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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VERNA PETERSON
COURT REPORTER

(COURT RESUMES AT 9:30 a.m., OCTOBER 23, 1991.)

(ACCUSED IN HOLDING CELL.)

THE COURT: Just for a minute before we bring the jury in I wanted to - when the jury do retire here they will be taking with them the indictment with the list of witnesses attached, and it seems to me the list of witnesses attached to the indictment at that time should be an amended list to reflect the changes that have been made in the Crown witnesses, some haven't been called, others have been substituted, and so on, and I don't suppose the Crown has their list of witnesses here at the present time?

MR. ALLMAN: Mine is on my desk and I could get it in one moment, but I mean we'll get our secretary to type up a proper revised list.

THE COURT: Actually, I have a list. What I was going to suggest is why don't I give to - the Clerk will get a clean copy and I will indicate to him the changes that I think have been made and he could show that to counsel on both sides and see if they approve of that or if it's clear. That's the simplest way of doing it.

MR. ALLMAN: That would be a very helpful suggestion.

THE COURT: There were quite a number whose - a line would simply be drawn through their name. There were others whose names or ranks were changed, there were a couple added and - well, there are about 15 or so changes, but the Clerk will be getting in touch with counsel and showing the amended list and you people check it over, if you would. The other thing was the Crown were going to come up with a list showing the pins, but you're doing that, I gather?

MR. ALLMAN: I believe Mr. Sleeth prepared that.

THE COURT: Yes, well, I meant don't leave it till the last minute. Perhaps if you could give it to the Clerk when you have it completed and I could look it over in the meantime to see if it's -

MR. ALLMAN: Was the idea that the jury would take that with them or -

THE COURT: I had in mind that the jury would take that with them.

MR. ALLMAN: That's fine by us. What I was going to do is just make reference to it in the course of my closing but certainly if that's acceptable we'll provide the list.

THE COURT: It doesn't preclude you from making reference to it but they would be taking it, but when you get that list prepared give a copy to Mr. Furlotte so he can see that he approves of the way the pins are described and so on, not only for inaccuracies but to ensure they don't convey evidence with them.

MR. ALLMAN: We won't put in anything like, "This is where Mr. Legere did such-and-such".

THE COURT: And give a copy to me through the Clerk so that I can look at it, too. Now we'll have the jury back.

(JURY CALLED - ALL PRESENT.)

(ACCUSED IN CELL.)

THE COURT: Now, you had a witness on the stand?

MR. WALSH: Yes, My Lord, I'd recall Dr. Ronald Fourney for cross-examination purposes.

DR. RONALD FOURNEY RESUMES STAND:

CROSS-EXAMINATION BY MR. FURLOTTE:

Q. Dr. Fourney, maybe you could tell us how you got involved with the R.C.M.P. Forensic Laboratory.

A. How I got involved?

Q. Yes.

A. Initially I was doing some studies with my first postdoc. which is immediately after receiving your Ph.D. You undergo a series of years of apprenticeship in some other laboratory, and shortly after I received my Ph.D. I was working on evolutionary and molecular questions in various other species. It became apparent that some of the genes that I was interested in I had accidentally cloned other genes at the same time. These genes were very polymorphic and it was apparent at that time what we had cloned and didn't know it were VNTR's, so that we were able to essentially distinguish differences between different groups of species within a population. In this particular case I was working on fish so we'd start to look at different groups of fish and where they were breeding, etc.

I went on to work on other projects after that but I kept thinking about it and contacted the R.C.M.P. at that time and suggested this would be a very interesting problem or possibly a project that could be worked on in conjunction with identification, and about four months later -

Q. What year was this?

A. Oh, that would have been in - it was just before Alec Jeffreys published his 1985 paper, because we didn't know what we had had, so it would have

been, I believe, in '85, I had just finished my Ph.D. in '84, and I contacted the R.C.M.P. and discussed this with them. They were intrigued and interested but we didn't pursue it. I went on to do my familiar cancer studies at the Cross shortly after that and I was interested in looking at the RFLP polymorphisms within specific cancer-causing genes, so I looked at many, many families using the same DNA technology that we currently use now.

Some of the material that we received at the Cross had been material from tumour repositories that had been in existence for about 17 years, and they were technically very challenging to work with because you had to obtain DNA from a very small amount of tissue that had been stored for long periods of time, and that's one of the things that I enjoy, and certainly the challenge of making a project and a technique work properly, and much of the application of the technology that we used at the Cross was directly applicable to forensics, so at that time I had contacted the R.C.M.P. again and actually they pulled my file, reviewed what I had said in the past, and offered me a position, and that would have been in '88, I believe, and that's basically how I got in forensic science.

Q. O.K., so the formation, I suppose, of the R.C.M.P. forensic DNA lab was - come about because you initiated the contact and convinced them that they should set one up?

A. Not exactly so. First of all, when Alec Jeffreys published his first paper there was a tremendous impact. There was an impact from all areas of

science including forensics but forensic scientists recognized the discreteness of this technology and the importance of it and immediately the R.C.M.P., after seeing this paper and others, put one of their operational support scientists, Gary Shutler, onto a project to search out the relationships of DNA and how it could be applied to forensics, so Gary Shutler at the R.C.M.P. actually started working on this. Shortly after that, I can't remember the exact years because I wasn't in the program at the time, but Dr. Bowen who had just finished his hair and fibre training in Edmonton suggested from his background, which was also in biochemistry and had involvement with DNA during his Ph.D., suggested that this technology could be applied to forensic DNA analysis in hair, for instance, so he worked on a cursory project in Edmonton, so there was a lot going on prior to the hiring of Dr. Waye and myself. What we were able to bring into the program, I think, was to jumpstart the entire program because the forensic community certainly knew what they had, they weren't exactly sure how to apply it, and much to the credit of the R.C.M.P. they decided that it was important enough to hire two outside experts and develop the technology accordingly, and since they have certainly supported the program wholeheartedly. I am essentially a research scientist working in the field that I want with tremendous support. They recognize the importance of carrying out this research for the support of their program. The other aspect is that Gary Shutler was sent back to

get his Ph.D. in molecular genetics at the university, so not only did they recognize the importance of bringing scientists from abroad into the program but they recognized that their own scientists had to be retrained in this technology.

Q. O.K., but basically you're one of the key persons behind the formation of the DNA lab in Ottawa?

A. I'm one of several individuals.

Q. So it's something you're quite proud of? It's your baby?

A. Well, I'm a scientist. I think if I didn't enjoy doing the work that I do that I wouldn't be doing it.

Q. And your project has been coming under attack by many scientists?

A. If I was back in cancer genetics my project would be coming under attack by cancer genetics scientists. Science is a fluctuating - I don't know the exact words here but there's nothing stable in science, it's continually moving. We're always changing the technology, we're looking for new questions or new answers to the questions that arise. It's certainly not a static environment.

Q. Would it be safe to say, Doctor, that although as a scientist you like to keep an open mind there is an inherent bias on your part in your opinion as to how well your laboratory is doing?

A. My bias is to do the best job I can possibly do and to maintain my credibility as a scientist. I would do that regardless of what project I was working on.

Q. Now, when did you begin - what did you have to do in order to build your lab for DNA testing?

A. You want the steps involved with building a molecular genetics laboratory?

Q. Well, not the steps involved but exactly when did you start bringing in the equipment to do your testing?

A. Well, some of the technology - or some of the equipment was in place in '88, the summer of '88. That would have been shortly after John Waye had joined. What they were not sure of is how to - what technology to use because there were several modifications, and the best equipment to utilize. One of my fortunate experiences had been when I moved to Edmonton I was charged also in that lab to set up the technology and the equipment that would be made available to the researchers in my group in Edmonton to do the DNA typing, so essentially I'd already reviewed a lot of the DNA equipment that was available, the techniques. I had modified procedures in Edmonton and these were brought with me when I came to the Cross, and also Dr. Waye had considerable experience, and I think it was the merging of what already was present at the R.C.M.P. Lab with the experience Dr. Waye and myself had brought that we began to build the program.

The other thing is that we're not building this in a vacuum. We had an excellent collaboration with other research labs both in the academic and the government community as well as other forensic labs. The FBI certainly deserves a great deal of credit for the amount of effort that they used to implement their program, and we certainly had an excellent collaboration with

them.

Q. O.K., but when you were setting up the facilities for DNA testing you had to use what, facilities that were used for other types of forensic testing?

A. Sure.

Q. So in your initial stages of setting up it was kind of a crowded situation?

A. It's difficult to be crowded when there's only two or three people in the program.

Q. But it was a little hectic?

A. I think any progressive research laboratory that is worth its salt is going to be hectic in the sense that it's always trying to look for new technology and to be doing experiments. If you're implying that we weren't prepared to do DNA, that's totally incorrect, and I might point out that our first case in Canada went to court in April of '89, and before it went to court Dr. Waye and myself were both satisfied, completely satisfied with what we were doing and with the equipment that we had had, but that certainly doesn't mean that we wouldn't modify the procedures to make things even more reliable in terms of efficiency and sensitivity.

Q. But your lab was constantly in a flux situation when you were originally -

A. I'm not sure what -

Q. Before you moved into the new facilities?

A. I don't know how - what you define flux. As a scientist I don't think I've ever stayed in one spot for very long. I mean I've been anxious to do my science, to continually interact with

people. My lab in Edmonton that I was involved in was - if you call crowded, we had 17 people in our group.

Q. O.K., Doctor, maybe the best thing to do is just tell you the statement you made and maybe you can tell us what you meant by that, if that's all right with Mr. Walsh.

MR. WALSH: First time he's asked me -

THE COURT: Is he saying something now that's different or -

MR. FURLOTTE: No, no, I just wanted a broader explanation or a qualification of his statement.

MR. WALSH: Well, I think he has to use it in terms of he's trying to contradict the witness on something he's said, then he can show it to him for the purpose of asking in what context it was made, etc.

MR. FURLOTTE: Well, My Lord, no, it's just that the witness said he didn't know what I would mean by the flux situation so I just -

THE COURT: Yes, well, put that book away, Mr. Furlotte, and ask him the question if you want to now. Get him to give the breakdown here. If he says something that disagrees with what he's said before, then revert to your Section 10 of the Evidence Act procedure, but until that becomes necessary let's keep what was said before out of it.

MR. FURLOTTE: Dr. Fourney, would you say that the lab was constantly in a flux situation where you were working with old facilities and getting all kinds of new equipment?

A. Yes, we were certainly working in a facility that

had not been renovated and we had modified our technology and were constantly getting new equipment in. I get new equipment in now. I have a brand-new piece of equipment that's due to arrive in November. It certainly doesn't indicate that we had problems previous to that.

Q. Would things be a little hectic at that time working with Dr. Bowen or Dr. Waye and trying to perfect their system or improve the quality?

A. Hectic? I would not use the word hectic, I would say exciting.

Q. You would say what?

A. Exciting.

Q. Exciting?

A. We were certainly challenged and I think that we were all very keen to do our best and we gave our 100% effort. We still do.

Q. Work long hours?

A. Yes.

Q. What kind of hours would you work?

A. You'd have to ask my wife that.

Q. Work more than five days a week?

A. Yes.

Q. More than ten hours a day?

A. Once again it depends. When I go home I don't pick up a novel, I usually pick up some transcripts or pick up a paper.

Q. I'm not just speaking for yourself either, Doctor, I'm talking about the lab technicians in general, yourself, Dr. Waye, Dr. Bowen.

A. I would say that scientists in general work long hours. They're dedicated and I think - we're certainly not paid by the hour.

Q. In general scientists, if you want to call them, call the lab?

A. Once again, scientists are constantly thinking of - they're dedicated, they're constantly thinking about what they're doing. When I'm at home eating supper I'm thinking about new experiments and things like this.

Q. Now, as I understand, you are also in charge of quality control and quality assurance?

A. That's one of the aspects that I'm involved in, yes, and I was instrumental in helping to set up the program and I am the R.C.M.P. member that certainly sits on many of the different boards or committees that have been set up in the forensic community, for instance, to get feedback from what is going on in quality assurance and bring it back to the R.C.M.P. Lab. At the present time we have an internal DNA committee right within the R.C.M.P., and for instance, the quality assurance guidelines that have been drafted for the R.C.M.P. have been drafted by the chief scientist in Serology, Pat Allain, primarily because she - quality assurance and quality control is something that isn't new to DNA, it had previously existed with all forensic disciplines, and she certainly was very qualified to draft the recommendations that we brought from our DNA committees back to the R.C.M.P., and within the current set of guidelines that the R.C.M.P. works under we were able to draft up a very respectable, I think, quality assurance program.

