare genetic disease, but again, here we're using common and rare relative to the category of genetic diseases, no one of which is all that common.

Q. O.K., for forensic purposes, when you say it's not in dispute that every pattern is rare, how common would a pattern have to be before it would be considered rare by the forensic community?

A. I'm sorry, I can't answer that. It's a semantic question, it is not a scientific question, and I can't say what other people would consider it.

Q. You mentioned you prepared a paper or a study for the National Academy of Science with someone else?

A. I have published a paper in the Proceedings of the National Academy of Science which is a scientific journal. This was not something prepared for the Academy, it was prepared for publication, and in fact, I've had several papers on different things appear in that journal over the years, but the one I mentioned was a study of 100 different DNA polymorphisms looked at in five specific populations from around the world. It's the largest study of DNA polymorphisms done in a global sense that's yet been published.

Q. O.K., any particular reason why the National Academy of Science was interested in that paper?

A. The Academy had nothing to do with it. It was one of my co-authors was a member of the Academy and so has the right to submit articles and have them published in that journal. It is considered a highly prestigious journal, but the Academy per se is neither interested nor disinterested in the

articles that are published.

Q. Do you know whether or not the National Academy of Science is interested in whether or not it's valid to use the Hardy-Weinberg formula and the product rule in the calculation of the frequencies by the forensic laboratories?

A. I know that there is a panel of the - constituted by the National Academy of Sciences to look into the applications of forensics, forensic applications of this DNA technology. I know nothing about their deliberations other than one day when I was present to present comments and others did. Their report has not been published and as far as I know is not public knowledge and what specific elements they were investigating or debating, I have no knowledge.

Q. Although the report hasn't been published there's many people that know the contents of the report?

A. If they do it's - if it's beyond the members of the panel, then it's unethical distribution of a document prior to publication if other people know about it. Those documents are, as I understand it, supposed to be confidential until they are finally approved and released, and I don't believe the final document has been approved.

Q. Do you know what degree of variation would be necessary between races or ethnic groups to be certain that it's necessary to have different databases for each?

A. No.

Q. Is there any mathematical formula which can be used to calculate it?

A. No.

Q. If you were to find a community who happened to show a lot of common bands, say on the 25 per cent level, would it be fair to assess somebody in that community with a general population database that maybe the FBI or the R.C.M.P. has?

A. You are asking a hypothetical question about a population where one band has a frequency of 25 per cent, is that the question?

Q. No, that happens to share a lot of common bands on a 25 per cent basis.

A. Well, I'm not sure what you mean by that because if there are a lot of common bands -

Q. If you picked five people - O.K., maybe I'll give you an example. If we picked five people at random in a community and out of those five people it showed that there was a 25 per cent common band sharing, which is almost on a sibling basis, would it be fair to assess a person from that community with the general population database?

A. I can't answer that question because I have no idea what type of situation you are really describing. There are many scenarios. I'm not sure what 25 per cent band sharing means. It is reasonably common in a random unrelated population if you look at a lot of loci to find several instances among five people where at least one band is shared, but if you're asking out of, say, five loci and hence ten bands, 25 per cent of them, something between two and three are shared for every pair of individuals, that is a very improbable situation. The type of population genetic structure that would be required to produce that I'm not sure is compatible with the

kind of reproduction that human beings have, so I think you're describing something that's an unrealistic situation and so I wouldn't know how to interpret it.

Q. Your position in support of the forensic DNA labs, have you ever written a paper and submitted that for peer review to the general scientific community?

A. I've had some 260 papers published and most of those - some have been book chapters but the majority of those have been peer reviewed.

Q. No, I'm talking about the position that you're taking in court today in support of the forensic DNA labs and in support of your no meaningful difference in a forensic field between substructures. Have you even attempted to get peer review on your opinion?

A. There are very few journals that will consider this sort of argument for publication because most of them consider it largely irrelevant to science. I have one paper that has been peer reviewed as a result of an invited talk I gave at an FBI symposium on PCR methodology, and that paper is published or is in press, it was peer reviewed. It was dealing with forensic implications of the kinds of population studies I am doing and the new kinds of molecular methodology that I'm developing in my laboratory, but it was not specifically related to this. This is not my career, my publications are primarily in other fields, but I clearly - or at least I think I have expertise related to this. I am not trying to establish a scientific reputation in forensics.

Q. With the National Academy of Science investigating the reliability of the forensic DNA labs and because of your great experience you didn't feel it was necessary to support your position with the National Academy of Science?

A. I was invited to come down and make a verbal presentation; I did. That clearly supports my position. I have not written a document. Clearly had I desired to they would have accepted it. Anybody who wanted to submit something in writing, they would take it, that's nothing in particular.

Q. Now, Doctor, basically I understand that before you can use the Hardy-Weinberg formula and the product rule two conditions must first be met, that it would be in Hardy-Weinberg equilibrium, that's one of them?

A. No, that's circular. All you need to show is that Hardy-Weinberg ratios do exist in the population, and then you use it.

Q. And there must be linkage equilibrium?

A. The implication of your question is trying to prove something that can never be proved. You can never prove there is linkage equilibrium, you can only prove there is not disequilibrium greater than your ability to measure, and in fact quite a few studies have been done in general in human populations. Virtually all loci in virtually all populations show Hardy-Weinberg frequencies. The hundred different loci we looked at in five populations around the world all show statistical agreement with what we would expect from Hardy-Weinberg. It's a very robust and general finding. One would need extraordinary deviations before one

questioned its applicability. The possibility of linkage disequilibrium at multiple loci, if one can show that there is not large amounts of substructuring then within a population it is also a reasonably robust assumption to proceed as though there is no deviation whatsoever, that any deviations that might exist will exist in both directions, so it is still a reasonable estimate.

THE COURT: Aren't we coming back, Mr. Furlotte, to an area that has been rather adequately covered already?

MR. FURLOTTE: I thought so, too. I didn't expect that kind of an answer. I just wanted a straight yes or no here. O.K., Doctor, basically - I can probably finish up with this witness in about ten minutes.

MR. WALSH: I'll have a couple of questions on redirect, nothing major. If that's the case, I know there's arrangements for lunch to be done. I'll leave it up to Your Lordship as to what you want to do. I'll be about ten minutes on redirect as it is and with his ten, that's twenty.

MR. FURLOTTE: Well, maybe we could break, then.

THE COURT: No, let's keep going, shall we, and then that will let the witness get away. Is that agreeable to the jury? You want to get away. I don't mean just from the court room, from New Brunswick.

MR. FURLOTTE: Well, Doctor, basically to be able to use the Hardy-Weinberg formula and the product rule you must be in Hardy-Weinberg and you cannot have linkage disequilibrium?

A. Of any substantial nature, correct.

Q. And the scientific community, at least the forensic field, or the field in general, has not proven that linkage equilibrium exists?

A. And as I have said, that is something that is scientifically unproveable. It has been proven in several databases that no detectable linkage disequilibrium exists and therefore any deviation from the assumption is small and it is safe to use.

Q. Is it unproveable or just impractical, that it might take a little too long or cost a little too much money to prove it?

A. In the absolute abstract scientific sense the null hypothesis is never proveable. If one wanted to test hundreds of thousands of people you could get much finer levels of deviation that could be tested for, and you might then find some. My assumption is that you would find some if you did a large enough sample and looked very - for very tiny deviations, because human beings do not assort completely at random, they don't mate at random the way oysters do, and so one might expect some. My point is the samples that have been studied are sufficient to show there is no big deviation and hence tiny deviations become the difference between buying one lottery ticket and two lottery tickets and I would say it is not relevant.

Q. Would you admit, Doctor, that the product rule cannot be applied to identifying characteristics unless a valid foundation is first laid for the probability assigned to each of the characteristics and unless mutual independence of each of

the characteristics is established?

A. That is a statement of what is in principle the belief in a mathematical sense, and if you want absolute precision, then that is true. One applies the product rule in a variety of circumstances with approximate answers recognizing what you get out after applying it is still an approximation or an estimate, and you don't need quite such rigorous underpinnings if one recognizes that.

Q. In science, Doctor, before an opinion may be acceptable within the scientific community, must the facts upon which you base your opinion first be proven?

A. Proof of facts is a different thing from proving linkage equilibrium. In many ways the existence of linkage equilibrium for most human populations within a single largely random mating population is adequately proved by examination of hundreds of loci, hundreds of traits, over decades of research in human genetics.

Q. Would you agree, Doctor, that without the knowledge of frequencies of certain alleles as represented by DNA fragment sizes in a population it is impossible to calculate the likelihood that a match could arise simply by chance?

A. I would certainly agree that one must have frequency estimates for the alleles before you can calculate a probability estimate.

Q. Now, Doctor, you said you have studied the autorads in this case?

A. That's correct.

Q. And you came to the same conclusion as Dr. Bowen?

A. With the exception that I noted I would have called a match for one that he called inconclusive.

Q. And how many different autorads would you have looked at?

A. I don't remember. I think it was about a dozen but this has now been four months ago. There was certainly - there were two completely different autorads and each one had been probed - I mean two completely separate loadings or filters and each one had been probed for each of the different loci.

Q. You didn't do any gel to gel comparisons?

A. Well, yes, I did some gel to gel comparisons because there were standards and there were samples of the defendant's DNA on two different gels, and I satisfied myself by comparing them that they were indeed the same on the two different gels.

Q. Which gels were those, do you recall?

A. I have no idea what numbers they were called or what numbers they are in evidence.

Q. Do you know how many different gels were taken of Mr. Legere's DNA samples?

A. I know his samples were run on two separate gels that I saw autorads made from. I do not know if there were more.

Q. Now, Doctor, on Page 8 of the OTA Report which has been read to different Crown witnesses it states: "Questions about the validity of DNA typing, either the knowledge base supporting the technologies that detect genetic differences or the underlying principles of applying the techniques

per se are red herrings and do the courts and the public a disservice". You would agree with that? I would hope you would.

A. I'm sorry, I did not hear clearly the first words of that quote. I'm not going to agree to something I'm not -

Q. I'll let you read it.

A. Yes, I would certainly agree with that.

Q. And here they're talking just about the typing, the initial stage of running your DNA profile?

A. I believe - I would have to look at the context more carefully, but I believe that's correct, it's mostly the DNA methodology.

Q. Right, and that's if the tests are run right and the Office of Technology says it finds that forensic uses of the DNA tests are both reliable and valid when properly performed and analyzed by skilled personnel?

A. Of course. Anybody can make a mess of a DNA test if they have never been trained in how to do it.

Q. So basically anybody who argues that you can't get a good DNA profile through this procedure, your Southern blotting and the works, that's really a red herring, that's nitpicking?

A. To say that it can never be done is certainly a red herring. It is perfectly possible to challenge any given set of results, and in fact, I was asked once by a district attorney to evaluate some DNA evidence and I told him he should not enter it into court, that the test was not done well and would be very bad to enter into court. If a given test is not done well it can be argued against.

Q. O.K., but the same thing cannot be said for the issue of population genetics and the calculation of frequencies? That's not considered to be a red herring by the general scientific field?

A. Certainly a very large number of the criticisms that have been raised in the past such an excess of single band patterns I would say were very much red herrings. They were taking one observation and quickly concluding that it absolutely demonstrated that Hardy-Weinberg frequencies did not apply when there were other far more simple technical explanations and it was a big brouhaha over nothing. I think it was a red herring.