Q. O.K., in your quality assurance guidelines is there any limitation to the amount of hours a

scientist should be working?

A. I don't recall that, no.

Q. An overworked person might be prone to make more mistakes than one who works a regular work week?

A. I think an inexperienced person is prone to make mistakes.

Q. And a tired person, maybe?

A. That's more of a personal opinion, I think. If I was a lawyer practicing law and I was tired I probably would make mistakes or maybe not certainly be as good as if I was doing it for six hours.

Q. There's a good chance we do, eh, anybody, just any normal person, no matter what profession you're in?

A. If you're asking me if a tired, overworked person could make mistakes I would have to say yes.

Q. More prone to make mistakes? Anybody can make mistakes, I think that's a - that's human nature?

A. That's part of being a homo sapien is that you're going to make mistakes.

Q. As head of quality assurance and control do you think it reasonable to put limitations on your lab technicians to ensure that they don't make mistakes?

A. I think the program that we have in place is such that, number one, we would detect a mistake that could occur. We have too many controls. That's part of the reason why the technology takes a little bit longer is that we have all kinds of inborn controls within the program, so if we had made a mistake we would certainly detect it. In terms of your question, should we put limitations

on our technologists and specialists, I think the people in our group are very dedicated, I think they're highly trained, they're skilled, they're experienced, and with the controls that we have in place and the fact that a second analyst reviews the case, if there is going to be a mistake we'll most likely pick it up. A clinical diagnostic lab -

Q. There'd be a lot of mistakes that could be made that it's impossible to pick up?

A. Pardon me?

Q. There could be a lot of mistakes made that it's impossible to pick up?

A. That's a theoretical question and I would think that even in a clinical diagnostic lab you could potentially make a mistake that you may not pick up. Human beings are prone to make mistakes. We've done everything I think is possible in our current program to counteract for that problem, and certainly if we make a mistake we can go back and figure out what went wrong with our controls.

Q. What's the purpose for open and blind proficiency testing?

A. An open and a blind proficiency test are essentially two tests that are given to a clinical lab or forensic lab to test the ability at that time how their techniques, their protocols, their quality assurance program is working, and if they can definitively make the right calls based on what they're trying to measure. In this case we want to know if our test is valid; i.e., we're going to be making a match or a non-match, and if it's reproducible and

reliable, and the open proficiency test is a test where essentially a clinical lab or a forensic lab is told, you are going to get a test, we know what the answer is ahead of time, but here's the test, I want you to do it in the current manner that you're practicing just like it was a case to go through all the procedures, come up with your conclusions, and then we hand that back and say, did we make any mistakes, how good were we, what's our measurement precision, did we make the right matches, did we make any non-matches. That's an open proficiency test.

A blind proficiency test, they're a little bit more difficult to set up but essentially it's we don't know it's coming, and a test will come in through a door to Operations, or in a clinical lab that's making a diagnostic for cystic fibrosis, they think it's a real case and they've handled it as if it's a real case because they don't know any different and when they've done the case it's reviewed. That's essentially a blind proficiency test.

Q. And that's tested because you know the results that are supposed to -

A. Well, any test, whether it be blind or open, would be difficult to interpret if you didn't know what the results would be.

Q. Now, in case work that you're bringing before the courts nobody knows what the test results are supposed to be?

A. We certainly know how the controls are going to work.

Q. Well, you know how to control your gels and to

run your monomorphic controls and your markers?

A. That's correct.

Q. Right, but as far as for the same proficiency - same mistakes that were made, say, in open and blind proficiency tests where you don't get the results you're supposed to, maybe by getting just samples mixed up in the lab or by getting DNA from a known source, mixed in with an unknown source, how can you control against that unless you have open and blind proficiency tests?

A. The open and blind proficiency test does not control for mistakes, it merely is another way of detecting mistakes, so you can't really get confused with controlling for something and testing for whether or not it occurred. The control for not making mistakes is in the procedure, the quality control, the quality assurance, that we practice, and the blind proficiency test or an open proficiency test, what that essentially does is test the analyst at that time who's doing that particular study, how good that person is working with respect to the technology that exists, and in a way it tests the entire laboratory procedure because it's a team effort. It's certainly not a one-man show.

Q. So the open and blind proficiency test, it's not a control to get better results, it tells you whether or not your technicians are making mistakes?

A. Proficiency testing is more an aspect of quality assurance. It's the documentation and the requirement behind whether or not everything is being practiced in the lab properly. Now, in our

particular case and the Technical Working Group for DNA Analysis in North America, that is the FBI and multiple forensic labs that are practicing DNA, our standard at this point of time is essentially two open proficiency tests per analyst per year and one blind proficiency test to each lab.

Q. Have those been started yet at the R.C.M.P. Lab?

A. Well, certainly before any analyst or specialist goes to court he has had his open proficiency tests. Whether or not we've had a blind proficiency test, I'm not sure, because I wouldn't know. In other words, I would advise them how to set up a blind proficiency test but if it's truly blind it has to come through the door with as few people knowing as possible, and it would be sent in from an outside agency. Now, at the time where Dr. Bowen was the initial person practicing DNA in our forensic group he was also in charge of operations, and it would be difficult for him to accept the case, review the case, and actually do it without knowing that it's a blind proficiency test, so it would have been difficult to administer a blind proficiency test to Dr. Bowen, but for instance, there is certainly a blind proficiency test in the works right now for the analysts that are going to court and are going to be tested by him in the future.

Q. If a blind proficiency test is conducted on any lab, the lab is usually informed after whether or not one was run?

A. That's right.

Q. And you people have never been informed that a

blind proficiency test had been done?

A. At this point I have not been notified that we have had a blind proficiency test, no, but we certainly have had open proficiency tests, and the other thing that we've practiced at this time, since January we have had four outside proficiency tests. These are independent tests set up by independent agencies that we don't know the answers. They come in and we, as well as many other laboratories, participate in. We've had a test administered by Collaborative Testing Associates which is a forensic community that has set up a testing program for all kinds of forensic disciplines including DNA. We have participated in a Cellmark proficiency test. We have participated in the National Bureau of Standards proficiency test. This is the test that the U.S. government is going to use as their quality control or their gold standard on which to assess all forensic DNA labs. We were not only involved with the testing of that, we were instrumental in helping to set up the program, and we have had three separate FBI proficiency tests that were sent out to all of the technical working group that were participating in what we call TWGDAM, so I think we've - one of the problems that people complain to me is that we're being proficiency tested to death, and I don't think that's a problem, I just think that's a safeguard.

Q. When did your proficiency tests that you just mentioned begin?

A. Well, for instance, before Dr. Bowen, certainly, participated in any case work he had his

proficiency tests. He's had -

Q. Who did the proficiency tests?

A. I would set that up.

Q. You set that up.

A. The first one I certainly set up, and he's had two since then.

Q. And that's like in your training process for doing forensic case work?

A. No, it's part of your ongoing quality assurance program. Even if you're fully trained unlike, say, practicing law, where once you've got your license you can practice forever, we like to bring our people back and say, "Let's see how good a job you're doing", every once in a while, so essentially they will get tested twice a year.

Q. So they know they're being tested?

A. In that particular case that's an open proficiency test, yes.

Q. So when you know you're being tested you're on your best behaviour?

A. If you're not knowing you're tested you're still going to be on your best behaviour because you're not going to make it in the program unless you're doing a good job.

Q. Now, you mentioned also that you were responsible for setting up the R.C.M.P. database?

A. I was one of the key people involved, yes.

Q. And you do some of the testing yourself, run some of the gels yourself?

A. At the beginning I ran a lot of the gels myself. When the initial database was set up Dr. Waye and myself had divided up the activities. He was doing a lot of the initial population database

work. For instance, he and the technologists in our lab at the very beginning had collected samples, they were actually there before - some of those samples had been there before I arrived at the R.C.M.P., and he had started running the gels shortly after, I guess, I got there in November. In the meantime I was looking at other aspects to set up the program. In particular we wanted to know what probes to use and we wanted to conduct reliability tests, etc., and that's what I concentrated my effort on and I think we looked at a great number of probes to select the very few that we used.

Q. O.K., but the ones you selected for your database are basically the ones we've used in this case here, those six probes?

A. Yes, the probes that we currently use in our data-base, most labs in North America actually use them, and many of those probes we had investigated even before they were commercially available or other laboratories had used.

Q. O.K., and I believe you mentioned on direct examination that as a member of TWGDAM there's a lot of forensic labs are members of TWGDAM?

A. I'm just trying to recall how many there would be. I know when I visit the FBI for our meetings there's probably about 40 people there, some of them are a couple of members from one or two labs, but I believe there's at least 20 laboratories participating at the current time.

Q. And out of the members of TWGDAM there's very few that are not directly involved with forensic laboratories? Most of them are employees of

police agencies?

A. Yes, that's true.

Q. And as a group you discuss your achievements so you can pass them on to each other?

A. We discuss our achievements, we discuss our problems, we discuss the technology, the advancements. The quality control program that's been set up that many labs are using, the initial draft document was drafted, certainly, at TWGDAM. It was TWGDAM that brought in population geneticists. These are people that are not forensic scientists who are interested in the data and the technology. We brought those together collectively to answer very important questions about sub-population and Hardy-Weinberg, and I think what TWGDAM essentially is the nucleus for the development and of the technology in North America, and the Europeans have a similar program as well, it's called EDNAP, which I think is European DNA Analysis group, or I'm not sure what the exact letters stand for, but it's a similar program to ourselves where a community of forensic scientists have got together to set up or draft up guidelines and standardization, because one of the things that we hope to get out of this is to bring the technology to the point where many labs are practicing the same safeguards, quality assurance, quality control, and in the same way that criminals can go across borders we want the technology to be easily transferrable from border to border so that if I screen a match, for instance, down at the R.C.M.P. Lab and the particular individual that we're interested in

happens to be an American citizen who might have committed a similar offence in another state, it would be important for that state to understand the technology, to use similar sets of principles and guidance and protocols so that they can interpret our results with respect to their results, because ideally we want this to be a North American approach for the analysis of DNA typing, the individualization.

Q. Doctor, the essence of scientific testing for their validity, those tests must be reproducible; would you agree with that?

A. Yes.

Q. Absolutely?

A. That's part of science is that people constantly look at someone else's results and say can we reproduce that, and once it's accepted within the community that it's valid, reliable, then generally scientists accept it and they don't rediscover the wheel. We would go on to build upon previous discoveries. We don't go back to rediscover something.

Q. O.K., when the R.C.M.P. built their database in order to obtain calculations of frequencies, out of the DNA specimens that they used how many times did they test them? Let me put it this way, your R.C.M.P. database is compiled of about 700 people, DNA specimens from about 700 people?

A. We obtained about 900 or so -

Q. You're up to 900 samples?

A. Nine hundred or so samples, and what normally happens there is that these are blood samples that are collected anonymously, and as I indicated

yesterday we got some from the Kingston group, there's some locally in Ottawa, and in actual fact from Vancouver it was from the Department of Pathology. It was from a clinical lab that they had there from patients who - most of them were healthy, had come in for routine medical service, so we would take those samples, they would be blood, and basically in the Vancouver group, for instance, we were very fortunate because we had worked with that individual, Dr. Lorne Kirby. He had sent his technologists up into our lab, we trained her and she actually -

Q. I believe you gave all that in direct examination but maybe if we could shorten up the day here somewhat and try to stick with answering questions. How many times would you -

MR. WALSH: That's a statement, my Lord, that indicates the doctor was not answering his question and I don't think that's correct.

MR. FURLOTTE: No, he's not answering my question and I just want to shorten it up. I think we're getting sidetracked.

A. Perhaps you could tell me what your question is.

Q. The question was how many times did you test the samples that are in your R.C.M.P. database.

A. Essentially those samples were run once.

Q. Once, so you don't know whether they're reproducible or not?

A. That's the database?

Q. That's the database, yes.

A. There are some of those samples that have been run subsequently. At the beginning when we were looking at our technology we would pick out 50

or so samples and run them multiple times, but once we were satisfied with the procedures, that it's working properly, we ran our database once.