Q. But the fact that substructures exist is not a red herring?

A. Substructures exist in some sections of the human species. They certainly exist in Bougainville and Papua, New Guinea, where we're collecting samples. They certainly exist in the Amazon Basin where we're collecting samples. One can possibly argue some about whether they exist in Europeans but I would say it is in Europeans mostly a red herring because of the bulk of other evidence that we have about DNA variation and about genetic variation among European populations.

Q. Now, Doctor, you mentioned you don't buy lottery tickets because the odds are too great?

A. No, they're too small.

Q. O.K., the odds are too great against winning?

A. Against winning, yes.

Q. So you're just as well off with no tickets as you are with a ticket?

A. That's correct.

Q. And there would be no difference in buying one ticket or ten tickets, no meaningful difference?

A. That's correct.

Q. Now, the odds against winning a lottery, they would be the same for every person?

A. If every person has one ticket, then the odds against winning are identical for all people.

Q. Do you know whether or not anybody wins lotteries?

A. Yes, they do, because hundreds of thousands of people buy tickets, so one considers the number of tickets as opposed to the odds. Certainly the probability of any single DNA pattern that occurs on an autorad, be it part of a database, random people, whatever, the odds of that pattern, the probability of it occurring may be one in ten billion, but it did occur. It's just how often is it likely to occur that then becomes the question. It's not whether it did or did not occur.

MR. FURLOTTE: No further questions.

THE COURT: Now, we've run somewhat over the ten minutes. I'll leave it to you whether you want to finish now or do you want to -

MR. WALSH: I'll finish now, My Lord. I'll restrict myself to a limited number of questions. I'll restrict myself to a couple.

THE COURT: How many?

MR. WALSH: I just have a couple, then, My Lord.

THE COURT: Can I ring a bell when you -

MR. WALSH: Yes, you can -

THE COURT: Is this agreeable with the jury to -

WITNESS: May I have the bell?

THE COURT: You'd like the bell. No, I'm going to keep

control of the bell.

WITNESS: I might ring it sooner.

REDIRECT EXAMINATION BY MR. WALSH:

Q. I understand, Doctor, that during your testimony Mr. Furlotte asked you a question about an affidavit of William Shields that you had been asked to comment on previously and you said something to the effect you would have liked to have seen the context in which the statement was made that you had made the comment on, is that correct?

A. That's correct.

MR. FURLOTTE: My Lord, I believe the Crown brought out William Shields' testimony on direct examination.

THE COURT: Yes, but the affidavit I don't think was brought out. You're referring to the affidavit now?

MR. WALSH: Yes, My Lord.

THE COURT: Yes, it was brought out on cross-examination.

MR. WALSH: I'll show you this particular document, Doctor.

A. Yes.

Q. Is that the affidavit that you were previously asked to comment on?

A. Yes.

Q. O.K., the place that Mr. Furlotte referred you to, the statement of Dr. Shields is on the bottom of Page 10, is that correct? There's a paragraph ahead of it and then the one it's contained in, would you just take two minutes and just read that to see the context in which you were asked to make the statement.

A. O.K., there is an added parenthetical remark here, "The estimated probabilities are predicted to be incorrectly lower when an individual is tested against a sub-population other than his own", and that component of the statement is definitely wrong. They may on average be, but it's going to be very genotype-specific. In some cases the probabilities will be greater if tested against the population other than his own if his type is, especially, rare in his population but common in the other population, and I think it was primarily that component of the statement that I was most opposed to. The earlier part of the statement -

MR. FURLOTTE: My Lord, I don't believe this witness is contradicting anything that he said in cross-examination here. The word - now he's saying is predicted. That's not a must.

THE COURT: He was asked on cross-examination why he had disagreed rather strongly with a statement contained in the affidavit made by Dr. Shields, and what the Crown attorney or Crown counsel now is seeking is to put the matter in context, and the witness is saying there was another paragraph on there which wasn't read to me and which caused the answer which gave rise to the answer I gave on the voir dire.

MR. FURLOTTE: Yes, but My Lord, what I'm saying is it's not contrary. The first term when I was - was, 'is expected', and now it's, 'is predicted'. I don't see any difference between is expected and is predicted.

MR. WALSH: Doctor, the opinion that you gave previously

when you were asked to comment on that affidavit, after seeing that particular portion is your opinion any different today than the opinion you gave previously?

A. My opinion of what Dr. Shields meant has altered somewhat. This is a semantic issue, I read his transcript from the voir dire which he - was after I had testified, in which he made it clear that he was talking about on average, and I clearly interpreted this when I first read it to mean is predicted, will always be, as being equivalent. The other interpretation is not outside of semantic bounds, so this is part of the problem of the English language and even scientists don't always agree on what a word means in all time. My position still stands that it is absolutely not universal. There will not necessarily be a bias against the defendant. It is going to depend upon the defendant's genotype and the specific frequencies in each of the two populations being compared.

THE COURT: Isn't that perhaps best left right there?

MR. WALSH: That's it, My Lord, yes. I only have one more question, in fact, and that would be my second one. Mr. Furlotte asked you a number of questions with respect to what is or is not in scientific dispute. Is there any scientific dispute over whether a five-probe or a four-probe match at these loci - is there any dispute as to the fact that they're rare?

A. I am not aware of any dispute about that. It is universally recognized that multiple locus matches are uncommon, rare events.

MR. WALSH: Thank you. I have no further questions. Just before the bell, My Lord.

THE COURT: Yes, you made it. Well, thank you very much, Dr. Kidd. Thank you for coming and I hope we'll see you back one day.

MR. ALLMAN: I hesitate to keep the jury any longer but I'll be a minute and you can time me. The matter that we've discussed before that we have to voir dire one of these days, this is the appropriate time to voir dire it, and I would suggest that we do that at 2:15, 2:30, whenever. I expect to be about 15 to 20 minutes on my part of the voir dire. I have no idea how long Mr. Furlotte expects to be, perhaps he can give you an indication and then you can tell the jury how long they need to be out. That was 30 seconds.

THE COURT: Well, perhaps Mr. Furlotte, though, isn't in a position to give much of an estimate.

MR. ALLMAN: I say perhaps.

THE COURT: Do you have any thoughts on this, Mr. Furlotte?

MR. FURLOTTE: I have some very brief law that I want to recite beforehand and then it depends on how long it takes with the witness.

THE COURT: Yes, well, the whole thing could take anywhere, perhaps, between one-half hour and an hour, is that a fair estimate?

MR. FURLOTTE: It definitely shouldn't go over an hour. I think half an hour might do it.

THE COURT: Well, why don't we come back at two o'clock, can we do that for a voir dire? Is that rushing it too much?

MR. FURLOTTE: That's rushing it.

MR. ALLMAN: Two-fifteen.

THE COURT: All right, 2:15, and can we tell the jury that they needn't be back until three o'clock, and they shouldn't, of course, come in the court room here but they'll come in by the back way, anyway, and I don't want to send the jury home now because we'll do quite a bit more after three o'clock, perhaps. So, if the jury, then, would retire, please?

(JURY WITHDRAWS.)

(LUNCH RECESS - COURT RESUMED AT 2:15 p.m.)

(JURY ABSENT - ACCUSED IN HOLDING CELL.)

MR. WALSH: My Lord, I was wondering if I could be excused during this voir dire?

THE COURT: Yes. You're not concerned?

MR. WALSH: No, My Lord. There's another witness come in and we want to have him ready as well.

THE COURT: Thank you. Well, now we're assembling here in a voir dire session. The monitor is working, Mr. Pugh?

CLERK: Yes, My Lord, it is working.

THE COURT: Now, I think the main question we had - perhaps you can carry on, Mr. Allman?

MR. ALLMAN: Yes. I thought Mr. Furlotte said just before we closed that he had some legal issues he wanted to address. I wasn't sure whether he meant before we do anything or at some later stage.

THE COURT: I took him to mean in connection with this application.

MR. ALLMAN: Yes, but I wasn't sure whether he meant he had law that he wanted to put to you now before

A. I was not present during his testimony. I took the opportunity to read his transcript. He states that he had met with me and brought it to my attention. I do not recall such meeting. That's not to say that it did not take place, however, but I do not recall bringing that to my attention and because I don't have recollection it's probably because it had no direct probative value to the Daughney case as I saw it at the time.

THE COURT: Did you have any part in the preparation of the composite drawing?

A. Absolutely not, Your Honour. No, My Lord.

THE COURT: And the obtaining of the statements?

A. No, My Lord.

THE COURT: He'd have no involvement, really, in that, is there?

MR. FURLOTTE: Well, let's find out.

THE COURT: All right, go ahead.

MR. FURLOTTE: No, no, I'm not concerned about that. I know he had no preparation of that. Was it brought to your attention at any time that the composite drawing prepared by the Williamses was comparable to the composite drawing of a suspect in the Russell case?

A. Are you asking me if in my opinion I feel that they resemble?

Q. Either you feel or it was brought to your attention by somebody else?

A. I do not recall Constable Fournier telling me this, however that's what he states, but I do not recall that conversation with him, and again I want to emphasize that I was not involved in the Doran and Russell case, I was not about to be

mentioned, wasn't it?

MR. FURLOTTE: O.K., now, I can deal with two at one time here. The statements by the Williamses and the copy of the sketch done by Constable Michel Fournier, do you recall when you came into possession of those items?

A. The sketch from the Williams?

MR. FURLOTTE: Yes, and the statements.

A. I don't recall when I came into possession. I mean there was countless files there that I was reviewing and this was one of them that I reviewed and concluded, but I don't recall when - I would presume - again I'm not sure but I would presume that it's shortly after the 14th of October when I became in charge of the investigation and if I recall, the Williams issue was brought to our attention around the 19th of October, or shortly after anyway, I'm not sure on the dates. They had called themselves to report the sighting and as a result the investigating officer saw fit to pursue, which we do in any case in tips of that nature, to take a statement from these people, as a result of the statement obtain a composite drawing, and that's pretty well it.

Q. O.K., I believe Constable Fournier testified that aside from discussing his evidence and taking the sketch with - I believe it was Constable Lockhart who took the statement from Williams -

A. That's correct.

Q. I believe Constable Fournier also testified here that he thereafter discussed this evidence with yourself; do you recall that?

we get into it or whether he wants me to call my witness and then get into it. I was going to do the latter.

THE COURT: Can we not even before you call your witness - you had had in mind calling your witness on the voir dire and asking him your questions?

MR. ALLMAN: Yes, and then seeing what Mr. Furlotte wants to ask and then seeing how much of that is legitimate to go to the jury.

THE COURT: Yes, but can you - well, O.K. Have you any better suggestion, Mr. Furlotte? I'd like some idea of just what the issues are here before we embark, though, on a -

MR. ALLMAN: Well, I don't know because the issues are Mr. Furlotte's, essentially. I don't want this witness, he's not my witness. The issue, I suppose, is what questions does Mr. Furlotte want to ask this witness and what of those questions are legitimate to be asked before a jury. What I would like to do is call him, lay a basic foundation with this witness, and then hand him over to Mr. Furlotte. Mr. Furlotte can then ask him any questions he deems appropriate and then I would want to make some submissions to Your Lordship. I may say that line of questioning is inappropriate; that line of questioning, that's fine; that line of questioning is inappropriate.

THE COURT: Yes, but I don't want to go on with an hour of cross-examination, you know, to get all the answers and so on.