Q. You ran your database once, O.K. I believe Dr. Bowen testified that if he run his DNA samples today and then he would run his DNA sample again next week that he could possibly fit in different bins on both occasions?

A. If a sample was very close to a bin boundary, that is an area where it crosses over into another frequency, yes, you could possibly get a different bin frequency, but you have to recall that's built into the conservative nature of our system.

Q. But we're talking here about measurement imprecision, the reason why he would fit into a different bin at different times?

A. Yes.

Q. And he said that his DNA, the measurement of the bands could be out by 2%?

A. It's possible.

Q. It's possible, and that could put him in different bins?

A. If he was right on the edge of the boundary, yes, he could.

Q. And if the DNA samples were out by 5% - your matching window is 5.2%, I believe?

A. You have to recall that part of the safeguard in a system, our window is certainly 5.2%, but the bins are much larger than 5.2% so the measurement precision is smaller than the actual bin, and that's part of the safeguard of the system because we wish to be as conservative as possible. We have very large bins. Our frequencies essentially

are such that they're very conservative.

Q. So to make it easier to identify the same individual the second time the larger the bins the better?

A. You're confusing something directly here is that to identify an individual you must declare a match. Match is completely independent of the actual binning process. A match is made primarily visually under the experience of the analyst. Something could certainly be within the same bin. If you had - this is one fragment, this a second fragment, and you had two other fragments, they're well within 5.2% but it would take very few seconds to recognize that those aren't a match, so the first thing you have to recognize is to divide up our system into match and to bin frequency.

Q. But if you wanted to, I suppose, describe a person's DNA pattern, DNA profile, whichever you want to call it, a pattern or a profile for five probes, you would recognize it according to which bin his RFLP's would have fit into?

A. It's sort of like a catalogue, if you like. For instance, if we wanted to know if we had a match and a large number of suspects the first thing we would do, we'd certainly look at the bins because that's a way of narrowing down those that are way out. Once we got the bins that we were interested in and those matches were fitting in with those bins the analyst would certainly take out those autorads and visually look and declare each match, so you could eliminate many of those matches based on the fact of your experience, they're certainly not matches. The measurement precision is a

safeguard built in for establishing the frequency. The match is still up to the analyst and their experience and training.

Q. What I'm saying, Doctor, again, is if my DNA profile was in your R.C.M.P. database -

A. Yes.

Q. - and I gave you a sample of my blood today and you run it through a test and you come up again with my DNA profile through your tests of, say, today, and you tried to cross-compare that with your database, there's a good chance you might not even find me in there, is that right, that I would not fit into the same bins and therefore you could say, well, my profile is not in that database, you couldn't match me with anybody in the database?

A. No, what would happen there is that you would be picked out readily. Certainly if you had a five-probe match I would definitely say this is the person.

Q. O.K., but you don't know if I've got a five-probe match unless I'm put in the same bins both times.

A. Bins have nothing to do with it there, it's the match precision, and then you would go back and look at the autorads.

Q. When you give me a catalogue number is that catalogue number not determined on which bin you would have put my RFLP's in?

A. If by catalogue number you mean - if you gave me two bands, say you were 1,000 and 2,000 - or 1,000 and 5,000, O.K., we'll separate them greatly, and I put a window of 5.2% on those and I searched through we would pick up the match of that regardless of the bins. The bins are simply a way of

giving a frequency to the non-discrete alleles that we're looking at, and it's a conservative frequency. The match in this case, we're looking at the measurement precision within the ability that we're able to look at. The technology we use is we can't say down to the exact base pair the differences here, so immediately we would pick up your two bands, I would go back to the autorads and actually compare those for a physical match.

Q. O.K., there were different gels run in this case with Mr. Legere's DNA samples?

A. Yes, and -

Q. Between the first gel and the third gel there was one band that was out by 5.5%?

A. Yes, that's true.

Q. So if you got that - if you were getting those kind of tests - I'll back up a bit, if you were going to run your R.C.M.P. database for the second time and the second set of tests were no more reliable than the tests between the first and third gel that was done with Mr. Legere, would you not get again a complete different identification or database?

MR. WALSH: My Lord, I think Mr. Furlotte is - intentionally or unintentionally has not stated the facts completely. He has stated to a point but not completely. He says that on one occasion -

MR. FURLOTTE: My Lord, Mr. Walsh has the opportunity to redirect and if he wants to raise it, if I don't clear it up enough on here he can raise it in redirect.

MR. WALSH: If he wants to put it in the form of a hypothetical, My Lord, yes, but if he's referring it

to this case, then I think he has the obligation to put the whole findings of Dr. Bowen with respect to that particular bin to the doctor, not just part of it.

THE COURT: Could you put your question again, Mr. Furlotte?

MR. FURLOTTE: In this test case of Mr. Legere there was a first gel and a third gel, and out of Dr. Bowen's interpretation between the first gel and the third gel he found that one band was out by 5.5%, which was outside the match window. That would be right, outside the match window?

A. 5.5 is bigger than 5.2.

Q. Yes, so it was outside the match window, so if you use - if those sizings were put into the computer it would show that there was no match?

A. In that particular case, yes.

Q. O.K., if those type of tests and interpretations were done from autorads, done again with your R.C.M.P. database, say you run all the tests over again in the R.C.M.P. database and used other DNA samples, not just run the probes over on the same gel, run all new gels, and you got those kind of results again, what effect would that have on your database?

A. Probably very little.

Q. Very little. Thank you. It would have no effect in the interpretation or in calculation of frequencies?

A. Well, once again the interpretation is the match and the calculations of the frequency is merely a measurement of how rare this is in the population. A match is still a match. What the 5.2% does is

essentially put an outside limit on what the analyst will declare a match based on the laboratory experience and the protocols that are in existence. I might point out that there are other labs in North America that have a 5% window, so everything within 5%. Ours is a little bit bigger but that's their program, their protocols, and their measurement precision. There are other labs, for instance in Florida, that have a 5.6% window. I believe there's one lab on the west coast of the United States that's even larger than 5.6, but it's based on the research that they have conducted in their lab to establish what they feel is their confidence limits for making a reliable call. What's interesting about some of the conservative nature of our system is that many people reflect that we're essentially throwing out our data, that we're too conservative. The fact that one match, one band, probably one band out of two, is slightly outside the window detracts very little from the nature of several autorads with multiple samples on it with multiple probings.

Q. O.K., you mentioned as a member of TWGDAM and your association with other forensic laboratories you share your joys and sorrows, so to speak, and any particular problems. Are you aware that the FBI in their database, they run the people's DNA in their database on more than one occasion, on three occasions at least?

A. I'm aware that they have prepared three different databases and they're not necessarily the same DNA and the circumstances were certainly not the same, so essentially if you're asking me if they run the

identical experiment three times, that's incorrect.

Q. You're sure of that?

A. Absolutely.

Q. Did they run it over on their own - some of the individuals that are in the database, they are FBI agents. Do you know whether they run their own FBI agents over again?

A. Their initial database when the FBI started out only had 250 members or individuals in their database, it was relatively small compared to our database, for instance, but many of the population geneticists said it was certainly substantial for the technology and the precision that we're using. They had decided partway through their program to switch markers. Now, these are the actual fragments that are run alongside with known standards so it's a different way of measuring the DNA, and much to the credit of the FBI and as mentioned in the Jacobetz case in the transcripts, they did the right thing. They re-ran their samples with a new set of markers to establish another database on their existing protocols at that time. The second database in fact had - some of those samples were different in it, and what's interesting about this is that here's a situation where two experiments have been run. Essentially you've got two different markers, you have perhaps 80% same samples, 20% different samples, and I think they've done the right experiment by using - if they're going to use the new markers they have to know what's going on with their database, they have to measure the precision and measurement

error, etc., with those new marker systems. Yet what I find curious is that many defence experts state that they didn't get exactly the same answers with the old and the new database yet in reality they were using slightly different samples so you would expect to get slightly different answers.

Q. And they ended up with different binning frequencies?

A. Certainly.

Q. And I believe they run it a third time?

A. I'm not sure about the third time.

Q. Not sure about the third time.

A. I do know that the database that the FBI have now, if you're calling that the third database, is I believe well in excess of 1,500 indviduals. I know it's 1,200 from talking to Dr. Budowle, so it may be larger than that now. The FBI has a visiting research scientist program where people come in, and part of the cost of going to the FBI is to bring about 100 samples with you and you basically process those samples, and depending on the reliability and validity of those samples and the accuracy they're added into the database, so like any database, even our own, it's constantly growing, so the database we use today will be slightly different than the database we use tomorrow, and I would suggest if you're interested in the impact that has on frequencies, etc., then Dr. Carmody would probably be your best person to talk to.

Q. Now, I understand you've calculated your measurement of imprecision or your 5.2% window on the

measurement of your monomorphic probes?

A. It was originally calculated on the monomorphic probes. It was since then calculated on our case work experience and on our control cell line data.

Q. And I believe your monomorphic probe, you say it has 2,731 base pairs?

A. That's the sequence size of the probe, or the DNA fragment that the probe recognizes it's important to -

Q. And you mentioned something about a ladder effect in the monomorphic probe, or what was that again?

A. Oh, essentially if you have a restriction digest that is somewhat incomplete, if you don't get the perceived 2,731 base pairs that's a constant intense band and you get multiples that seem to be of the 2,731 base pair fragment all the way up. That's an indication that there's been incomplete digestion. In other words, instead of cutting the piece of string in six defined place you might have cut it in five defined places or three defined places, and if you add them all together you'd get the same size that you started off with. What we would like to make sure of and what we take extra caution is that the piece of string is cut consistently each time, so our molecular scissors, the enzyme, is cutting that piece of DNA into the respective fragment size that we're looking for or are interested in.

Q. So on the autorads for the monomorphic probe how many bands should you have in each lane?

A. The one that we're primarily interested in is a very intense 2,731 base pair band. You will get other fragments showing up and those are of

interest mostly to individuals who are looking at the relationship of satellite DNA to the human chromosomes. For instance, Dr. Waye in his doctoral thesis had worked extensively on satellite DNA. All we're interested in is that that one fragment that comes up that's easily identified, I believe there's about 800 copies of this in each cell that we have, gives us within our measurement precision the 2,731 base pair size.

Q. So how would you identify that from the other ones that might be in the way?

A. Because it's a very intense band.

Q. More intense than the others?

A. Absolutely. Most of the time you can see the satellite fragment band within hours of auto-radiography. We don't have to go overnight, for instance. I can put on the X-Ray film on our membrane and go out for lunch and come back and we probably have that 2,731 base pair band there. It's very intense.

Q. What if there's other ones in there that are just as intense?

A. I'm not familiar with that. It's a hypothetical situation.

Q. Maybe if I could find it here you can explain - no, it's O.K. Could you tell me what reverse band shifting is?

A. I have no idea.

Q. Do you know what band shifting is?

A. Certainly.

Q. What is band shifting?

A. Band shifting is a phenomenon that we see very

rarely but other labs seem to experience it a little bit more. Essentially you might have a fragment here and you have what you consider to be the same fragment is shifted either up or down slightly, and that's essentially a shift in the band, band shifting.

Q. Which you assume to be the same fragment?

A. Not necessarily. You'd have to go through a series of tests. If you see the same shift consistently in the same direction in a number of probes you would assume that's band shifting, and certainly the nice feature about our monomorph which is one of the controls is that if we get a shift in the band we can usually detect it relative to that 2,731 base pair fragment, so if you have a straight line of fragments at 2,731 and all of a sudden you get one that's slightly higher, then we know that there's a potential band shift there.

Q. And there was no band shifting in this particular case?

A. If there was any band shifting there it was minimal and I can't recall anything that was of any significance.

Q. When you reviewed the test results of Dr. Bowen in this case, when did you review the test results?

A. I'd have to refer to my notes but from memory I seem to recall I reviewed them in December of 1990.

Q. Did you know what Dr. Bowen's interpretation was before you reviewed it?

A. No. When I review a proficiency test or when I review a case I like to look at the autorads by

myself and make my own interpretations. From there I go back and talk to the analyst or the person that conducted the proficiency test.

Q. I believe you also mentioned in direct examination that there's a lot of scientists that will study the different databases of the organizations belonging to TWGDAM just out of purely academic interests?

A. Yes.

Q. So it would be maybe a cheap and convenient way for them to study population genetics?

A. It's some science results, data that are very interesting, and certainly we encourage people to look at our results. We're not doing this in a vacuum. The other thing that one must recognize is that many of the results we have in Caucasians, for instance, they're so insignificant with respect to the shift that if a research scientist were to apply to a university granting agency, for instance the Medical Research Council of Canada, they probably would not get the grant to do this because, one, the review of the literature would be such that they would think that the changes are so minimal that it would not be worth funding, so many of the studies that we actually do couldn't be done in a university because they wouldn't be considered significantly different enough to pursue.

Q. Now, you mentioned that there were a lot of criticisms within the forensic fields of the R.C.M.P.'s techniques and databases?

MR. WALSH: I might be mistaken, maybe I missed that. When did he say that?

THE COURT: Well, I don't recall that, Mr. Furlotte.

MR. FURLOTTE: I recall on direct examination mentioning criticisms within the forensic field, and one of them being that the British system says that -

THE COURT: You put a leading question suggesting there had been many criticisms but the witness didn't say that.

MR. FURLOTTE: On direct examination did you state that within the forensic field there was criticisms of the R.C.M.P. by the British for being too conservative?

A. Yes.

Q. So those were criticisms within the forensic field?

A. That's coming from forensic scientists who are my peers suggesting that we're being very conservative.

Q. And do you recall on direct that you used that word, within the forensic field?

A. I presume I used that word, yes.

Q. Now, there are also criticisms from without or outside of the forensic field, the general scientific population?

A. A criticism of what, specifically?

Q. Mostly not on the DNA testing and establishing profiles but on the fixed bin approach and the calculation of frequencies there's been criticism?

A. There are people out there who are advocates of the system and there are people out there who seem to feel that there are changes warranted. In science there's going to be criticism. When there is no critique in science, then it's time to leave.

Q. Now, within the forensic field I suppose it's safe to say that your methods of calculation are considered reliable by the forensic field of scientists?

A. I think Dr. Kidd is certainly not a forensic scientist and he would certainly agree that they're reliable even outside the forensic field.

Q. By some members of the general scientific -

A. Certainly, members who are familiar with our program or those programs that are similar to ours certainly seem to think that what we're doing is certainly adequate. I would not understand why a lab would want to enter into a collaboration with us if they didn't think what we were doing was correct.

Q. That's right, but from outside the forensic field like Dr. Kidd and Dr. Carmody who's going to be testifying, I suppose we could consider them independent witnesses because they don't have any direct interest in forensics?

A. Is that a question?

Q. Yes.

A. They'd be probably independent witnesses, yes.

Q. And there's a lot of independent witnesses aside from - like Dr. Kidd and Dr. Carmody who oppose the forensic field from determining probabilities the way you do it?

A. There are going to be opponents in any system and I think if you had a large enough population and you pooled the population you would find people out there who would suggest the earth is still flat.

Q. In the general population of scientists there are

probably more who oppose it than who confirm it?

A. That would be like counting noses, and essentially if you had 12 people that said the earth was flat and you had one person that said it wasn't flat, who are you going to believe?

Q. Police agencies have a difficult time in getting scientists to come to court and support their position, independent scientists like Dr. Kidd and Dr. Carmody?

MR. WALSH: I thought we had objected to this question the other day and I thought the Court had ruled on it, I might be mistaken, as to whether this was an appropriate question.

MR. FURLOTTE: It's an attempt to count noses, My Lord.

THE COURT: I don't think it's a realistic question, really. I suppose there are all sorts of factors that enter into it. Dr. Kidd expressed yesterday his reluctance to become involved in forensic work, he has other motives, and I suppose perhaps he may fix his fee to discourage being asked to take part in forensic cases. Perhaps, I don't know. Perhaps the cost of getting people outside the police laboratories is a deterrent. There are so many factors I - we're getting into a field that's - I should imagine to use common layman's sense that most scientists or a lot of scientists don't want to become involved in forensics and do everything they can to resist it. I suppose others do. However, if you can comment on this, you can comment more intelligently than I can, perhaps - if you care to. What was the question again?

MR. FURLOTTE: That's a good question.

THE COURT: No, it wasn't a good question. I think it was a nonsensical question, but however, ask it again.

MR. FURLOTTE: It's difficult, Doctor, for police agencies to find independent expert witnesses to come in and support the reliability of your ability to calculate the frequencies in these cases?

A. I think there are going to be scientists out there that will support us in court like Dr. Carmody and Dr. Kidd. These are independent, respectable scientists. The major problem with scientists, I think, entering into a court system is the fact that it's completely different than science, the background environment that they're involved in. In court precedent seems to be extremely important, in science it's facts. A lot of scientists out there do not believe there's even a problem with the DNA and don't even recognize that it's necessary to go and support the technology in court.

The other aspect is that if you're truly an independent scientist I don't think there'd be any problem with us having our data going out there for review or to collaborate on a project and that person gets something back from the project in the sense that they've looked at our data and they're interested in it, etc., they think it's good data, and it's been of interest to them, but to actually call a scientist who is probably working on cancer genetics into a court room to testify on something that he's used for ten years and it's totally accepted, he'd first find it nonsensical, secondly

it would be a waste of his time, and three, he's not in it to make money as a legal expert, he's a scientist. You heard Dr. Kidd himself say he's not a paid legal expert. So I think part of the problem, if you're considering it a problem, of getting people to come to testify is that they certainly haven't identified this as being a problem, and secondly, they have other careers, but I think there are certainly very respectable scientists out there, Dr. Ranajit Chakraborty, Dr. Bruce Weir, there are many scientists out there that would certainly support us in court, but they're not doing this as a profession.

Q. No, that's fair, and there's a lot of scientists out there, Doctor, who just couldn't care less what the courts do with this type of evidence?

A. Is that an opinion?

Q. Yes, would there be lots out there like that, they have their own interests and they don't want to get involved?

A. I think there are a lot of people who have their own interests and don't like getting involved.

Q. Right.

THE COURT: There are a lot who don't want to have to subject themselves to direct examination or cross-examination by laymen, would that be correct?

A. Sometimes it's very difficult to be a scientist in a court setting.

MR. FURLOTTE: But in your monitoring the different techniques from the different forensic laboratories, how different scientists are approaching, say, the problems of dispute, the R.C.M.P. monitors all of the different court cases?

A. I think that would be impossible to do.

Q. Well, many of them.

A. We're certainly interested in court cases and we'd like to know if there have been cases that have direct applicability to us. I think most of the monitoring of court cases are more for the benefit of the lawyers that are going to be trying our court cases because it gives them a perspective on how to set up their direct and cross-examinations, etc.

Q. O.K., but I believe Dr. Kidd testified yesterday that in one case he was testifying in the defence lawyer hit him with a list of different lawyers who testified for the defence in these cases and a list of lawyers who testified for the police agencies in these type of cases and it seemed that there was about three times as many opponents to this process than there was proponents?

THE COURT: You were saying lawyers, you meant scientists?

MR. FURLOTTE: Scientists, I'm sorry, that there appeared to be three times as many scientists coming to court and opposing this type of reliability as the police agencies were able to get. Is there any reason why it's easier for the defence lawyers to get scientists to come in here and testify against it than it is for the police agencies to get them?

A. I don't know if that's really true, number one, and two, it's like any profession. I think if someone has the time or perhaps is interested in a case or perhaps their research is not taking up all their time that they may want to go to court, they may need the extra money. I don't know what

motivates a person to testify in court. There certainly seems to be a lot of people out there testifying in courts that seem to make a lot more money than I do.

Q. Do you know whether or not some of the defence experts have actually went to court and testified for nothing, no payment?

A. I wouldn't know that.

Q. Now, Doctor, the mere fact, then, that maybe one side or the other can come to court with more expert witnesses, we shouldn't be nose counting, should we?

THE COURT: Well, that's a legal question. I'm going to explain to the jury in due course that the number of experts on one side or the other doesn't have any bearing, it's the quality of the evidence that counts, so that's not for this witness to say.

Q. O.K., Doctor, do you think it's important to recognize the fact that a DNA analyst should have the population database with respect to the area that it's going to do an analysis?

A. I think what's important to have a database for this DNA analysis, essentially have a database that is going to support the conclusions or the reliability of the tests that you're first going to conduct, i.e., has the database been run properly, do you have enough samples, etc. Whether or not you have the correct database, I assume what you mean are different ethnic group databases, is that what you mean?

Q. Well, no, with respect to the area, not different ethnic groups.

A. With respect to the area, in other words I would

have to have a Caucasian database for Nova Scotia and use a Caucasian database for Saskatchewan?

Q. If it was necessary.

A. I don't think it's necessary.

Q. Do you feel it's necessary for each country to generate its own database?

A. In certain circumstances, no, and others yes. One of the reasons why a database is important is that it's usually one of the initial ventures that a forensic lab gets into to support the technology, so it gives them a lot of training and of using their protocols. If you've done 600 individuals it certainly will test your system before you get into case work, so I think part of the reasons why a lot of forensic labs generate their own database is to gain the experience, but for instance if I was a state starting out a forensic lab service where - at this time in the DNA program, I would most likely use the FBI database or the TWGDAM database which is quite large, and that would be perfectly adequate for my purposes provided that the technology I was using was the technology that was used to establish the database, i.e., if I was going to use the FBI database I would want to be using the FBI system. It wouldn't serve me any purpose to use a HinfI enzyme Cellmark protocol if I'm using the FBI database, but there are other instances, for instance, where we've been asked by Bermuda to look into the possibility of setting up a database for Bermuda. Not having any expertise in the population of Bermuda I would generate an opinion that it would be necessary to make a data-base for Bermuda.

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

THE COURT: All right, we'll recess now. I would just say something before we do recess and that is that I have in mind instructing that the accused be returned to the court room after the recess. I'm not going to give any instructions or advice as to what his conduct or behaviour should be because he appreciates it as well as I do, what the standard is or should be that prevails in the court room, and when conduct intimidates witnesses or intimidates jurors or intimidates the court setting, the trial setting, then something has to be done about it and it's the duty of the presiding judge, of course, to intervene and to do something about it. The only thing that one can do is to put an offending person out of the court room, and I won't hesitate to do that again if it re-occurs, so Mr. Pugh, you'll see that the accused is returned after the recess, please.

Thank you very much. Fifteen minutes or so recess.

(**BRIEF RECESS - RESUMES AT 11:25 a.m.**)

MR. FURLOTTE: My Lord, before we call the jury in, Mr. Legere has asked me to request to this Court to be excused for the rest of the morning, that he has a migraine headache and I believe he has been given some medication for it and he's been, I believe, suffering from these quite some time while -

THE COURT: He what?

MR. FURLOTTE: He has a migraine headache -

THE COURT: Yes.

MR. FURLOTTE: - and he's been given medication for it and he's had it for the past two days and he's been given medication at the detention centre in Fredericton and it's a common thing, I believe, that he suffers from, so he would like to be excused for the rest of the morning and probably this afternoon he might be able to come in. I believe under Section 650, paragraph 2(b), that the Court may permit the accused to be out of court during the whole or any part of his trial on such conditions as the Court considers proper.

THE COURT: Yes, well, do the Crown have any comment, Mr. Allman, on this?

MR. ALLMAN: No.

THE COURT: The Court has the authority, of course, to require an accused to be present but in the circumstances I'd certainly grant permission for the accused to remain in the holding cell. Is the machine operating, Mr. Pugh?

MR. PUGH: Yes.

THE COURT: That permission can extend into this afternoon if necessary, Mr. Furlotte. Perhaps you'd keep in touch witht he situation and let us know this afternoon.

MR. FURLOTTE: Yes.

THE COURT: All right, we'll have the jury in, please.

(JURY CALLED - ALL PRESENT.)

(ACCUSED IN HOLDING CELL.)

THE COURT: I explained to the jury before the recess that I was lifting the order in respect of the

accused and I did make that order but just before you've returned here the accused has made a request through his counsel to the effect that he has a migraine headache and would prefer to stay in the holding cell the rest of the morning or perhaps for longer, and I've granted permission for that as I am authorized to do under the same section of the Criminal Code that I spoke of before, and I'm saying that merely to explain why he isn't present in the court room at the present time. Now, you're continuing on, Mr. Furlotte, with cross-examination?

CROSS-EXAMINATION OF DR. FOURNEY CONTINUES:

Q. Basically, Dr. Fourney, the controversies associated with the forensic application are primarily dealing with the aspects of population genetics?