MR. ALLMAN: But I have no control over that, that's Mr. Furlotte's part in this business.

THE COURT: Well, we may be arguing it when the first

question is asked. I mean you may be posing an objection at that point and -

MR. ALLMAN: I think I may very well, but I have a scenario in mind, I think it will work. Let's give it a try.

THE COURT: All right, you go ahead.

MR. ALLMAN: O.K., I'll call Sergeant Poissonnier.

SERGEANT VINCENT POISSONNIER duly sworn on the voir dire, testified as follows:

DIRECT EXAMINATION BY MR. ALLMAN:

MR. ALLMAN: My Lord, I propose to lead this witness just for a little at the beginning on matters that I take are totally not in dispute, and if I'm wrong I can be corrected.

THE COURT: Yes, that's all right, and you can abbreviate it, perhaps. Confine it to just what you require for this purpose.

MR. ALLMAN: Your name is Sergeant Vince Poissonnier?

A. Yes.

Q. And Sergeant Poissonnier, you were originally on the witness list of potential witnesses for this case?

A. Yes, I was.

Q. The purpose of doing that was to deal with continuity of one item, namely the Ident-A-Kit photographs?

A. That's correct.

Q. Subsequent to that you were advised that your name had been taken off the witness list and we weren't intending to call you as a witness?

A. That's correct, sir.

Q. Subsequent to that you were advised that the judge

had ruled that we had to call you as a witness?

A. That's correct, sir.

Q. And that would be just last week, or a few days ago?

A. That's correct.

Q. After we advised you of the judge's ruling did you proceed to talk to Mr. Furlotte?

A. Yes, I did.

Q. For what purpose?

A. Because I wanted to have an indication as to what he was seeking from me as evidence.

Q. Why did you want to know that?

A. Because - to prepare myself accordingly.

Q. Rather than go back over the entire area?

A. That's correct.

Q. And did Mr. Furlotte give you an indication of the areas that he wants to get into with you?

A. There was three issues that he brought to my attention, yes.

Q. Let's deal with those three issues one at a time.

A. The first issue is whether or not I had any involvement in an unrelated investigation concerning the assault of Russell and Doran case in the Newcastle area.

Q. Did you?

A. I did not.

Q. Any information you may have in your position regarding either the Doran or the Russell case would have come from what source?

A. From an R.C.M.P. officer that apparently worked on the case subsequent to the investigation conducted by the Newcastle Police Department and brief conversation with Mr. Fred Ferguson, Crown

Prosecutor involved in that case.

Q. With regard to the R.C.M.P. officer who gave you information, would that include information which he himself had obtained from other R.C.M.P. officers?

A. I presume.

Q. Apart from that kind of information do you have anything that you could tell us about the Doran and Russell matters?

A. No, I don't.

Q. What was the second aspect of the matters that Mr. Furlotte wanted to get into?

A. It was the composite drawing that was obtained from father and son, Mr. Williams, Sr. and Jr. That was obtained during the course of the Daughney investigation.

Q. Did you take statements from the two Mr. Williamses?

A. No, I did not.

Q. Did you take any part in the preparation of the sketch?

A. No, I did not.

Q. The information that you have about the Williamses, their statement and their sketch, would be given to you by whom?

A. By the investigating officer that was assigned that to.

Q. Have you been advised that both Williamses have testified in this court?

A. That's correct, sir.

Q. Have you been advised that Constable Fournier, the police officer who prepared the sketch, testified in this court?

A. That's correct.

Q. Have you been advised that Constable Charlebois, who was apparently involved to some extent, testified in this court?

A. Yes, I have.

MR. ALLMAN: I'm going to be arguing that this witness shouldn't get into this matter at all but I'm going to still ask him some questions just to clarify the situation. Could you just tell us basically and as briefly as you can what you know happened about the two Williamses' statements and the Williams sketch?

A. This particular tip, when it was assigned, basically it's in relation to their testimony, of course, it's the -

THE COURT: May I just interrupt for a moment just to get it sort of clued in on the background to this, would you care to ask the witness a couple of questions about his overall involvement in this thing?

MR. ALLMAN: All right, let's break off for a moment, then, and go back. You've already told us the Doran and Russell you had no involvement.

A. I had no involvement, no.

Q. What was your involvement in the Flam matter?

A. I had no involvement in the Flam as to the conducting an investigation.

Q. What was your involvement in - or your capacity and your involvement in the Daughney matter?

A. I was in charge of that investigation.

Q. What does that entail? As a person in charge what would be the sort of things you would be doing and what would be the sort of things the people under

you would be doing?

A. Being in charge of an investigation of this nature, because of the complexity, I was assigned investigators. My duty was to oversee the duties of these investigators, assign investigations, review the files that were returned to me as a result of these investigations, assess these investigations and priorize them and conclude them according to the information that I had.

Q. Is that the sort of thing, then, that happened with the Williamses, somebody was assigned to speak to the Williamses, somebody was assigned to make a sketch?

A. That's correct.

Q. O.K., coming back - I hope that answers -

THE COURT: Yes, that's fine.

Q. O.K., coming back to the Williamses, then, I've forgotten where we got to. Could you just start again and tell us what happened about the Williamses?

A. When I read the file which had been completed by the assigned investigator I decided that when I was preparing the court brief for this case that in my opinion based on the opinion of the investigator that it was not probative to the case.

Q. The Williamses, then?

A. The Williamses. Now, having said that it came -

Q. O.K., let me just stop you there. As a result of that did the information about the Williamses, that is to say their statements and the sketch prepared under their instructions, get into either the Crown's brief to be called to court or the disclosure brief of matters not to be called but

disclosed to the defence?

A. It was not disclosed to neither party.

Q. Could you now go on and explain how in fact it came about so far as you know that the Williamses did come to court, did give evidence?

A. As I was told, that the subject of this sketch which had been prepared by Constable Fournier was brought to the attention of the Crown Prosecutors handling this case. After looking into it further themselves, felt that it may have a probative value to it, and therefore they decided to call these witnesses.

Q. So the decision that the Williams aspect should go into court was a decision made by the Crown?

A. That's correct.

Q. Prior to calling the Williamses that fact was made known to Mr. Furlotte and what the Williamses said was made known to Mr. Furlotte?

A. That's correct.

Q. You mentioned three aspects of the evidence that you wanted to get into, one was the Doran - or Mr. Furlotte said he wanted to get into, Doran, Russell, the Williamses; what was the third?

A. The third was concerning the issue of a notice concerning a person who was the object of interception, and pursuant to Section 196 of the Criminal Code and in this matter here Mr. Legere was served a notification on the 8th of February, 1991, to that effect.

Q. So that's the third aspect of matters that we are concerned with and want to ask you about?

A. That's correct.

MR. ALLMAN: I have no other questions.

THE COURT: Well, Mr. Furlotte, how do you want to tackle it? do you want to just explain verbally what types of questions or what areas you want to examine on or do you want to actually ask - start asking questions, at any rate?

MR. FURLOTTE: Well, I think I can give a general statement, My Lord. I think that would be sufficient.

THE COURT: I would think the general statement would serve better to -

MR. FURLOTTE: Well, basically, My Lord, in continuity that he had at the photo line-up. I believe I'd be entitled to ask him as to what his purpose was for having continuity and whether or not he showed it to any witnesses for investigative purposes. That would be the first issue with the photographic line-up. The issue of the Russells, I believe that we can take those two issues in -

THE COURT: Just on that first question, why did he have continuity?

MR. FURLOTTE: Yes, but -

THE COURT: Why did he have possession?

MR. FURLOTTE: What was the purpose of him having the possession or continuity of the photo line-up.

THE COURT: He didn't have continuity, he had possession.

MR. FURLOTTE: Well, he had possession for a while, I understand it, and I would like to know what the purpose was.

MR. ALLMAN: I have a distinct recollection, I can't remember when, but I thought the officer already answered that, he had it at one time because some policeman had to go somewhere and - anyway, I have no objection to that question being asked and answered now and then if Mr. Furlotte wants to ask

it in the presence of the jury we -

THE COURT: Yes.

MR. FURLOTTE: O.K., maybe we could ask that question now, what was the purpose of you having a photo line-up?

THE COURT: Yes, O.K., go ahead.

A. Constable Proulx had the exhibit in question and had used it in the course of an investigation in Montreal. The exhibit in question had been originally prepared by Corporal Godin. I was proceeding to Newcastle, again on this matter, and Constable Proulx only asked me as a courier to return this particular exhibit as Corporal Godin would apparently be in the Newcastle Detachment that particular day, so rather than hanging onto it he saw - he knew that I was going to Newcastle. Basically my duty in this particular exhibit was as a courier, actually, and when I got to the Newcastle Detachment I met Corporal Godin and I handed it over to him and that was the extent of my involvement with this.

THE COURT: This is the line-up photo, is it?

MR. ALLMAN: Yes. Maybe we can deal with these things one a time. If Mr. Furlotte feels it's necessary to call Sergeant Poissonnier to get in that piece of evidence I have no objection.

MR. FURLOTTE: Well, because of that, and you didn't show it to anybody?

A. Absolutely not, no, sir.

THE COURT: Well, that pretty much settles that.

MR. FURLOTTE: Pretty much, and I don't have to have him for that purpose.

THE COURT: But that was outside the three items

involved in that matter, and if anybody should have been concerned with it, it's probably the Newcastle Police Department, and again I will presume that they were informed of that.

Q. O.K., as the chief investigator of the Daughney case would it not raise your curiosity that it may be the same - you may be dealing with the same suspect as in the Russell case?

A. Again the composite drawing, as in other investigations that I've been involved with, is an investigational aid. For me to give an identity, positive identity, to a composite drawing would be very dangerous. For me to say that this composite drawing does resemble this one, I mean it's a question of opinion, so if I recall the composite drawing on the Doran and Russell that was put in the paper by some other sketch artist, I don't know his or her name, the nose was different -

Q. The composite sketch artist was from California.

A. Were they both made by the same person?

Q. Yes.

A. You see, so I was not even aware of who had done the composite on the Doran Russell, that's how little I know about this case. The nose is different, it may look similar to you, it may not be similar to me. It's a question that I have difficulty answering.

Q. But at no time during your investigation of the Daughney case did it raise a suspicion that you might be dealing with the same individual who was involved in the Russell case? I'm not asking about proof or a positive identification, I'm talking about suspicion here.

A. Of course, yes.

Q. It did raise a suspicion?

A. Well, as an investigator with all the violence that was going at that time, of course you would say well, perhaps maybe it's the same person responsible for all these assaults. Again maybe.

Q. And did you check whether or not in the Russell case that the suspect may have been of Indian descent?

A. No, sir.

Q. Did you check in the Russell case as to the description at all of their assailant, the Russells?

A. No, sir.

Q. So while it may have been a suspicion there you did nothing to investigate that possibility?

A. With the Russell connection?

Q. With the Russell connection.

A. I did not investigate.

Q. And do you know whether or not any of your police officers, in particular Kevin Mole, stated to Mr. Legere, "And I'm going to tell you something right now, now that you're in jail I don't think they're going to look for anyone else, do you follow me"? Do you know whether or not that was the attitude of the R.C.M.P.?

A. Absolutely not. Absolutely not. The issue of a possible accomplice was always in the back of my mind. Unfortunately we have been unable to date to ascertain that speculation. There has been a lot of talk about this issue and after almost two years into this investigation I have yet to receive information to indicate that other people

were involved.