A. I would say that there are some population geneticists out there who have different opinions and that's primarily where, if you want to call that controversy, yes, that would be the major area.

Q. I believe two scientists who maybe would oppose the ability to calculate the frequencies as claimed by the forensic laboratories would be Dr. Lewontin and Dr. Lander?

A. Yes.

Q. Do you know who Dr. Lewontin is?

A. Richard Lewontin?

Q. Yes.

A. Yes. He's a population geneticist who has testified several times in the past.

Q. Yes, and he's probably rated as the best in the

world?

MR. WALSH: My Lord, at this point I'm going to raise an objection. First of all, I don't mind so much this as the fact that Dr. Fourney has not been declared an expert in the field of population genetics. He's not providing testimony in that particular regard. Mr. Furlotte is asking questions now with respect to other population geneticists, and the other risk he has is that I'm afraid Mr. Furlotte would like to try and - I'm just anticipating where he may be going. If he's trying to get any opinions of these doctors on any specific issue and on any particular case or on any particular lab, then that's not a permissible thing to do. I don't have the right to cross-examine or to look and see what this case - what they would say with respect to this case, so I'm anticipating where he's going and I'm also objecting on the basis that Dr. Fourney has not been declared an expert in the field of population genetics and he's transgressing into that particular field.

THE COURT: Yes, well, without hearing you, Mr. Furlotte, on that, on the first part of it, the question of whether the witness is competent to comment on Dr. Lewontin's credentials, well, the witness will have to decide that, whether he is or not, based on his own expertise. On the second question, if either of these gentlemen have views there's nothing to prevent your posing, perhaps, a theory or a principle to this witness and saying do you agree with that, but not to attribute it to either Lewontin or Lander, because you would be, then, as

Mr. Walsh points out, trying to slip in evidence from Lewontin and Lander in a way that wouldn't be permissible under our rules of evidence. If there are - I mean the mere fact you mentioned these gentlemen would suggest perhaps there's some reason for Mr. Walsh to suspect what he does suspect.

MR. FURLOTTE: I don't want to get into the specific testimony that these witnesses may have given in other court proceedings or any papers they may have produced.

THE COURT: No, you can't do that, no.

MR. FURLOTTE: I have no intention of doing that, but as we know, expert witnesses are entitled to base their opinions on what they have heard from the expertise of other scientists in their fields or in that area and -

THE COURT: Yes, but as Mr. Walsh says, you can't be slipping in evidence that Lewontin or Lander might have given in other cases or even general views they have under the guise of questions that you're putting to this witness. If you know there are theories out there somewhere that you want to say, look, do you agree with a certain theory, as I say, that's O.K., but not to attribute them to Lander or Lewontin or anyone else.

MR. FURLOTTE: Would Dr. Richard Lewontin be considered probably the best scientist in population genetics in the world?

A. I don't know how I'd evaluate that.

Q. Well, let me put it this way, many scientists believe him to be?

A. That would be their opinion.

Q. Yes, and -

THE COURT: By that answer do you mean yes or do you mean if they thought that it would be their opinion? I'm not just quite clear on what you're -

A. Well, he's proposed the fact that there are other scientists who are more familiar with Richard Lewontin and find him a very credible witness or scientist in that he's considered in high regard. I don't doubt that. In terms of my own expertise, if he was a molecular biologist, for instance, I could probably render you a better opinion. I have not read everything that Richard Lewontin has written and I think Dr. Carmody, who has actually worked with Dr. Lewontin, could probably render a better opinion towards that.

Q. And what about Dr. Eric Lander, do you know him?

A. Once again the only time I had an opportunity two weeks ago to hear him talk for the first time, and it was at the 8th International Congress of Human Genetics, and he strictly spoke on mouse genetics and looking at various gene clusters in mice, so I would say he seems to be a very credible scientist as well. As to the finer points, once again I think that should be left up to possibly a population geneticist to evaluate.

Q. And Dr. Eric Lander was a member of a panel or a consultant for the Office of Technology Assessment Report?

A. There are many scientists that were consulted. My own chief scientist, Barry Gaudette, who's head of the entire program at the R.C.M.P., he's also been consulted in the OTA Report.

Q. And I believe the National Academy of Sciences has

attempted to take onto itself the responsibility of trying to settle the controversies between the forensic DNA laboratories and scientists in the general population?

A. I think they've been requested to look into the situation and to render an opinion, yes.

Q. And Dr. Eric Lander has been appointed also on that board?

A. Once again I believe he as well as many members have been appointed onto that board. I'm more familiar with Dr. Tom Caskey, for instance, who's also a member.

Q. Dr. who?

A. Tom Caskey.

Q. Do you know when he was made a member?

A. Well, he's on that board.

Q. He's on that board. Apart from quality control and technical proficiency in the conduction of these tests there are several bona fide scientific issues at the heart of this controversy; not just one, there's several?

A. Could you give me an example?

Q. Both the number and the type of loci being analyzed besides the population genetics issues?

A. I wouldn't think that that's a situation now. Perhaps at the beginning when we were starting out where we had less information, people were interested in looking at all sorts of probes. I think the number of probes that we use is very consistent with that being used in North America and the loci have to be those loci that will work within your system. There's no sense in using something that won't work with the type of gel,

the probing, the membranes, etc., that we're using, so I don't think that's that controversial. In fact, in the R.C.M.P. system we probably run more probes than many programs.

Q. Well, that's because you used the monomorphic probes?

A. That could be - that's another probe that we run, yes.

Q. But the monomorphic probes, they're a control probe, it's not a probe that assists in identification?

A. No, that's correct.

Q. Now, you're a co-author of a paper entitled, "Forensic analysis of restriction fragment length polymorphism", along with Doctors John Waye and John Bowen?

A. That's the Promega paper you're referring to?

Q. This would be the Promega paper, I believe.

A. Yes, I'm one of the authors.

Q. And apart from - well, on Page 119 of the Promega paper you state: "Recent debates have brought into question the ability to achieve genetic individualization based on the analysis of a limited number of genetic loci", and you quote King, Lander and Lewontin, and you state, "Apart from quality control and technical proficiency there are several bona fide scientific issues at the heart of this controversy". Now, would you state what those several bona fide scientific issues are?

A. O.K., first of all we have to put this in perspective. That paper was written, I believe, in 1989, so that was a number of years ago, and

at that time some of the issues that were of concern, for instance, were whether you use a monomorphic, how you quantitate DNA. People were not completely sure of what was happening with band shifting, for instance, or how to control for it, but many of these issues have certainly been addressed and what was in the past possible bona fide issues I think have been more or less been flogged to death at the point that most people think that the technology that we currently use, if it's done properly, is very valid and reliable, to the point that I believe on Page 8 of the OTA Report they point that out.

Q. But they're only talking about the DNA profile, obtaining your profile. They're not talking about there the population genetic aspect of it, are they?

MR. WALSH: That's the very point I made. Dr. Fourney has not been declared an expert in the field of population genetics. If Mr. Furlotte wants to get into the field of population genetics I've got a man sitting back here that's going to be happy to talk to him about them.

MR. FURLOTTE: I'm not asking him to describe population genetics, I'm just asking him that he recognizes that it is a controversy and a problem.

THE COURT: Well, let the witness answer that.

A. In my view I'm very - I've looked at the research and I've certainly looked at the information that's been made available to me and I feel that the program and our databases are more than adequate to do the job that they're intended to do. If you have questions of the specific

controversies, many of which are minor controversies or points of interest that only a population geneticist would understand, then I would suggest that perhaps Dr. Carmody would be the best person to address those.

Q. O.K., but you said you're satisfied that your databases are good enough to do more than what they're supposed to do. On the other hand -

A. Once again, I'm not a population geneticist but -

Q. Right, but on the other hand not being a population geneticist you're really not qualified to form that opinion?

A. This is a little of a circular argument. To do the work that I have to do I have an understanding of the principles involved. To address some of the finer points of population genetics, then I would suggest that I'm not a qualified expert, no, you're correct, but the basic issues of population genetics, the principles involved, the correct use of the technology that we currently have, I would say that I have an understanding of that, yes. Some of the controversies you're relating to seem to be points that only would be understood or possibly of concern to the more academic technical issues of population genetics.

Q. What guarantees do you have that anybody from New Brunswick is in the R.C.M.P. population database?

A. We don't.

Q. So although the R.C.M.P. population database is up to some about 900 people you can't state for a fact that anybody from New Brunswick is in it?

A. That's correct.

Q. I believe we have here for Item 110 the

calculations would be one in 7,400 for sharing two probes?

A. Yes, that appears to be what that chart says.

Q. If you were to search your database and find two probes that match, two different individuals who found they matched at two different probes, would you calculate it this way to find something like one in 7,400, or if you had a database of 700 people would the chance be one in 700?

A. I would address the issue based on the Hardy-Weinberg equation based on the sampling population. I think the principles involved, and Dr. Carmody certainly is prepared to discuss this in detail, he has charts, etc., to band matching. I think what is more relevant here, if I may add, is that we did take the patterns that were present in Mr. Legere and searched our database and he can be excluded as of matching the entire 974 people on the basis of two probes. In other words, after two probes we do not find anybody that would match Mr. Legere's pattern.

Q. But then again it's possible with Mr. Legere that if he was in the database originally you still wouldn't find a match with him because he even falls outside the match window with his own tests?

A. No, we would certainly find a match.

Q. And, Doctor, as a scientist and using the Hardy-Weinberg formula and the product rule you're basing your calculations and your ability to use the Hardy-Weinberg rule and the product rule - you're basing that on some kind of a theory or model?

A. You're talking about linkage and dependence?

Q. Yes.

A. That's correct, and there have been reasons for the fact that we can do that, and once again I'm not an expert in that and Dr. Carmody is going to address those issues.

Q. Now, I believe that you can never prove a theory, you can only disprove a theory?

A. That's the nature of science.

Q. So what you're saying by using the Hardy-Weinberg formula and the product rule and whether or not they're in Hardy-Weinberg equilibrium or linkage equilibrium, you can't prove that, you can only disprove it?

A. Yes.

Q. Do you know of any way that a scientist could prove that it is improper to use the Hardy-Weinberg formula and the product rule in this case or in any case, forensic case?

A. If it's improper to use this formula?

Q. Yes, how would we prove your theory is wrong?

A. I think that's part of the problem, actually, is it's difficult to address those issues and how many samples you have to have. What they originally tried to do was to look at the number of single band patterns versus double band patterns, and this formula would tell you the number of what we call homozygotes versus heterozygotes, and the fact that they're a variation over what was predicted and what we actually had indicated that the Hardy-Weinberg equation did not stand up to it, but on the other hand, reviewing that data and recognizing the limitations of the technology and the fact that people are missing

the bottom bands in some cases, it quickly became apparent that the limitation was not in the Hardy-Weinberg, it was the limitation of the technology, but in terms of hypothetical technology and how to address issues of population genetics, how to test those principles, I think that has been done by the experts in the field. Certainly there's a paper out in "Science" by Bernie Devlin's group that addresses the Hardy-Weinberg issues. There was another paper in the "American Journal of Human Genetics" this spring, Dr. Chakraborty has got one or two papers on this, so I think the population geneticists are certainly looking into this.

Q. O.K., but part of the Promega paper that you and Dr. Waye and Dr. Bowen did was to test for the amount of homozygotes?

A. That's absolutely correct.

Q. Right, and at that time you felt that that would be a proper test?

A. At that time that was the only test that we could apply.

Q. And as a matter of fact that test would prove that you could not establish Hardy-Weinberg, that you were out of Hardy-Weinberg?

A. The way that we applied that test that's exactly what it said. It has since been shown through Dr. Carmody that that doesn't appear to be a concern.

Q. And for some of the probes basically you would have to have - to be within Hardy-Weinberg you should only have about ten per cent of the people should be homozygotes for each probe?

A. It's very dependent on the probe and the

technology.

Q. Yes, but roughly; you used the 90% or the ten per cent standard?

A. Well, for instance, the homozygosity of some of those probes is quite a bit lower than - or the polymorphism, the heterozygosity, is quite a bit lower than what, you know, 90% I believe. D-16 was around 16% or so.