Q. Now, that brings us to the issue of notice of wiretap information served on Mr. Legere -

THE COURT: Well, let's dispose of that one first.

MR. ALLMAN: It seems to me it would make sense because that's the first two issues. They're discrete issues, to use the language the scientists have been using all the time, I think we'd make sense to argue the Doran Russell, Williams matter now and then Mr. Sleeth's going to argue the wiretap because that's a topic that he's much more fully informed than I.

THE COURT: Yes, well, what are your objections to the - those are the extent of your questions?

MR. FURLOTTE: Well, those are the areas, and I expect I'll not remember the questions word for word but that's -

THE COURT: What do you say?

MR. ALLMAN: What I say is this. First of all, so far as the Doran Russell is concerned this is clearly hearsay and it's a bunch of questions asked of a man who doesn't know the answers, and if he knew the answers he only gets those answers from other people. He apparently got his information from another police officer who probably got some of his information from another police officer who probably got some of his information from other police officers and from Fred Ferguson, who heaven knows where he got his information from. It's classic hearsay and I would refer Your Lordship again, as I have, to Canadian Criminal Evidence, McWilliams, 3rd Edition, Paragraph 8.10400.

> "The rule against hearsay applies equally to answers given on examination and in cross-examination. Just because an answer is given in cross-examination does not dispense with the rule."

They quote two cases, **Laverty**, 1979, 47 C.C.C., 2nd, 60, Ontario Court of Appeal, and **Forsythe and The King**, 1943, 79 C.C.C., 129 Supreme Court of Canada. **Laverty** is quite an interesting case. In that case the question was whether an expert who had died - a certain expert had died. They wanted to ask some questions of another expert about that expert's notes, the dead expert's notes, and they said no, you can't do that, that's hearsay. This is a classic instance of hearsay. That's the legal basis upon which I object. The practical basis upon which I object is we're going to have a lot of questions which yet again are going to be getting into investigating the investigation and investigating what if any disclosure has been made in this case. Those are not matters that are appropriate for the jury.

The Williamses were in court, they gave evidence, they were cross-examined. Fournier was in court, he gave evidence, he was cross-examined. Constable Charlebois was asked questions about this, he was cross-examined about this. There's nothing that this officer can say except about what he thought about the Williams sketch, rightly or wrongly, and whatever he thought, how it then came out into court because of the decision made by the Crown. That's not the sort of thing that the jury should be getting into.

I'd like to read Your Lordship a little bit of what you said when we were dealing with a

portion of Constable Charlebois's evidence. We were talking about disclosure and the investigation there, though that particular one was about some hair and a report of Gary Verrett.

> "It's not a matter for the jury, this matter of what disclosures have been made, and I'm not going to have all this. This is just a red herring as far as the jury is concerned. If they were to hear it, it would be and I'm not going to have discussion of this matter."

Later on you say again, "My ruling is I will permit no questions with regard to disclosure before the jury".

The Crown's respectful submission is that legally this is all hearsay and practically it's irrelevant.

THE COURT: Insofar as anything pertaining to the Russell case goes, that is a no-no, we're not investigating the Russell case and I'm not going to permit any questions dealing with investigation.

MR. FURLOTTE: My Lord, may I argue first?

THE COURT: All right, go ahead if you want to, I'm sorry.

MR. FURLOTTE: I mean, I think I'm entitled to full answer and defence in this.

THE COURT: I'm sorry, you go ahead with full answer and defence. I wasn't going to hear Mr. Allman on the matter, as a matter of fact. Go ahead.

MR. FURLOTTE: In **Ewaschuk's** under cross-examination, Page 16-16, Paragraph 16:2330, it says:

> "Cross-examination generally involves the questioning of an opposing witness and thus is broader in scope than examination in chief. Its main purposes are to impeach the witness's credibility on testimonial factors such as opportunity to observe, actual observation, recollection, narration and ability to communicate, and integrity, including bias, interest or corruption, to bring out additional aspects

> of the witness's evidence in chief and to elicit new testimony favourable to the cross-examiner's position on any relevant issue. Leading questions even with favourable witnesses are permitted and, unlike the American practice, Canadian practice permits a wide-open cross-examination as to relevant matters and credibility."

It also states that there are - in **McCormack's on Evidence**, 2nd Edition, it's at the bottom of the page, it states that - they're just referring to McCormack's on Evidence - states that:

> Five areas of general attack on cross-examination as to credibility are prior inconsistent statements, bias" -

which the defence would be claiming in this case -

THE COURT: On the part of?

MR. FURLOTTE: On the part of the investigation of Allan Legere.

MR. ALLMAN: Of this witness?

THE COURT: The part of this witness?

MR. FURLOTTE: As a member of the R.C.M.P., yes, on the part of this witness.

> - "bad character, defects of testimonial capacity, and inaccurate testimony."

My Lord, the Crown is quite right, part of the cross-examination is to investigate the investigators. Part of the defence, and it's often been said offence is often a good defence - in this case the Crown is submitting that what I have to question this witness about is all hearsay evidence because it has been said by somebody else, but the purpose of the defence here in cross-examining this witness is not to prove the truth of whatever has been said to this witness or whatever this witness may have uncovered during his investigation of the Daughney incident, the purpose of this cross-examination is to show that

there was a failure on the R.C.M.P. to conduct a proper and a thorough investigation, that they narrowed their suspects to one person and only one person. They weren't concerned about finding any - or they didn't show enough concern, I won't say they weren't concerned, but at least maybe that they didn't show sufficient concern in looking for other suspects other than Mr. Legere.

It's a question of bias. I suppose I could have also asked this witness what was the police's attitude towards Mr. Legere even before he was recaptured. The evidence was, official police reports, that Mr. Legere would be charged with all these offences that he's charged with today even before they had any evidence whatsoever in the Smith case to lay a charge against Mr. Legere, so that would show bias on the investigator's part, and I believe the jury is entitled to know as to whether or not there was adequate police investigation in any and all of the matters which are before this Court.

MR. ALLMAN: I don't want to keep Your Lordship. Do you wish me to speak specifically to the Doran Russell matter or do you have a ruling on that already?

THE COURT: Go ahead but you're - this is rebuttal, is it?

MR. ALLMAN: I have a general observation on all this, two things.

THE COURT: I'm losing track here of what is direct argument and what is cross-argument. This is rebuttal?

MR. ALLMAN: Yes, I think it is. Two things: first of all I think Mr. Furlotte's argument illustrates perfectly, though I don't want to go back over

all the ground why I shouldn't have to call Sergeant Poissonnier. He's manifestly and obviously intended as a defence witness. Having said that I accept Your Lordship's ruling I have to call him. The quote is:

> "The main purposes of cross-examination are to impeach the witness's credibility on testimonal factors such as opportunity to observe, recollection, narration, integrity, bias", etc.

On testimonal factors, it is not - it's to say the testimony that you gave isn't credible for the following reasons, but he isn't giving any testimony. Mr. Furlotte is coming in from the beginning. The purpose of the testimony is to show bias, and in my respectful submission that's not what that's talking about at all. When the Crown or one side calls a witness and the witness gives evidence, then the other side can seek to show bias to undercut that evidence, but that isn't what's happening here. The only purpose of this cross-examination is to show bias.

THE COURT: Well, what **Ewaschuk** is saying is two things. On cross-examination the examiner may ask leading questions and he may explore much more thoroughly or is given a much wider range of type of question than is the person conducting the direct examination. That's recognized, that's a standard rule, but when it talks about bias it's not talking about bias of an investigation, it's talking about bias of the witness. Questions may be asked of a witness to show that evidence he's given on examination in chief have been influenced by a bias on his part and that he's not telling the absolute truth because of that bias. That's what

they're talking about in bias there. The primary question that applies to evidence on cross-examination, just as evidence given on direct examination, is that it must be as **Ewaschuk** says based on any relevant issue, as the words used in the quotation which Mr. Furlotte read, and it must be a relevant issue, and anything here dealing with the Russell investigation is not a relevant issue and therefore questions cannot be asked on that.

There is no relevant issue insofar as the statements or the composite drawing - the statements of Williams insofar as this witness is concerned - nor in respect of the composite drawing which was prepared by the artist, Fournier, was it, as the result of the descriptions given him by Williams, and whether or not this witness compared those drawings with - of which he has no recollection, but whether he did or not compare those with drawings prepared in the Russell and Doran case, I believe was the name of it, is not a relevant issue in this case and those questions can't be asked, so I've disposed of everything up to this point.

Now, the third point was the question of the - or the fourth point, perhaps it is, is the subject of the interception of 8th of February, 1991. Mr. Legere - apparently an order was made and -

MR. SLEETH: My Lord, if it please the Court, before proceeding on that I would like to bring to the Court's attention and to Mr. Furlotte's the provisions of Section 193. I've made a copy, My

Lord.

THE COURT: Section 193 of the Code?

MR. SLEETH: Yes, My Lord, and I've marked with a highlighter for the Court and for Mr. Furlotte the sections which concern the Crown.

I would start by noting, My Lord, that this type of evidence, the type of evidence that would be obtained by using this particular technique, has not been offered and will not be offered. That being the case, My Lord, all the exclusionary principles that would protect this witness from an action under Section 193 at the outset in the prohibitive sections do not apply. We're not dealing here with an evidentiary use or disclosure, evidentiary disclosure -

THE COURT: Excuse me just a minute until I read over Section 193.

MR. SLEETH: Yes, My lord.

THE COURT: Yes, O.K.

MR. SLEETH: There being no such permission, My Lord, before us, no express consent as indicated in the fourth or fifth line of 193(1), this shouldn't even be discussed.

THE COURT: I'm sorry, I just don't get the gist of that. There was no consent so therefore -

MR. SLEETH; Yes, My Lord, either from the originator or the person intended by the originator thereof to receive.

THE COURT: So therefore it would be an offence to use -

MR. SLEETH: It would be an offence for this witness to be referring to it, My Lord. There is provision obviously contained there and we can have a consent if my learned friend wants to obtain it

from the person who would be the originator of various things or intended to receive, and we all know who that would be, but until that is done this witness is not able to answer, he's statutorily barred.

THE COURT: Yes, well, I'm not just sure what we're talking about here. This was a conversation -

MR. SLEETH: We can't even disclose it, My Lord -

THE COURT: I suppose not.

MR. SLEETH: - the existence of it. Perhaps we can have two minutes simply with my learned friend. We might get around the problem in that but in the absence of - and I'm sure he must realize the sort of document in mind - we can't even talk about it, and this witness certainly cannot.

THE COURT: Mr. Furlotte, what do you have to say about that?

MR. FURLOTTE: I'm sorry, My Lord, some stupid lawyer drafted this thing and I'm having a hard time to get the gist of it.

MR. SLEETH: My Lord, the drafter of that was not a stupid lawyer, the drafter of that particular thing was a person interested in protecting the privacy of Canadian citizens.

THE COURT: Draft of what, this is the draft of the section, is it?

MR. SLEETH: Yes, My Lord. I should add, perhaps, in fairness, My Lord, that if my learned friend overcomes that particular barrier I have others.

MR. FURLOTTE: Well, My Lord, I believe I'm acting on behalf of my client and my client was the -

MR. SLEETH: My Lord, the word express is there.

MR. FURLOTTE: The word what?

MR. SLEETH: Find it for yourself.

MR. FURLOTTE: My Lord, I wish Mr. Sleeth would be a little more civil. Let's have a little more -

THE COURT: Yes, don't get too excited, Mr. Sleeth.

MR. SLEETH: My Lord, I will certainly be as civil - treat Mr. Furlotte as civilly as he did with the witness -

THE COURT: Civil and unexcited.

MR. SLEETH: And unexcited as well, My Lord. The reference there is very clear, "the express consent of an originator or of a person intended by the originator to receive a communication". The consent must be expressed, the mere appearance of counsel does not indicate an express consent and it could be denied later.

THE COURT: I suppose it must actually have been expressed before the reception, would it?

MR. SLEETH: Before disclosure, My Lord.

THE COURT: Oh, before disclosure, but I was wondering about before reception as well. Well, that wouldn't make sense, would it. Well, this is without disclosing the nature of anything, we're talking here about what some telephone message - something just said by the accused in this case? Mr. Furlotte, you must know what we're talking about.

MR. SLEETH: My Lord, I guess the best way to describe it is we're talking about an investigative technique.

MR. FURLOTTE: My Lord, we're talking about an investigative technique and I'm not interested in what the content of the private communication was. What I'm interested in is the conditions of which the R.C.M.P. are allowed to obtain such an order,

O.K.? Section 186(1) -

MR. SLEETH: My Lord, we're getting into disclosure again.

THE COURT: The Crown here have made no use of any - apparently, as I gather, have made no use of anything that may have been disclosed. You're suggesting, as I understand, Mr. Furlotte, that the Crown has illegally wiretapped or illegally intercepted a -

MR. FURLOTTE: Oh, no, I'm not submitting that at all, they got a court order. I'm not submitting it was illegally done. What I want to submit in cross-examination is the bias of the R.C.M.P.

THE COURT: In what?

MR. FURLOTTE: In their investigation. Basically, My Lord, I'd read 186(1) to you. It says, "An authorization may be given if the judge" -

THE COURT: What is this, 186?

MR. FURLOTTE: 186, paragraph 1. It says,

> "An authorization may be given if the judge to whom the application is made is satisfied, (a) that it would be in the best interests of the administration of justice to do so and" -

and, My Lord, I might state and, it's not or -

> "and that other investigative procedures have been tried and have failed, other investigative procedures are unlikely to succeed or the urgency of the matter is such that it would be impractical to carry out the investigation of the offence using only other investigative procedures."

Basically the position of the defence is that at the time that this order for interception with private communications was obtained was merely two months before Mr. Legere was charged. I don't have the exact dates but I believe they were in September and October of 1990.

THE COURT: My understanding of the law is this, that if the Crown here, for instance, endeavour to put into evidence information which was obtained as the result of an interception of a private communication, whether it by wiretap or otherwise, for which an order was unlawfully obtained purporting to permit that, then you could resist the adducing into evidence of that evidence on the ground that the order was improperly obtained, but this isn't a case of this. You're questioning the bias of the - are you using bias in the same term as **Ewaschuk** used it a minute ago, because I explained that a minute ago, what **Ewaschuk** means by bias.

MR. FURLOTTE: My Lord, also in **Ewaschuk's** at Page 16-17 under paragraph 16.2370 it says,

> "Cross-examination regarding unprovable allegations and outstanding charges."
>
> "Counsel is generally entitled to put questions in the course of cross-examination of a non-accused witness which are based on material which he is not in the position to prove directly. However, unless the matter relates to a fact in issue or example to bias or state of mind counsel will generally be bound by the answer."

So I am able on cross-examination to put to a witness in relation to any issue which I'm not in a position to prove directly, and I'm not in a position to prove this directly.

THE COURT: What do you want to ask him, then?

MR. FURLOTTE: I want to ask this witness as to how they were able to get an order, one, from a judge to interfere with private communication of Mr. Legere when the only condition of which they can get that order is that other investigative procedures have been tried and have failed - "other investigative procedures are unlikely to succeed or the urgency

of the matter is such that it would be impractical to carry out the investigation of the offence using only other investigative procedures".

MR. SLEETH: My Lord, my learned friend once more, it's not the first time, misstates the law. Those words are there -

THE COURT: Just a minute now, Mr. Sleeth. Mr. Furlotte still has the floor and may not have finished yet.

MR. FURLOTTE: What I'm questioning, bias and credibility of witnesses and credibility of this investigation and the charges against Mr. Legere. How can they be on one hand saying that we have sufficient evidence to prove you guilty beyond a reasonable doubt and at the same time telling a judge that the other investigative procedures have been tried and have failed and that there is - "have failed and that other investigative procedures are unlikely to succeed or the urgency of the matter is such that it would be impractical to carry out the investigation of the offence using the other investigative procedures". As you will recall, the DNA -

THE COURT: Who do you want them to charge if they don't charge your client? Who do you want them to charge? Isn't the duty of the jury here to decide whether or not the Crown have put their eggs in the right basket or not? You know, if they're charging and trying to make out a case against the wrong man and they fail in the evidence they adduce the jury presumably will find the man not guilty or bring in not guilty verdicts.

MR. FURLOTTE: The jury has every right to do that and the R.C.M.P. has every right to do it, but I also

think the jury has every right to know what tactical maneuvers the R.C.M.P. are using in order to try and bring evidence which they consider on one hand - one side of the mouth they're saying it's sufficient to bring before a jury to convict. On the other side of the mouth they're going before a judge and saying, we don't have enough evidence, all within -

THE COURT: Where do you find any support for that proposition?

MR. FURLOTTE: Well, that's what I want to be asking this witness in cross-examination.

THE COURT: No, but I'm talking about a legal precedent for that type of proposition.

MR. FURLOTTE: Well, before a judge can issue an order for interception of private communications the condition must be met. It says, "An authorization may be given if the judge to whom the application is made is satisfied that it would be in the best interests of the administration of justice to do so and that other investigative procedures have been tried and have failed, other investigative procedures are unlikely to succeed".

THE COURT: I don't have any authority to look into the reasons that some other judge may have granted that order, or whoever did grant the order, I didn't myself.

MR. FURLOTTE: I would assume that the R.C.M.P. give an affidavit stating the conditions upon which they wanted to get the interference with private communications.

THE COURT: The only circumstance under which I would

have any authority to look into those reasons would be if this witness or some other witness here - the Crown through this witness or some other witness were trying to adduce evidence which you or the defendant contended was illegally obtained, and then I would have to look into the question of whether that order was properly obtained or not, and there's no suggestion here, you make no suggestion, that there's any evidence being adduced in this trial gained as a result of this order that you refer to.

MR. FURLOTTE: No, that's quite right, My Lord, but if I want to argue to the jury in my address as to how much weight they should be putting on the evidence that's brought before them I believe I would be entitled to tell them, well, look, the R.C.M.P. didn't think there was enough weight to be placed on it because they had to go to a judge to get an interception of private communications.

THE COURT: That's a matter of investigation and it's not relevant to this trial. That's my ruling on that point.

MR. FURLOTTE: That's fine, My Lord.

THE COURT: Does that dispose of -

MR. ALLMAN: Well, that being the case of the four issues I think the first issue Mr. Furlotte said he doesn't need to raise. The remaining three issues Your Lordship has ruled he can't raise. Do we need to call Sergeant Poissonnier; I think not, but I await Your Lordship's ruling.

THE COURT: I say you don't have to call him, or there's no necessity for calling him.

MR. ALLMAN: I'm obliged, My Lord.

THE COURT: We'll have a recess here for ten minutes and then we'll continue with the jury.

(BRIEF RECESS - RESUMED AT 3:20 p.m.)

(JURY CALLED - ALL PRESENT. ACCUSED IN CELL.)

MR. WALSH: My Lord, the next witness on the indictment list would have been Dr. Carmody, then Dr. Fourney. I've spoken to Mr. Furlotte. Dr. Fourney would, I expect, be the shortest of the two and it would make more logical sense to put Dr. Fourney ahead, and I would seek your permission, then, to call Dr. Fourney.

THE COURT: All right.

DR. RONALD FOURNEY, called as a witness, being duly sworn, testified as follows:

DIRECT EXAMINATION BY MR. WALSH:

Q. Would you give the Court your name, please?

A. Ronald Mitchell Fourney.

Q. And your present position?

A. My position is Section Head of Research and Development at the R.C.M.P. Laboratory in Ottawa.

MR. WALSH: My Lord, with your permission I'd like to take him through his C.V.

THE COURT: O.K.

Q. Dr. Fourney, you have a Bachelor of Science in Biology with Honours from Queen's University, is that correct?

A. Yes.

Q. And a Master of Science in Biology from Queen's University?

A. Yes.

Q. And a Ph.D. in Biochemistry from Memorial University?

A. Yes.

Q. You had a National Cancer Institute of Canada Research Fellowship and a National Cancer Institute Research Fellowship with the Alberta Heritage Foundation?

A. Yes, it's actually Alberta Cancer Board Research Fellowship, a National Cancer Institute of Canada Fellowship; there's two separate fellowships.

Q. O.K., thank you, Doctor, for correcting me on that. You were a Postdoctoral Fellow at the Molecular Genetics and Carcinogenesis Laboratory of the W. W. Cross Cancer Institute in Edmonton, Alberta?

A. Yes.

Q. What if any kind of work were you doing there, Doctor?

A. Primarily my work was concerned with looking for the molecular triggers that cause cancer. In particular we were looking at the genes, what are called oncogenes, and one of the hypotheses is that certain times these oncogenes will go awry or there will be a problem there and that the final offshoot will be cancer. Part of the technology that we use to study the activation of these cancer-causing genes are the molecular genetics and molecular biology technologies that we use, for instance, in forensic science, so most of my work at the Cross Cancer Institute was solely involved with looking at the DNA from families of members who had cancer, a predisposition, to ask the question what possible

molecular linkage or genetic relationships in the DNA could be a predisposition to cause these cancers to occur.

Q. I understand that you had a number of publications in the scientific literature stemming from that postdoctoral research?

A. Yes. In fact, one of my first publications was developing the technology of Southern blotting and an alkaline blotting for the detection of these particular genes. The sensitivity was enhanced, etc., because we were working with smaller samples at that time. I was also involved with a breast cancer project where I was particularly interested in diagnosis of breast cancer at a very early stage, such that if we could come up with a molecular test which will help the clinician predict those patients that will have a particularly bad metastasis towards disease, then we could possibly do something else, perhaps give chemoadjuvant therapy to these patients, so the bottom line is that certain patients would come in with a very early breast cancer. We would look at the DNA from the tumours of those patients and try to assess their levels of what we call oncogenes to see if there is a molecular diagnostic indicator there, so if the level was particularly high we would go back to the clinician and say, I think this patient has a good chance of recurrence and the risk is high, therefore you should take extra caution in treating this patient. Many patients would come in and they wouldn't have a recurrence. We were particularly interested in the very early onset of those 16% of the patients

that would have a predisposition towards breast cancer.

Q. I understand as well, Doctor, that some of the work that you actually did there, particularly in the area of the breast cancer screening program, has been adopted or followed or is now being used in science, is that correct?

A. Yes. I was part of a time which developed a rapid diagnostic procedure using DNA to make a prediction on breast cancer, and I believe there's a pilot project ongoing right now in, certainly, Alberta and other places capitalizing on this ability to detect cancer at an early stage.