Q. Maybe before we go too far you could explain to the jury what is homozygotes and what is heterozygotes.

A. Essentially what we're trying to do here is tell the difference between one-band and two-band patterns, and if the parent of an offspring has the same band the child will inherit what looks like a single band and that's called a homozygote, and if the parents have two bands, then one or the other band gets inherited from each parent and you get two bands or a heterozygote. In reality Dr. Kidd would be the first one to express his concern over this because at the present time it's difficult for us to really tell whether we've got a true one-band pattern or a two-band pattern because of the limitations of the agarose electrophoresis. We can only resolve a fragment so fine, so there may be two bands so close together that we call it one band or there may be a band that has run off the bottom of the gel. What's important to realize there is that we recognize the limitations of this and in a fixed bin paper with the FBI principal officer Dr. Budowle we designed our binning, our fixed bin, with such conservatism that it would take that into account,

but with forensic application the match is what I find to be the most important.

Q. O.K. Now, in order to be in Hardy-Weinberg you would have to be within the expected range of homozygotes within a population?

A. That's one of the tests that people use and some ways it's fairly naive.

Q. The expected range would be somewhere like about ten per cent of the people would be homozygotes, their two bands would be the same size?

A. You'd have to do the calculations.

Q. And if you were basically more than that, then you would be outside of Hardy-Weinberg, there would not be Hardy-Weinberg equilibrium?

A. In instances where there are more homozygotes than expect there's been another hypothesis called the Wahlund effect which suggests that the reason for this homozygosity increase has to do with what is called sub-populations, so there's a small group there that are breeding and you get more single band patterns, but in reality to really address the issues of Hardy-Weinberg and the Wahlund effect you've got to really know your population genetics and the statistics, and I would hesitate to suggest that most molecular biologists, certainly myself, we can do the principal tests, but to do the rigorous testing necessary to find out if you're at the limits of your technology and whether or not this is all making sense with the population statistics and genetics that are known today you'd have to go to experts in the field, and that's what we've done. Well, Dr. Carmody, for instance, I would consider

him a very credible expert and he has tested our program. We're working with Ranajit Chakraborty. When the FBI have a similar problem there's more homozygotes or single bands than they expected, they went to Bernie Devlin's people and they did extensive work on this, it's not a trivial problem and their conclusion was -

Q. O.K. to get into hearsay evidence now, eh, Mr. Walsh?

MR. WALSH: Well, you know, what's - I shouldn't say funny, but what is kind of ironic here is I posed an objection on the basis that Mr. Furlotte was delving into the field of population genetics. He doesn't mind doing that as long as he's getting answers that help him, but when he gets into it and he doesn't get the right answers, then he doesn't seem to be very happy about it. My point is why get into that field with him at all.

THE COURT: He's still happy because he hasn't stopped the witness. You've got the witness under your control, Mr. Furlotte.

MR. FURLOTTE: I'm just saying that Mr. Walsh is not objecting now because it's hearsay evidence. As I understand, you had your preliminary tests showed that you were not in Hardy-Weinberg?

A. Yes.

Q. That's basically. Someone in your forensic laboratories claim because they could not find themselves within Hardy-Weinberg that well, the smaller fragments of the bands would run off the end of their gel so therefore they were left with one band, right?

A. That's one of the possibilities, yes.

Q. And so they tried to explain away because they couldn't find themselves within Hardy-Weinberg, well, we've lost a band at the end of the gel, it's really a two-band pattern but we only show one so let's ignore it; is that right?

A. What a scientist does when he's confronted with something that seems to be slightly different than expected, they go back and test it, and one of the things they did was use another enzyme and found in fact there were two bands there, which confirmed their hypothesis.

Q. And the R.C.M.P.'s explanation as to why they have too many one-banded patterns is because in your lab you can't have small fragments go off the end of the band, they all stay on - or the end of the gel, I'm sorry.

A. No, that's incorrect.

Q. That's incorrect?

A. We could have small bands go off the end of the gel, very small bands. I mean we're looking - you know, if you had a band that was ten or twenty base pairs we'd probably never see it.

Q. So then your explanation, then, besides that would be that well, maybe we have two bands that are hiding behind one another, shows up as one?

A. That's another possibility, yes.

Q. That's another possibility. Now, these are possibilities to show as to why you're not in Hardy-Weinberg, and if you're not in Hardy-Weinberg you can't use the 2pq formula and you can't use the product rule so -

A. What I find interesting about the Hardy-Weinberg, the debate, is that it seems to be a debate

amongst population geneticists, and in my experience, certainly, in court, we have had defence experts including Bill Shields come in and say it's not even an issue, Hardy-Weinberg, so it's difficult for me to know what I should say with respect to Hardy-Weinberg because we have some population geneticists say don't worry about it, from both the defence and the prosecution side, and others say that well, we think there may be a little bit of a problem here, but the problem rests not so much in the use of the technology, it's maybe we don't have the exact number, and it's a probability, we're not generating an exact number.

Q. But in your Promega paper, your tests that yourself, Dr. Waye, and Dr. Bowen performed, where you should have got about a 90% heterozygotes, two-banded patterns, I believe out of the five probes that you run you've failed in four of them? There was only one that fit the pattern?

A. Using that limited test for Hardy-Weinberg it did not fit the Hardy-Weinberg equation, that's correct.

Q. And for the MS1 probe it was 89% when it maybe should have been 90, that's not too bad a failure, right?

A. I'd have to - I think there was one one probe there that was in Hardy-Weinberg, if I recall from that data.

Q. Yes, the D2S44 was in Hardy-Weinberg, it was at 91%? I'll show you your paper, Doctor, Table 4.

A. O.K.

Q. D2S44 was at 91% and it was the only one that

passed. Your D4S139 was at 86%?

A. That's correct.

Q. Your D16S85 was down to 69%?

A. Yes.

Q. And your D17S79 was down to 68%.

A. Correct.

Q. 22% off. Why would you be off, say, in D17, off by 22% one probe and the other probe actually shows that you're within?

A. I'm glad you asked that because, for instance, D17S79, the polymorphism, it's highly polymorphic, but the actual area that it's polymorphic in is a very small region of the gel, so that we have many, many different alleles compressed into a small region, and my guess in that case would be that they're hiding over one another. This other one, there's another explanation for D16S85. It's a probe that's characteristic of small bands so you'd expect to have small bands off the end of the gel.

Q. O.K., but the D17S79 you say they all seem to fit in one small area of the gel. Maybe your gel is that long and they all fit in one small area?

A. It's more of a compressed region of the gel, yes.

Q. So it would also be more difficult to tell whether or not fragment lengths are distinguishable from one another?

A. There's certainly that possibility, yes.

Q. So again that may be one way to prove that your theory would be wrong and you can't use the theory. Is there any other way?

A. I think possibly Dr. Carmody would be better to address that because these are issues that are

being looked at from a population genetics point of view.

Q. O.K., how about if you found that if according to your theory you were supposed to be - some matter or event was supposed to be predictable within your theory but for some reason or other the results of that event was utterly ridiculous? Could that prove your theory wrong?

A. It would certainly be a matter of concern.

Q. Do you agree, Doctor, that ultimately it would be desirable to define alleles discretely to be correctly genotyping not just phenotyping VNTR profiles, and to reduce measurement imprecision that then it would be legitimate to apply the Hardy-Weinberg equilibrium?

A. I think the context of that sentence or that paragraph, maybe, is from the fixed bin paper, is that correct?

Q. Yes.

A. And the issues there are ultimately what we want to do is to find a better system with respect to sensitivity and measurement precision, so I would agree with that, but since we're already applying the Hardy-Weinberg equation and it seems to be acceptable to most population geneticists that I've talked to, anyway, then I would disagree with the aspect that we can't apply it in our present circumstances.

Q. But the basic position of the FBI and the R.C.M.P. is both that while it's not really legitimate to use the Hardy-Weinberg formula because we are not using discrete alleles we do have measurement imprecision, but because of our binning system

we'll make it conservative to take in the fact that we're not allowed to use the Hardy-Weinberg?

A. The binning system is allowing for any inadequacies that may be in the Hardy-Weinberg. The other aspect of Hardy-Weinberg equation you have to recognize is the biological aspect. To use the Hardy-Weinberg equation there are certain conditions that have to be met in a population and there are very few populations that meet that, yet population geneticists totally accept this.

Q. In the calculation of frequencies Dr. Carmody is going to come to court and suggest that we put upper confidence intervals around these figures, is that right?

A. I believe so, yes.

Q. Before this case or before the R.C.M.P. was made aware of discoveries made by Dr. Shields did the R.C.M.P. suggest the use of upper confidence intervals?

A. Yes.

Q. Was it ever provided in court before? Did you have expert witnesses going to court and suggesting the use of upper confidence intervals?

A. I think since there was only two cases at that time, in the first case we didn't use it and - we didn't use it before in court, no.

Q. So that's being used in court as a result of Dr. Shields -

MR. WALSH: That's not what the witness had said. He answered that question and he re-arranged it incorrectly, flat incorrectly. That's an improper method of cross-examination, My Lord. I've tolerated this and what he does is he takes an

answer, rephrases the question, and gets an incorrect - completely incorrect, it's an incorrect use of cross-examination.

MR. FURLOTTE: My Lord, the Crown must forget that I can lead witnesses.

MR. WALSH: He's not leading them, he's putting a hood over their head.

THE COURT: Don't raise your voice, Mr. Walsh.

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

THE COURT: You know, I have a theory that when counsel has to raise his or her voice it means that the quality of bis argument is very weak, but I don't accept that in this case necessarily because I think your point is well taken. I think you are just twisting that a little, Mr. Furlotte, in your follow-up question, because that's not what the witness said.

MR. WALSH: My Lord, I apologize. I appreciate that is well-known, that you don't have to yell to get your point across. Unfortunately I let my anger get the best of me.

THE COURT: And it's well-known that when you do yell you've got a weak case?

MR. WALSH: No. I realize, My Lord, that that is an accepted statement, you shouldn't yell to get a point across, but I'm just saying that I was angry at what counsel had did and that's the only reason that I expressed it in that fashion, and I apologize to the Court and the jury for that.

THE COURT: Oh, that's quite all right. I just saw an opportunity to make that observation. I usually find that when I make it once during trial counsel never again shout. O.K., would you like to

rephrase your question just a little here, Mr. Furlotte?

MR. FURLOTTE: Back to the question, Dr. Fourney, before Dr. Shields got involved with the Allan Legere case the R.C.M.P. never had expert witnesses coming to court recommending upper confidence intervals?

A. No, I think that's incorrect.

Q. That's incorrect?

A. I think that Dr. Carmody testified in the Bourguignon trial voir dire, and that's when we first introduced confidence intervals, and certainly Dr. Shields is only fairly new on the stand with respect to coming to court.

Q. Dr. Shields or Dr. Carmody?

A. Dr. Shields. Ken Kidd previous to that used confidence intervals in many of the cases that he had testified in in court in the U. S.

Q. That's hearsay evidence again, is it?

A. No, you can read the transcripts.

Q. Now, you mentioned that Dr. Eric Lander was a member of the National Academy of Science which is looking into the disputes over the reliability of the forensic application of DNA evidence?

A. No, you brought that up.

Q. Yes, but you did agree that he was a member of that panel?

A. Yes.

Q. And that report should have been out before now, should it not have?

A. It's difficult to know how agencies and government agencies, etc., work. I'm not sure when that report is supposed to be out.

Q. Did the forensic laboratories have anything to do with the delaying of that report becoming public?

A. I wouldn't know.

Q. Are you aware of what the report was going to be -

A. All I can say is that -

Q. - in relation as to whether or not it is proper to use the Hardy-Weinberg formula and the product rule?

A. The report is in a draft form. Until it gets published I don't see how - I don't have the final copy of that report and I don't think I've seen anything that I would attribute to the report as being credible. I'm not sure what you're getting at. It's a document that's in process. They have interviewed a number of individuals. I had an opportunity to talk to people who were at - I believe they met in Washington to interview scientists about the aspects of forensic DNA typing to render their opinions in the same way that Ken Kidd was involved. Some of the forensic labs that I know of took part in that, but in terms of the final consequences of that report, no one has any idea what's in that report except the people that are drafting that.

Q. And to your knowledge they didn't tell anybody?

A. I'm not - I think in the States there was possibly some documentation that was leaked out in a defence case where a defence expert brought it up, and so there may be a few pages of parts of that report here and there. The only problem with that is that at best that report is preliminary, and number two, it's completely unethical to do that. From a scientific point of view it would be

like some scientist going into a lab looking at another scientist's data and then going out and publishing the results, you can't do that, so I think it's very invalid to render an opinion on a report that is not out there. The final copy is certainly not available. I believe it's December.