Q. What if any use did you make of the process of Restriction Fragment Length Polymorphism technique in your work in the Cancer Institute?

A. Well, at that time when I was working at the Cross we had a little over 2,000 cell lines. This is cells taken from patients or people who had a predisposition towards cancer, and also family members that didn't, and we were able to grow up these cell lines, extract the DNA from them, restrict or cut the DNA into small pieces, and then look at different parts of the DNA to find out if there's any predicting mechanisms there that we could detect using our DNA probes which would help us understand the mechanism of cancer in some of these patients, so most of the work that I've done at the Cross were primarily related to DNA, RFLP detection of small quantities of DNA. In particular I worked with tumour material which was formaldehyde-fixed in formalin material that it took special precautions and

technology had to develop to use this material to make DNA on which we could do our tests.

Q. I understand as well, Doctor, you were a research adviser on nucleic acid detection on membrane supports with a company called Gelman Sciences Inc.

A. Yes.

Q. What if any work did you do there that would have application to what we're doing or what's happening in the forensic laboratory?

A. It gave me the direct ability to look at many of the membranes, for instance, that we currently use in Southern blotting or DNA diagnostics, so that I was able to refine the technology so that we could get cleaner answers with less material, more sensitive detection.

Q. And Gelman Sciences Inc., what if anything do they provide in the scientific community, or did at that time?

A. At that time they were a major producer of membranes and they still are, as far as I know, a producer of many molecular products that are used for the detection of DNA products.

Q. You also were a molecular genetics specialist at the Molecular Genetics Section of the R.C.M.P. Central Forensic Laboratory in Ottawa, is that correct?

A. Yes, I was initially hired shortly after Dr. Waye, and Dr. Waye and myself were tasked with the role of implementing the DNA technology for the Royal Canadian Mounted Police for forensic use such that the technology and experience that we gained in our respective clinical backgrounds could be

transferred towards the forensic community.

Q. And then your position there changed to in charge of operational support at that section. What if any duties did you have in that particular area compared to the duties that you had when you first entered?

A. To tell you the truth there wasn't a great deal of difference. When Dr. Waye and myself joined the R.C.M.P. there were basically us, the two of us, and one or two technologists, so we could each have our own roles and call us whatever we want but basically the task was to develop the technology. As more people entered into the program we started to divide up the roles and the responsibilities we had such that as the DNA test was being used within the court systems and as particular restraints were put on the technology they became important for the Operational Support Section, that is the section I was involved in, to try to get around any of the problems we would have with sensitivity; for instance, the requirement for making population databases, etc., so a lot of the science or development that was behind the R.C.M.P. program to put this forth into the courts was being done by Operational Support.

Q. Now you're the Section Head, as you've indicated, of Research and Development of the Molecular Genetics Section of the R.C.M.P. Laboratory?

A. That's correct.

Q. What role do you play there?

A. At the present time I have - let's see, it changes but I believe I have one, two, three individuals, we're hiring a fourth, so there's five of us

counting myself in the program, and our main task is to develop the technology, remain current in the field, and to support the operational section as it may be required in court. Much of my responsibilities now lie in the field of quality assurance, quality control, to make sure that the tests are done properly, and also to remain current in the recent developments that are ongoing because this field is very rapid and the changes are quick such that the technology we use today may in fact be replaced with a more sensitive technology in the future, and one of the things that the R.C.M.P. wants to do is remain current, and my responsibility in doing so is to conduct research so that we can certainly be on top of our program.

Q. You are also an Adjunct Professor at the Department of Biochemistry at the Faculty of Medicine at the University of Ottawa?

A. Yes, I am.

Q. And in that particular - as an Adjunct Professor there do you have anything to do with DNA or DNA typing?

A. I have a limited teaching role there, such that I teach actually to undergraduate students some of the technology that we currently use in the forensic lab, that is DNA typing and the quantitation procedures. I also lecture in the general format of how molecular biology and genetics are used in industry or in the community, and I also have responsibilities to several researchers over in the university such that we collaborate back and forth sharing our new development and

technology.

Q. I understand, Doctor, you're a member of the American Society of Human Genetics?

A. Yes.

Q. And the Canadian Society of Forensic Science?

A. Yes.

Q. And the International Society of Forensic Haemogenetics?

A. That's correct.

Q. What is haemogenetics?

A. Essentially it was a society that was originally started to use conventional protein marker systems for forensic and paternity purposes. It would be what we would consider serology. That has been superseded now by DNA.

Q. You are also a member of the Technical Working Group on DNA Analysis Methods?

A. Yes, I am.

Q. And you're on the Editorial Board of Biotechniques and that's the Journal of Laboratory Technology for Bio-research?

A. Yes.

Q. And you're a member of the Canadian Society of Forensic Science DNA Committee?

A. Yes.

Q. What is that DNA Committee, what does it do?

A. Essentially it was a committee set up under the auspices of the Canadian Society of Forensic Science to develop a series of standards, quality assurance, and proficiency recommendations for DNA typing in Canada.

Q. You have also, Doctor, recently been appointed the Canadian representative on the International DNA

Committee. Would you explain what that is and what the role of that committee is?

A. Yes, as DNA typing is becoming accepted throughout the world it's important that we remain current with not the technology that's ongoing here in Canada and the U.S. but also in Europe, and recently in Germany a committee was formed under the auspices of the International Society of Forensic Haemogenetics, such that a number of individuals would come together and collaborate to develop a global or worldwide perspective on quality assurance, proficiency, DNA typing, and the future developments that this may lead for forensic purposes and also for paternity as well. There are three North American representatives, I'm one of those three. There's a number of European representatives, of course.

Q. As well, Doctor, I understand that you were in this particular case the reviewer of the test results conducted by Dr. Bowen?

A. That's correct.

Q. You also, Doctor, have a number of publications. I've previously mentioned that you had a number of publications related to your cancer research, is that correct?

A. That's correct.

Q. You have also a number of publications in the forensic DNA field?

A. Yes.

Q. You've published with Dr. Waye and Dr. Budowle of the FBI and several other individuals on a simple and sensitive method for quantifying human genomic DNA in forensic specimen extracts and that's a

publication in "Biotechniques"?

A. Yes.

Q. You have also published with Dr. Waye a paper called, "Agarose gel electrophoresis of linear genomic DNA in the presence of ethidium bromide: band shifting and implications for forensic identity testing", in "Applied Theoretical Electrophoresis"?

A. Yes.

Q. As well you've published with Dr. Waye on the identification of complex DNA polymorphisms based on variable number of tandem repeats and restriction site polymorphism?

A. Yes.

Q. In the "Human Genetics Journal", and you also, Doctor, have published with Dr. Waye and Dr. Bowen on the forensic analysis of restriction fragment length polymorphism: theoretical and practical considerations for design and implementation in the proceedings of the International Symposium on Human Identification at Madison, Wisconsin?

A. Yes.

Q. And you have also published with Dr. Waye and Dr. Bowen and others on case work examples of sensitive and specific quantification of human genomic DNA?

A. Yes.

Q. And you are one of the authors on the paper, "Fixed bin analysis for statistical evaluation of continuous distributions of allelic data from VNTR loci for use in forensic comparisons"?

A. Yes.

Q. And you are yourself the sole author of a recent

paper that's in press on standardization of methods and data sharing for DNA typing laboratories in the proceedings of the Second International Symposium on Human Identification?

A. Yes.

Q. Among others, Doctor, you've also - there are other publications as well?

A. Yes, there are.

Q. And you also have attended - you have been involved in a number of abstracts and presentations at various meetings throughout the world?

A. Yes.

Q. Particularly related to forensic DNA and DNA typing?

A. Oh, yes, that's basically my primary responsibility.

Q. Do you have occasion - without going through each and every one of them do you have occasion in your work to meet with other scientists worldwide to attend meetings in other areas, to visit other laboratories, etc.

A. Absolutely. Science is not a stagnant process and we're routinely updating our procedures, making the technology more sensitive, refining all the aspects of the DNA typing procedure and other technology that we're bringing in, and it's important to not only present this to your peers, other scientists, but also to be able to critique people and to get back information so that you can make your program better, because science is not done in a vacuum.

Q. And you've actually acted as moderator or chairperson at many of these meetings?

A. Yes.

MR. WALSH: My Lord, at this time I'm going to ask that Dr. Fourney be declared an expert in the field of biochemistry and in the area of DNA technology and testing procedures and forensic DNA typing.

THE COURT: Do you have any questions, Mr. Furlotte?

MR. FURLOTTE: I have no questions.

THE COURT: No? Well, I would declare the witness for the purpose of this trial an expert in the fields of biochemistry, especially in the area -

MR. WALSH: DNA technology and testing procedures and forensic DNA typing.

THE COURT: - of DNA testing procedures and forensic DNA typing. Does that cover you?

A. Thank you.

MR. WALSH: Dr. Fourney, you had mentioned when we were going through your background - you had mentioned quality assurance and quality control. Would you explain to the jury, please, what quality assurance is and what quality control is?

A. Yes, well, quality control are the steps taken by a laboratory to make sure that you have a valid reproducible and reliable procedure or test, and quality assurance is the documentation that supports that that quality control has been done.

Q. And what application would quality assurance and quality control have with respect to your section, Research and Development?

A. It's fundamental to assuring that we get the proper results and that the results are valid. Without good quality control you can't really derive any kind of perspective on what you've done.

Q. With respect to quality assurance what was done, if anything, to ensure that the lab uses top quality materials?

A. In respect of quality control, really.

Q. Excuse me, quality control.

A. Well, to start off with one of the things that we want to make sure that we use is the best quality material, and although there are a number of products out there and a number of different suppliers we are particularly choosy at the R.C.M.P., so fundamental to the technology that we use, for instance, is the membrane support. That's the nylon membrane that actually the DNA sticks to, and although there are three current manufacturers in the world we literally screen a particular lot of membrane and evaluate it extensively before it even gets used within the operational section, and we go through a number of steps to ensure that the membrane will meet our specifications so that we know that it will work properly. The agarose, for instance, that's the gel material that we make our gels out of, we have not haphazardly picked up just any old agarose. We've taken a number of steps to ensure that the agarose we use will give us reproducible and reliable results and that we would maintain a high level of quality control in that agarose we've taken a measure to actually buy a specific lot of agarose, and I've since learned that that agarose now is being actually sold as a forensic grade agarose to all international and national markets doing forensic DNA typing. The enzymes that we use, for instance the Hae III enzyme, that's our

molecular scissors, we want to make sure that we have the right pair of scissors to cut the DNA so we go through a number of steps to ensure not only have we got the best enzyme that we could possibly get at that time but that it will be consistent throughout the entire lot, so we will purchase an entire lot of that enzyme so that just a small deviation from one lot to another won't cause a fluctuation on our test, and it takes approximately two to three weeks just to test an enzyme out before we release it into operations. The probes, these are the final requirement in our procedures, the detection, and we want to make sure we have the right probes and that the probes that we do have will give us a very sensitive and reliable result, so we go through a number of steps of membranes that we already have known DNA sequences on that will give a respective result, and we would use the probes initially on those membranes before any of this is released into operations, and that's why it's separate from the operational section, that case work section. My section in Research and Development, we're supposed to find the problems before they get into operations and we're supposed to solve those problems before they get into operations as well.

Q. Apart from the quality of the materials could you review with the jury, please, the controls that are actually placed in the - when it's operationally being used?

A. Once the protocols and the actual material is released into operations, then we want to make sure that the technique has been followed

properly. Fundamental to this is the ability to get a result on the controls. These are known samples of DNA that we have looked at extensively and we know that within the limitations of our technology what the size of those fragments will be, what the expected result will be on that, and if we don't get that result on the membrane, then basically we can't use that test, and you'll find, for instance, there are two control samples on the membrane, there's a male and a female cell line control, or a male and a female DNA sample, and essentially we have to have those on because some of our probes are sex-typing probes, and without a male typing control on there we would never know if it has worked properly because you would get a negative result with a female.

The ladders that we use, the molecular weight markers, they've been very carefully selected to cover the entire range of our gels so that we can get a reliable molecular weight measurement. If those ladders are inconsistent in any way, or if they're deviant, we would immediately pick that up when we probe those ladders, so the ladders themself act as a sizing control on the membrane, or on the original agarose gel.

Other controls that we would use would be basically we would always be able to look back at previous test results, for instance, and I'm not really sure what other controls -

Q. What about monomorphic, the monomorphic probes?

A. Oh, O.K., beyond the actual probes, I should say what we load on the membrane, the DNA, we use a monomorphic probe. This is a little bit different

than what we call the VNTR probe. Unlike the VNTR probe which is highly different from individual to individual, the monomorphic probe essentially will find a major single band that is constant from individual to individual. Now, you may ask why do you have one band and it's not different from person to person. The whole reason for that is that we know the expected size, when we probe a membrane we know that the fragment size should be 2,731 base pairs, so this has been previously sequenced, very accurate, and when we use this probe on the membrane if we get anything else that's different, then we know there's a problem here, there's been a shift in the DNA or something has occurred that we would question the results, and the universal feature of this monomorphic probe is that it will bind to all the DNA on the membrane, that is human DNA, and give the same pattern, so it's very easy to look at and tell whether or not the test has worked properly. The monomorphic probe would not only give you a measurement and precision estimate because we know the size, but if you've got a result that looks slightly different, for instance if you get a laddering effect with the monomorphic probe, then you know your enzyme hasn't worked properly so you would question the enzyme hasn't cut properly, so it would give you a reliable estimate on what we call restriction digestion.

Q. What about, Doctor, the steps that are carried out, for example in this case by Dr. Bowen, the various steps? What if any record keeping is maintained associated with that step or what if

any photographs are taken along with it?

A. Oh, there's extensive record keeping. One of the things that I quickly became aware of coming from a clinical genetics program where we looked at cancer, I would have my research notebooks, I thought I kept good records. When I got to the R.C.M.P. the forensic continuity is such an issue that from the minute a sample comes through to every single step that is taken, it's documented. For instance, in the DNA typing program the DNA is extracted, it's recorded on particular log sheets when, where, the enzyme lot that was used, if there's any problems occurring with the extraction, the time of the extraction, the whole works, so it's accurately - then we would go to a test gel and they would look at the test gel, and this gel evaluates whether or not you've got a big piece of DNA. You want as large an intact piece of DNA as possible, we don't want to degrade a piece of DNA, and this test gel is a little bit of DNA is run on this gel to evaluate whether or not you got an intact piece of DNA to work with. That's photographed under fluorescence with ethidium bromide stain which is basically a fancy stain that interacts with the DNA to produce a colour that is easily photographed. The photograph becomes part of the record, the negative becomes part of the record. Each step along the way, the restriction digest, that's to ensure that everything has happened properly, a test gel for the restriction digest is run so that we would see a smear of the DNA pattern which I'm sure you heard about last week. There are certain bands

within that pattern that remain constant because they're satellite bands and we could tell by just looking at that whether the restriction digest has worked properly. That's photographed, the negative itself is put into the records.

Besides the photographic process, the membrane itself, it's still around. You can probe that membrane again and the X-Ray itself is the automatic or direct impression of your test result and that's part of the whole program.

Q. We had evidence last week from Dr. Waye with respect to a particular form of - I think it was called slot blot quantification, or quantifying your DNA to determine how much human high quality DNA you have before you proceed through to the test.

A. That's correct.

Q. You were involved in that as well?

A. Yes.

Q. Has that been used or being used by any other forensic labs now besides the R.C.M.P.?

A. There are a number of labs within the U.S. system that are currently using the slot blot quantification and there's a new technology that's around the corner that's going to be a little bit more sensitive, perhaps, called polymerase chain reaction, and there it requires even a smaller amount of DNA and our test is really the only test that can be used to predict the quantity of DNA that's on there, and the nice feature about the slot blot quantification technology is the fact that it detects a hybridizable human DNA material such that once we - we not only know how much DNA

we have there but we know that it's also of human origin.

Q. Doctor, would you explain to the jury what validation studies are?

A. Validation studies are studies that are undertaken to test whether or not the results of an experiment, for instance, would give you the reliable, predictable and valid result. In other words, what you're trying to test and ask, are you going to achieve the correct answer using this procedure, and one of the conseguences of forensic science, unlike clinical diagnostics where you might be handed a frozen piece of material from an operating theatre that you extract DNA from, in the forensic realm which is truly different from the clinical realm we would get a sample that may have been exposed to environmental insult, sunlight, temperature, it might have been a stain that's been around for several days. We would undergo tests ourselves, other laboratories in collaboration, to test whether or not we would get the result that's predicted from the controls, so there we would take, say, a blood standard from an individual and put it on a stain and deliberately leave that out for several days drying, several weeks in fact, and we would extract the DNA from that and compare it back to the fresh liquid blood and ask the question do we get the same results. That's a validation study.

Q. What if any validation studies were done with respect to a laser called a luma-light?

A. That was a study undertaken by Gary Verrett, for instance, at the molecular genetics section at

the R.C.M.P. where part of his project - each person that is trained at the R.C.M.P. has to undergo a mini-research project where he designs a project and develops the technology or asks the question and goes through the procedure, sort of like a mini-experiment, and one of the experiments was the luma-light procedure which is a light that detects bodily substance at a particular wave-length, and one of the questions we wanted to know is if the police use this light, for instance, and pick up a semen stain or a blood stain, is there anything that we should be worried about with the exposure of this light to the stain; in other words, will it have an effect on the DNA, the ultimate pattern, and the answer from that was fairly definitive that no, it doesn't have an effect.

Q. What about a substance called permount?

A. Permount is a substance which is used when you make a tissue section or it is used in hair analysis in the forensic lab where you can put this material onto a slide and it fixes - it binds the tissue, it's like a glue, and then you can put a cover slip on top of this slide and the whole works goes into a microscope stage and you look at the hair, for instance. The basic question was if you had a hair that was stuck in this glue, this permount substance, does it have an effect on the DNA, does it have an effect on the hair such that we won't be able to obtain a large piece of DNA that we could work with, and Dr. Bowen actually did some fairly nice tests with that. It definitively showed that we've had excellent results of

obtaining DNA from hair, for instance, that had been fixed for many years.

Q. I understand as well tests have been done either at the R.C.M.P. or collaborative with things like temperature, heat, cold, soil, fabric, solvents, things of that particular -

A. That's correct. We formed at the very early onset of our program three or more years ago now an international collaboration with the FBI because it quickly became apparent that this technology would be grasped in forensics and used extensively and in order to carry out the studies that we wanted to do it made a lot more sense to carry it out in a collaborative way so that we could divide up certain parts of the projects. Part of the project that we were involved or tasked with was to look at the different probes that were available. There are many more probes than what we have but we wanted to pick out the best probes for sensitivity and to give the reliable or reproducible results, so we looked at different probes. On the other hand, the FBI under the direction of Dr. Bruce Budowle at the Quantico Research Laboratory, they underwent extensive studies for validation on environmental insults, the effect of temperature, light, whether samples are stored in the dark, stored in the light. Many, many substances were put onto stain material, gasoline, various bleaches, detergents, anything that essentially would be a household product was exposed to DNA and the question was simply asked does it render a result that was different from the normal control and for the most purpose is the

reason forensic scientists like DNA, it is highly stable.

Q. When you say highly stable, I understand, Doctor, that you were at a recent Promega meeting in which there was examples given of DNA molecules that had been subjected to intense environmental insult?

A. At that particular Promega meeting there were different groups of scientists speaking from an operational point of view, from the point of view of research, and there was extensive discussion on - and actually the good results that we would get from samples that you would normally not expect to get a result from. I think probably what you're suggesting is some of the work that the Armed Forces Institute of Pathology had undergone during the Desert Storm and Desert Shield operation where they wanted to identify the remains of soldiers killed in action. They used various forms of DNA typing procedures and often the remains that were left after a soldier was killed in combat had been exposed to very high temperatures and incineration, but there is different forms of DNA typing. I believe at that particular meeting there's been over 3,500 cases now done by the FBI, they've accepted over 4,000. There's been over 2,000 cases done by the European group in London for the British Home Office and the Met Lab, I believe, so that there's been extensive tests on validation and actual case work experience.

Q. This particular experience that the army pathology had, this is what particular scientist was involved in those studies?

A. That was Major Victor Wieden who is heading up this program by the American military where essentially they want to develop the DNA typing procedure so that they will be able to ultimately identify every single individual who is killed in action.

Q. What kind of success did they have in relation to the stability of the DNA molecule? What if any conclusions could they draw from the work they did?

A. They were very encouraged with the number of samples that they had that they got definitive results using the different procedures. They tried a number of procedures, all involving DNA, of course.

Q. Hypothetically speaking, Doctor, if you were to extract high molecular weight human DNA from a substance that has been subjected to environmental insults would you expect the environmental insult to have an effect on the typing process?

A. No, I wouldn't.

Q. What role did you play, if any, Doctor, in determining the match window presently used by the R.C.M.P. and how was it determined and why?

A. At the very beginning Dr. Waye and myself when we were developing the program it became clear that there was essentially two different aspects to DNA typing. There is the aspect of match, do we have a match, do we not have a match, and then there's the aspect of if we do have a match what significance can play on that, and that's where the role of measurement precision and error rate came in, and essentially what we wanted to ask was what

kind of match window within the limitations of our procedures that we currently use was necessary to get a valid and reliable, reproducible result, and what we proceeded to do, for instance, is initially we used the monomorphic probe, that's the probe that only finds a major band at 2,731, and we essentially screened our entire database. I believe at that time we had 600, it's certainly much larger now, and we actually measured the deviation of all 600 individuals at 2,731 base pairs and asked the simple question how off can this measurement be, and that established from a monomorphic point of view our window at 5.2%.

The other thing that we did was as we gained more experience and had more case work experience we would measure known and unknowns from our case work and ask where we know that there's two individuals or two people here from a forensic point of view what's the reliability of our match window or how far can we go before it becomes beyond the limitations of our technology, and essentially we found that we had very reliable results up to 5.2% which essentially means that the band has to be within 5.2% of the other band, plus or minus 2.6, so 2.6 down and 2.6 up makes a window of 5.2%.

Q. What if any opinion, Doctor, do you hold about the RFLP system at the R.C.M.P., its ability to produce accurate, reliable and reproducible results?

A. I think there's no question about it.

Q. What if any role did you play or have you played or do you now play with respect to the compiling

of the R.C.M.P. databases for DNA typing?