Q. Do you know whether or not that as a result of the so-called leak of what the report was going to be that the forensic laboratories submitted that another population geneticist be appointed to the board before the final report comes out?

A. It's really - I don't know how I'd answer that question. First of all I don't know if it's true. One of the concerns I would certainly have in that report, I can tell you, is that there are only - in the population side there's only Eric Lander, George Sensabaugh and Mary Clare King who are the people responsible for population genetics. Mary Clare King was sick most of the time that the report was being drafted and had very little input and Dr. George Sensabaugh, although he's an eminent forensic scientist, is certainly not a population geneticist, so you come down with the situation there's essentially Eric Lander is the sole population geneticist on that board.

Q. And of course the forensic labs don't like Eric Lander's opinion?

A. I think his opinion is changing. Actually, if you're read the most current letter to the editor in the "American Journal of Human Genetics", I think he's certainly changing his opinion.

Q. Not as much as you'd like?

A. Do I think he's going to be a prosecution expert

witness, in other words? I don't know.

THE COURT: Let's leave Dr. Lander for the moment. Can we move on to something else?

Q. Do you have any idea when that report will be made available?

A. At the Eighth International Congress meeting I had an opportunity to talk with several members who were on that group drafting up the report and they tell me that possibly December.

Q. Do you know if anybody new has been appointed to that board or panel?

A. No.

MR. FURLOTTE: I have no further questions.

THE COURT: Thank you. Now, re-examination, Mr. Walsh?

MR. WALSH: It will be in a much lower tone, My Lord, I'm not angry any more.

THE COURT: Oh, I don't mind your tone that much, really.

MR. WALSH: Dr. Fourney, Mr. Furlotte had -

MR. FURLOTTE: I'm sorry, My Lord, I had one more area to address.

THE COURT: All right. Go ahead, Mr. Furlotte.

Q. Dr. Fourney, I believe you did some kind of a computer search of the R.C.M.P. database matching probes to see what kind of matches you could get out of it?

A. What happened with our computer search is that it became apparent that the type of search that we are able to do is we would look for coincidental matches, say within the 5.2%, and take the numbers that we would generate between two matches and then compare those numbers with another group of numbers, etc., and you'd go all the way down until you get to five probes. We've done a search

similar to that. It's very technically demanding on the computer.

Q. And when you did that search you found five sets of individuals who shared five probes?

A. Yes.

Q. And because you found these five sets of five individuals who shared the same probes you threw five of them out?

A. No.

Q. You took them out of your database?

A. What we did was we concluded once you get a five-probe match you've got a duplicate in your data-base so that's -

Q. Otherwise it would destroy your theory?

A. Well, my professional opinion as a scientist is a five-probe match is a duplicate or an identical twin, and as a scientist what you'd have to do is test that, so what we did is we went back where we identified what we thought were five duplicates. We have a problem here because they're anonymous samples, you can't go back and get the exact person to confirm if it's a duplicate, so what we would do is we pulled the samples out, we had some of the material still available to us, the blood, re-extracted the DNA, re-ran those and they came out as duplicates across not only five probes, it came across as six probes, on the monomorph, on the sex-typing probe. We extended that to other probes with other enzymes, they're all duplicates, so once you get a five-probe match you've either got an identical twin or it's a duplicate in the database.

Q. But there's no way you can trace those samples

back to the individuals who contributed to them?

A. Absolutely not.

Q. So you're again assuming they're duplicates because it would destroy your theory?

A. No, in my professional opinion they are duplicates, I'm not assuming. As a scientist knowing the background of what constitutes a match, not only my opinion they're five duplicates, it would be the opinion of others, and I've actually sent these samples out to independent labs for confirmation with other probes.

Q. But other than using your own testing facilities which created the problem to begin with there's no way of proving that they come from specific - they are specifically the same person or that they come from the same individual or different individuals?

A. There's no way of saying it's come from the exact same person, no. When we contacted the Red Cross we were advised that although they're happy to -

Q. O.K., I don't want to get into hearsay evidence. I have no further questions.

MR. WALSH: I would like, My Lord, that the doctor be permitted to complete the answer to the question Mr. Furlotte posed and I expect -

MR. FURLOTTE: Not if it involves hearsay evidence, My Lord. I've got to get back here somehow.

MR. WALSH: Well, the scientific opinion of a doctor, he's entitled to rely on - in the terms of when he's investigating as he was there with those five duplicates he's certainly entitled to rely on the opinions of others and what he's told, things of that nature. Mr. Furlotte got into that field, I didn't, and I think Dr. Fourney should be entitled

to complete his statement.

THE COURT: You don't want him to tell? You don't want Dr. Fourney to tell what he knows?

MR. FURLOTTE: Well, Dr. Fourney already testified he doesn't know anything, he can't tell. Now, he can testify as to what other people may have told him and as maybe to help him form the opinion.

THE COURT: But you don't want him to give his explanation of this last point?

MR. FURLOTTE: Let's go for it. Go ahead, Doctor, give your explanation.

A. When we contacted the Red Cross and explained our situation they informed us through their charter that they could not do this. It's prohibited to give out individual information on any blood donors, it's protected information. The only reason they have that information is in the event that one of these donors may have an infectious disease so they can notify that individual because that's part of their screening program, so number one if we could -

Q. I believe you testified to that on direct evidence, didn't you?

A. I don't believe so, not the exact nature. When I explained our situation they informed me that although they've tried everything possible to prevent duplication the fact that there appeared to be what looked like a clear duplicate could have occurred from several circumstances; number one, they have a series of identical twins that give samples on a routine basis, and secondly, even though advised by us specifically to take a single tube of blood from - what would happen,

you would go in, you would donate blood, they take off a small sample of blood on which they do their testing. If the test proves that your blood is in fact non-infectious they would go on to make blood products for the hospital. What we get are the expended tubes. Sometimes the technologist would take two tubes of blood from that individual, and because the tubes are coming in anonymous from us we wouldn't know that the two tubes are from the same person. The other possibility is that the blood donor clinics that we were involved in were far enough apart that it's possible that the donor could have come back twice, and the last circumstance, which I was quite amazed at from talking to the people in Montreal, for instance, there are people out there who like to give blood on a routine basis, and even though they have an identification card that tells them who they are, they'll have two or three of these cards and they may donate blood up to five or six times a month, for whatever reason I don't really know, so these are extenuating circumstances beyond our control.

Q. Is there one more possibility?

A. And what would that be?

Q. Whoever was running the test could have run it, the same sample, twice or got the samples mixed up and run it in two different lanes?

A. That's quite possible.

Q. So there could have been a mix-up of samples in the lab?

A. That's always a possibility in any clinical analysis.

Q. And if you're so sure that all the independent

tests that you run and a scientific opinion that they are duplicates, why would it even be necessary to go out and search all the other avenues as to identical twins or maybe the same person coming back twice or maybe the same person giving blood under two different names or -

A. Well, for one thing, I'm a firm believer that a five-probe match is not concidental, and it's beyond that in the European laboratory, a three-probe match is considered not coincidental, so from a scientific point of view it certainly pigued my interest.

MR. FURLOTTE: I have no further questions.

REDIRECT EXAMINATION BY MR. WALSH:

Q. Mr. Furlotte had mentioned that Dr. Bowen on the third gel, comparing the third gel to the first gel, the third gel being an exclusion on a hair, comparing it to the first gel which would be the one with the 22 lanes across it - you mentioned that on one band on the third gel when you compared it across it was - Dr. Bowen found on the probing that it was outside the match window. Do you remember that?

A. Yes, it was slightly outside the match window.

Q. Dr. Bowen also testified in this trial, Doctor, that on the re-probing of that because the markers appeared to be overblown on the re-probing that they fell within the match window?

A. That's correct.

Q. And is what something that you would expect when you have markers that are overblown, the computer may have difficulty picking it up?

A. That would be one of the things that we would look at, yes.

Q. Mr. Furlotte asked you about numbers of scientists and lists of scientists and things of that nature. Dr. Bowen testified in this trial that he has consulted with defence lawyers, and Dr. Waye has indicated the same -

MR. FURLOTTE: My Lord, I didn't raise that in cross-examination.

THE COURT: Let's hear the question first and then we'll decide.

MR. WALSH: Well, Mr. Furlotte had asked him a number of questions about having difficulty, a long list of defence experts and the short list of Crown experts, and what I was trying to get at, Doctor, is whether or not there are scientists who will testify for either side depending on how good a quality the work is in the particular instance?

A. That's absolutely correct. A scientist is only concerned about facts and the data in front of him.

Q. Mr. Furlotte asked you a question to the effect that you can't state for a fact New Brunswick people are in your database and you said no, you agreed with that. Would you explain - so there's no confusion would you explain to the jury why you say that?

A. Well, once again the samples are collected anonymously and we really don't, when we get these samples, have a little checklist saying you were born in Prince Edward Island, you were born in New Brunswick, etc., and we file out our samples, so for that reason we have no reason to believe

that - they may be from New Brunswick as well. I mean, it can work either way, but what we tried to do, and I think what we're certainly going to get into, is by going to Canadian Forces Base Kingston we got a breakdown of the population that was present at that time at the base and their descendants and we found out that there were certainly New Brunswick people represented in that population, so unless there is a strong aversion to New Brunswick not donating blood I would suggest there are people in there from New Brunswick.

Q. And the final question I have, Doctor, Mr. Furlotte questioned you with respect to excess homozygosity which is - and you mentioned the Wahlund's test. Were you in court yesterday when Dr. Kidd testified?

A. For part - I think yes, I was.

Q. I was wondering whether or not these same issues were addressed to Dr. Kidd.

A. I believe Dr. Kidd covered all these issues.

Q. The test for excess homozygosity that you tried at the very beginning of your laboratory commencing, is that an accepted test now?

A. It's a very weak test and we recognize the limitations and that's why people like Dr. Carmody and Dr. Kidd got involved. First of all it was an academic interest, and second of all it was certainly necessary to find out what was going on.

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

THE COURT: Thank you very much, and I guess that

finishes with you, Dr. Fourney, and thank you very much for coming.

Now we'll recess until this afternoon at two o'clock.

(LUNCH RECESS - RESUMED AT 2:00 p.m.)

(ACCUSED IN DOCK.)

(JURY CALLED - ALL PRESENT.)

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

DR. GEORGE R. CARMODY, called as a witness, being duly sworn, testified as follows:

DIRECT EXAMINATION BY MR. WALSH:

Q. Would you give the Court your name, please, and your occupation - your position, I should say.

A. George Richard Carmody. I'm Associate Professor of Biology at Carleton University.

MR. WALSH: My Lord, with your permission I'd like to take Dr. Carmody through his C.V.

THE COURT: All right.

Q. Dr. Carmody, you received your undergraduate degrees, particularly your doctor's degree, in zoology from Columbia University in New York, is that correct?

A. That's correct.

Q. And would you explain for the jury what zoology is and whether or not the human species comes under that particular heading?

A. Certainly the human species comes under the heading of zoology. Zoology is the one branch of biology - if you were to break it down into animals and plants zoology is the study of

animals, botany is the study of plants, so my degree was in the study of animals versus other people who would be studying plants.

Q. And how does the human being come within that particular division?

A. The human species falls within the animals.

Q. You were also, Doctor, a postdoctoral fellow in population biology at the University of Chicago?

A. That's correct, from the years 1967 through '69.

Q. And population biology, what does that mean?

A. That's an area of biology that encompasses both the study of organisms, how they interact with each other, as well as populations of organisms including population genetics.

Q. And you also worked for a time at Harvard University, is that correct?

A. No, that's not correct.

Q. I'm sorry, you worked with someone that is presently with Harvard University?

A. That's correct. When I did my postdoctoral fellowship at the University of Chicago, for those two years I was working with Dr. Richard Lewontin who is a population geneticist.

Q. You were also a senior fellow in genetics at the University of Nottingham in England?

A. That's correct, and a sabbatical year in 1967 through '77.

Q. And what field of genetics would you have been working in?

A. That's in population genetics with Professor Brian Clark there.

Q. You were also a visiting researcher in genetics at the National Institute of Environmental Health

Sciences in North Carolina?