A. It is certainly one of the programs that I'm in charge of and essentially all the requirements necessary to make a database goes through my office, and essentially my people in my program are the ultimate individuals that compile the databases. Once the databases are compiled I review everything to make sure that it's been done properly and then we generally would bring in an outside expert such as Dr. Carmody or Dr. Kidd to look at various aspects of our databases.

Q. Has your Caucasian database been looked at by others in addition to those people?

A. Oh, absolutely. I've taken my database down to the FBI as part of the technical working group of DNA analysis methods, that's called TWGDAM. It's hosted by the FBI. All the members that are currently - members of forensic labs that are currently working with DNA meet approximately every three to four months and it's a working relationship where we show our results, we produce documentation, and we share our databases, and our database has now been given to that group such that I believe the TWGDAM database is well over 7,000 Caucasians, for instance, so it's been extensively looked at by not only the members within the TWGDAM group but also there's a lot of scientists out there from a purely academic point of view who are quite intrigued by the data that we're collecting in terms of migration of individuals, certainly evolution, and we've given our database or we're making arrangements now, certainly, with many prominent molecular

geneticists, population geneticists. Dr. Bruce Weir, for instance, has our database, he's looking at that in the same way he's looked at the FBI.

Q. Who's Dr. Weir?

A. Dr. Bruce Weir, he's one of the foremost population geneticists in North America.

Q. The Caucasian database, we've had evidence with respect to the Caucasian database, were you involved in the compilation of that database?

A. Yes, I was.

Q. Could you tell us, please, briefly, how that data was actually gathered?

A. O.K., our Caucasian database has come from three different areas in Canada. I could refer to my notes, I know the entire database is 974 individuals in what we call our combined database. I believe there is 526 members from Kingston, there were three hundred and - perhaps I should refer to my notes. We have 356 Caucasian samples, individuals from Vancouver, 526 from Canadian Forces Base Kingston, 92 individuals from Ottawa, making a total of 974 individuals. Now, this represents one of our databases, this is our Caucasian database, and we have numerous others that we're also compiling as well.

Q. Why was the Caucasian database important for the R.C.M.P. in a country like Canada?

A. Primarily because we're almost 94% Caucasian. In Canada we certainly don't have the ethnic diversity, say, of the southern United States where there are certainly more blacks and Hispanic groups, so the Caucasian database would be our most relevant database.

Q. And why CFB Kingston, why did you choose CFB Kingston?

A. CFB Kingston was an interesting example of luck, really, because what we were looking for is a large number of samples that we could document as Caucasian, but at the same time our samples have to remain anonymous. Because they're collected through the Red Cross their charter forbids us from knowing the identity of the individuals, and what was important about Canadian Forces Base Kingston, there was I believe two or three blood donor clinics run on the armed forces base and the members that would be able to give blood at those clinics would be presumably the military personnel or their direct dependents. Consequently, they represent pretty well in a micro sort of way all of Canada, because Canadian Forces Base Kingston has a training electronics school, one of the largest in Canada, so people from all across Canada come there to train. They have a land staff college, the Royal Military College, there's a number of specialized groups such that the individuals that would be at Canadian Forces Base Kingston would pretty well represent all provinces of Canada, and in one or two blood donor clinics from that area we would essentially have a very nice Caucasian database that would represent Canada.

Q. Going through the Red Cross, how does that compare with data method collections other places?

A. Well, in Vancouver for instance we didn't go through the Red Cross for our Caucasian databases.

The way our samples were obtained in Vancouver was through Dr. Lorne Kirby in the Department of Pathology who through his appointment at the hospital had access to particular samples and which he made available to us, such that in Vancouver, for instance, the samples were screened for familial relationships, brothers, daughter, for instance. Also it was screened for duplicates and I believe at that time they were able to identify and by my name accept whether the individual or not was Caucasian. Contrary -

THE COURT: Did you use corpses in the -

A. No, no, that was a maternity clinic and patients coming into the hospital that would come in for normal testing, etc. No, we would not use corpses.

THE COURT: Well, I thought perhaps in the Department of Pathology you might have some available.

A. Well, actually, that would probably be one of our validation studies. We would probably want to know how long after a person is deceased the quantity and quality of DNA that we could obtain from various tissues, and that's certainly a study that's been done recently in the Centre of Forensic Science by Pam Newell's group. It's a very nice study.

Q. How does the size of the Caucasian database of the R.C.M.P. compare with other forensic laboratories worldwide?

A. Well, when I started this I used to brag that it was one of the largest databases. I think now that with more and more of this technology being used by larger and larger organizations that we're

certainly one of the largest but we're probably not the largest database. Our Caucasian database, just under a thousand individuals, is quite large by forensic lab standards, but for instance, some of the paternity labs that use this on a routine basis, in North Carolina, for instance, I believe it's genetic design, they do 500 tests a week. Their database is quite enormous now.

Q. Doctor, what have you or your lab done or participated in to hold out the R.C.M.P. RFLP typing system and/or the database to general scientific scrutiny?

A. Well, we like to certainly make all our data available to scientists because it's a two-way street. If we can help others through a collaboration they can certainly help us, and that's the fastest way to make significant advances in science and also by us releasing our data, our databases, our technology, to other groups it allows groups that are not forensically orientated to test, utilize our data, and to basically render their own impressions through a peer review process whether or not they accept our technology and our databases.

Q. And what ways do you do that? What are the different ways that you actually expose the R.C.M.P. system to scientific scrutiny?

A. Well, for instance through my adjunct professorship at the university I certainly teach students. Some of these students want to do mini-projects and I may collaborate through that means. We've had co-op students come from different universities through our lab, we have visiting

scientists programs where people would come in for a couple of weeks to train with us and pick up the technology. These are forensic scientists. We often go to other laboratories to take the technology that we have and transfer it and have their technology transferred back to us. The Quantico, for instance, at the FBI, I routinely go down there for working laboratory studies that were ongoing. The other aspect is through our collaboration with both academic, government, and business orientations we certainly release our information and our data. The Canadian Red Cross, for instance, approached us a year or so ago, they wanted to have more accurate means of determining the success or failure of bone marrow transplant. These are patients who may have leukemia, have leukemia or various forms of cancer, and they've had their bone marrow irradiated and replaced with another bone marrow. One of the questions the Red Cross wants to know is in the case of relapse is it because the old bone marrow has come back with the cancer or has the new bone marrow replaced - has had a mutation that has caused a new type of cancer. Well, the technology that they had in place couldn't answer those questions so they came to us and we've transferred our technology to them, so essentially they do a DNA typing on the recipient, on the donor, before and after for the recipient to determine whether or not what percentage of the DNA has come from what bone marrow transplant as tissue so that they could render their impression on the success and failure based on the acceptance of the bone marrow

from the new donor.

Q. You mentioned the Red Cross and you've mentioned the government. What if any government departments have actually looked at your lab?

A. Health and Welfare Canada, Dr. Rene Aubin, who's in charge of a new biotechnology program there. These are scientists who have been assigned by Health and Welfare to review and look at the various biotech spin-offs from molecular biology, recombinant DNA drugs, these are drugs made through DNA in various organisms. Some of the technology that he's requested to look at, cell lines and various experiments, this is technology that we're transferring to their program. They've adapted our hybridization procedures, for instance, to look at another nucleic acid within the body called RNA, and they're using it to study gene expression, so much of the technology that we use in our program has direct spin-offs with many programs and essentially it's used universally in clinical diagnostic labs throughout.

Q. Doctor, you've indicated that particularly in the forensic area you have travelled throughout North America and I believe outside North America as well, is that correct?

A. Yes.

Q. Could you tell us, please, what if any criticism is levelled at the R.C.M.P. forensic system in the forensic field by others in the world or in North America?

A. We've been criticized certainly by the British system as being much too conservative. In actual fact, we throw out our data, so that our numbers

could be a lot more incriminating, but we prefer to remain conservative.

Q. You mentioned the British, we've had testimony earlier this week and last week with respect to multi-locus probing versus single locus probing.

A. Yes.

Q. As a result of your travels and your research interests are you aware of what if anything the British are actually doing in relation to their multi-locus probing technique that they began with?

A. Oh, yes. What one has to recognize is the multi-locus approach is the first generation of DNA technology. When it was originally developed in Alec Jeffreys' laboratory around 1985 that was the current mode that people were using where it detects many, many bands. Well, it quickly became apparent that that technology would not be directly applicable to forensics for several reasons. One, it's not sensitive, you needed too much DNA; two, with all these bands it's very difficult - we're talking thirty, fifty bands sometimes. How would you determine a mixed sample where you had blood from one individual and blood from another individual, it would be a nightmare to try to sort that out, and the other aspect that was a concern at that time was the genetic relationships, Mendelian pattern of inheritance was really not well-established, so over a period of time certainly the major labs have switched to single locus probes and you'll find, for instance, in the British system now, the British Home Office and the Met Lab, that's

what you would call Scotland Yard, they use single locus probes. They do very, very little work with multi-locus probes in forensics.

Q. Single locus probing being the technique that's used here?

A. The technology that we're using, exactly. They use a slightly different enzyme than us, they use another molecular scissors which is called HinfI but it essentially does the same thing as our Hae III.

Q. Doctor, you were the case reviewer, if that's the proper term, in the R.C.M.P. Forensic Lab with respect to the case of The Queen versus Allan Joseph Legere, is that correct?

A. Yes.

Q. Would you explain what you would do as a case reviewer?

A. As a case reviewer I am the second analyst with the R.C.M.P. to completely review the case, to look at all the data that's been processed and collected in this case by Dr. Bowen and to render my opinion based on what I've seen in the report and the autorads and all the information that has been developed in the DNA typing procedure, to render an opinion as to what my conclusions would be respective to those samples.

Q. And did you do so in this case?

A. Yes, I did.

Q. And what if any opinion did you arrive at as with respect to the opinion that Dr. Bowen had arrived at?

A. It was the exact same opinion. I think Dr. Bowen did very careful examination and rendered a very

valid and reliable result.

Q. Did you also check the method of frequency calculation and the figures that he generated, the best estimates that he provided?

A. Yes, I did.

Q. And how did they -

A. I would concur with Dr. Bowen completely.

Q. And, Doctor, we've had evidence that the summary chart introduced through Dr. Bowen as P-162, this chart here - are you referring to those particular results?

A. Yes, I am.

Q. Doctor, in your experience, apart from identical twins and without even putting a probability figure of best estimate or any kind of a mathematical figure to the four or five-probe match as shown in that summary chart, in your experience have you ever seen a four or five-probe match between different individuals using these highly polymorphic type probes?

A. No, I haven't.

MR. WALSH: My Lord, that concludes my questions. Thank you.

THE COURT: That's your direct examination. Mr. Furlotte, I gather you're going to be perhaps a little while with this witness? It's twenty after four.

MR. FURLOTTE: More than nine minutes, My Lord.

THE COURT: More than nine minutes. Well, I think we'll recess here, then, and you'd prefer to wait till morning to start?

MR. FURLOTTE: Yes.

THE COURT: So we'll adjourn till 9:30 tomorrow morning

and my usual caution I will express generally without going into the detail, please, so we'll see you at 9:30.

(JURY WITHDRAWS.)

And you, of course, Doctor, aren't to discuss the case with anyone until all of your testimony is completed. I'm sure you understand?

DR. FOURNEY: Yes, I do.

(COURT ADJOURNS TO 9:30 a.m., OCTOBER 23, 1991.)