A. That's correct.

Q. And I understand that's a Federal United States Government Lab?

A. That's right. There was a group there in population genetics that I spent a sabbatical year working with.

Q. In population genetics?

A. In population genetics.

Q. You have also been a visiting professor in genetics at the University of Hawaii?

A. That's correct, in 1989-90.

Q. And that dealt with the area of population genetics?

A. Yes.

Q. We have had some instruction on this particular aspect but from your own view what is population genetics and how does it apply to what we're doing, briefly?

A. Population genetics is the study of the behaviour of genes in populations of organisms. Genes don't exist alone, they exist within organisms, and those organisms as species occur in populations. There are phenomena particularly in the study of evolution that we're interested in to know how the genetic composition of populations change in the course of time through various forces and how different different populations are genetically.

Q. And what application would that have to what we're dealing with here in forensics?

A. Well, specifically when we're looking at VNTR loci that are being used for genetic identification

we're interested to know what the frequencies of the different types of DNA profiles are in human populations, and we're specifically wanting to know whether there is geographic difference, ethnic background difference, racial differences, and whether those differences would cause significant changes in the way we would do our calculations.

Q. And you've already touched on this, Doctor, you've indicated that there are various life forms that are studied under the umbrella of population genetics, animals and plants, etc. What if any other specialties or sub-specialties are under that particular umbrella?

A. In population genetics we can break down that field to people who study specifically different groups of organisms. First you could say animals versus plants, you could say within animals those that study insects or invertebrates, those that study within plants, who study conifers versus deciduous trees, and whatever. Another division of population genetics is to break it down into a theoretical area as well as an experimental area. I would classify myself as an experimental population geneticist where I do experiments and collect data and have studied populations with the idea of trying to understand how well the theory predicts what we see empirically when we go out into the world and to see whether in fact those formulae that have been developed by theoretical population geneticists in fact can be used to predict what we would see in the real world.

Q. And you use these predictions. What kind of work

are you involved in when you use these particular predictions when you're looking at populations experimentally?

A. Specifically we use the statistical ideas to test whether in fact the predictions of theory correspond to the observations that we're making.

Q. We have heard the term drosophila. Would you explain to the jury, please, again? Drosophila, we understand is a particular form of - it's a fruit fly that's used in population genetics as a basic form of study. Where is your expertise in relation to that kind of organism?

A. My training was in drosophila population genetics. I have worked primarily with the fruit fly as an experimental organism both in laboratory experiments as well as field experiments where we collect the organism from various geographic places around the world and at different times in the season to see whether in fact there are genetic differences occurring. I have also worked with a number of other organisms and done studies in population genetics on lake trout in Algonquin Park in Ontario. We've looked at crayfish populations in some rivers of Ontario, we've looked at cave spider populations and cave beetle populations. One of the reasons for working with invertebrates is that they occur in relatively large numbers, they're easy to collect, we don't have to get special permits to work on them, and they just facilitate the studies and have many more generations enduring a particular period of time, so we can study evolution in a much better way than if we were dealing with

larger organisms that had very long generation times.

Q. Would you explain to the jury what if any experience or what if any work you've done in relation to humans, the homo sapien?

A. My work with homo sapiens, that is humans, has been confined to my helping the people in the Central Forensic Labs in Ottawa with collection and analysis of their human VNTR population database. That has involved predominantly statistical tests, statistical consulting. I give them advice as to what size populations would be necessary to form proper databases and they allow me then to analyze that and I give them the results of my analysis.

Q. You indicated that you would consider yourself an experimental population geneticist. The organism that you primarily work with, does that permit you as well to use your experimental theories or your experimental work and apply it to homo sapiens?

A. Yes, it does. The analysis is virtually identical when you're testing for things like Hardy-Weinberg equilibrium, linkage disequilibrium, representativeness of samples, differences in frequencies between different samples. Whether they were samples of plant populations, drosophila populations or human populations the techniques and statistical methods are identical.

Q. Dr. Kidd was declared an expert in this court in human population genetics. Would you explain what if anything he has over and above a population geneticist, in particular when we're dealing with humans?

A. Yes, he has in fact for most of his career spent that time looking specifically at human populations and looking specifically at populations of humans, of native populations or indigenous populations in quite remote places in the world. He has knowledge about pedigree analysis of these populations and inbreeding coefficients in these populations that in addition to his clinical background in human genetics puts him in a different category from myself.

Q. The theory of population genetics generally and the principles and the working formulas that you use, are they applicable to the human population?

A. Yes, they are. They are completely applicable.

Q. And you have looked at human populations using these particular statistics and mathematical formulas and working models?

A. Yes, I have.

Q. You've indicated that you were an Associate Dean of Science at Carleton University?

A. That's correct, from 1987 through 1989.

Q. I also understand, Doctor, that you are Chairman of the Integrated Science Studies at Carleton University?

A. Yes, I am.

Q. And could you tell us, please, what kind of teaching duties you would be associated with as a professor of biology at Carleton?

A. I have taught an introductory genetics course for the last - not every single year, but over the last 22 years, and I'm teaching it this term. I teach an advanced course in population genetics, fourth year level course, I teach that roughly

every other year. I also teach a graduate course with a colleague at the University of Ottawa in evolutionary genetics.

Q. Evolutionary genetics, what if any application would that have to what we're dealing with in population genetics of humans?

A. Well, my interest in population genetics is very much to understand the kinds of change that occur during time, and those changes that occur during time we would see simply as an evolution that occurs in species of organisms, so the population genetics is kind of a way of analyzing evolutionary phenomena in a rigorous mathematical way.

Q. As Chairman of Integrated Science Studies at Carleton - what is integrated science studies, what is involved there?

A. It is a unique program to Carleton that allows our undergraduates who are studying science to combine a study of a particular area of science with a minor concentration in a non-science area. We have people in this program, there are roughly 40 students enrolled in the program at the current time, who combine various disciplines. Some that come to mind, we have people studying biology combined with philosophy, looking at things like the new reproductive technologies where there are many philosophical questions and ethical questions that come up. We have people studying a combination of science with business with potential of applying business principles to biotechnology, things of that nature. We have people combining biology and psychology, biology and anthropology. It is a very exciting program and we have a great

many students who feel that that serves their interests best. Rather than having to concentrate within one area of science they can combine this multi-disciplinary approach of science in their undergraduate degree.

Q. Doctor, you're a member of the Genetic Society of America and the Genetic Society of Canada and the Society for the Study of Evolution, is that correct?

A. Yes, I am.

Q. You have indicated in your C.V. that your research interests - under research you have indicated that among them are molecular evolution of DNA sequences and genetics of population differentiation?

A. Yes.

Q. And again, just so we're clear, what application does that have to population genetics?

A. Well, both of those interests are within the domain of population genetics. The evolution of DNA sequences is a relatively young area where now we're able to get the exact DNA sequence of organisms and be able to see what kinds of actual differences there are between individuals of a species as well as to see how those differences might be changing in the course of time. As well, by studying a closely related species and by studying different populations of the same species we can get an idea of the amount of genetic diversity there is between species and between different populations within a species.

Q. You mentioned that you work with statistics as an experimental population geneticist.

A. Yes.

Q. Could you explain to the jury your experience with statistics and what if any expertise you have in the application of statistics?

A. Well, when I was a graduate student I took a number of courses in probability theory and statistics. I have used statistics in most of the publications that I've produced. I use statistics in advising my graduate students. In most of the work that I'm involved with I use statistics. I guess I would call myself an amateur consultant in statistics, I have a number of people in the Biology Department and, in fact, the way I got involved with the R.C.M.P. was that they consulted me first over some statistical questions and found that my recommendations were useful.

Q. You are not a member of the R.C.M.P., Doctor, are you?

A. No, I'm not. I have no contractual or financial connection with the R.C.M.P. My salary is completely paid for by Carleton University.

Q. Why do you do this work for the R.C.M.P., then?

A. I do it out of academic interest, in fact. This is an area where there is great interest to me to in fact be able to look at populations where there are the great amount of information being produced by people for forensic purposes. I'm very interested particularly in the analysis of the data that they are amassing on native populations. There's sort of an anthropological aspect to that to see what we can say about the background and potential evolution of various

native populations in the new world, and I'm very interested in that aspect of it. I also am interested in it in terms of some of the statistical questions that come up. They can be quite challenging given the fact that with humans we can't do experiments for obvious ethical reasons, and because of the long generation times and in general small family sizes we can't do the kinds of experiments that we could with drosophila, for example, so it's an interesting challenge to try and analyze this data within the limitations of analyzing human populations.

Q. I understand, Doctor, you've been an invited lecturer at the Technical Working Group, TWGDAM, formed at the Quantico - FBI Training Centre at Quantico, Virginia?

A. Yes, I was invited to address the Technical Working Group in early July of this year to talk about the forensic population genetics issues.

Q. And you're also an invited lecturer to the Canadian Society of Forensic Science on the same types of issues?

A. That's right, it was just last month in Montreal at their annual meeting I was invited to give them an address there as well.

Q. And you've just recently attended the Eighth Congress of Human Genetics in Washington?

A. That's right, where we presented a paper - I presented a paper jointly with Doctors Bowen, Fourney, and Dr. Lorne Kirby from University of British Columbia in Vancouver.

Q. And if we could sum up, Doctor, could you tell us, please, what your field of science would be?

A. I would classify myself as a population geneticist.

Q. And of a further subdivision?

A. Experimental population geneticist.

MR. WALSH: My Lord, I would ask that Dr. Carmody be declared an expert in the field of - before I do, Doctor, you've testified in courts in Canada before on these same issues?

A. Yes, I have. I've testified in two other cases.

MR. WALSH: My Lord, at this time I would ask that Dr. Carmody be declared an expert in the field of population genetics.

THE COURT: Yes. Have you any questions?

MR. FURLOTTE: I have no objections and no questions, My Lord.

THE COURT: For the purpose of the trial and no other I qualify you as an expert in population genetics.

MR. WALSH: My Lord, at this time Dr. Carmody during his testimony - I understand, Dr. Carmody, you're going to be using a number of slides?

A. That's correct.

MR. WALSH: My Lord, so that we will not have all the slides entered into evidence we have arranged for copies, schematics of these, to be filed as an exhibit. We don't certainly have them mounted on charts or anything and I don't think there's any necessity to give them to the jury other than to have them filed as an exhibit that they could refer to later at any time they wished, and if I could I'll move them into evidence one at a time so we have them straight.

THE COURT: You mean you're not going to tender the slides themselves?

MR. WALSH: There will be two I have to tender and I'll get to that because I don't have copies, but the majority of them I don't want to tender if I could help it. The first one is entitled, "Canadian Population by Province", and the best way is to put in brackets beside that, "(Numbers)".

THE COURT: Chart?

MR. WALSH: Yes, it's a chart, a schematic diagram of "Canadian Population by Province (Numbers)".

THE COURT: You're familiar with these, Mr. Furlotte? Do you have any objection to them going in as exhibits?

MR. FURLOTTE: No, I have no objections.

MR. WALSH: If we could have one exhibit number and perhaps number them one through whatever.

THE COURT: All right, so this would be P-164(1), the first one.

MR. WALSH: The next one, My Lord, would be "Canadian Population by Province", and in brackets you could put "(Percentage)".

THE COURT: P-164(2).

MR. WALSH: The next one would be "Profile of Canadian Ethnic Groups Per Cent Representations by Single Ethnic Origin".

THE COURT: P-164(3). We'll give that a short title, "Profile of Canadian Ethnic Groups".

MR. WALSH: The next one would be "Canadian Caucasian Profile - Geographical Origin".

THE COURT: P-164(4).

MR. WALSH: The next one would be "Percentage of Ethnic Population Distribution in Canada and New Brunswick".

THE COURT: P-164(5).

MR. WALSH: The next one would be titled "R.C.M.P. Caucasian Combined Database".

THE COURT: P-164(6).

MR. WALSH: The next one would be "Kingston Military Personnel and Dependents - Per Cent Composition by Birthplace".

THE COURT: P-164(7). Let's call that "Kingston Birthplace Distribution".

MR. WALSH: That's fine, My Lord, and the next one would be the same thing except it's done in a pie chart form.

THE COURT: P-164(8).

MR. WALSH: The next one would be "CFB Kingston and Canada - Composition by Province".

THE COURT: P-164(9).

MR. WALSH: That should be nine, My Lord, one exhibit number with nine. There's two other slides on the projector but when we get to that later in the testimony I could mark those at that time. Dr. Carmody, are you familiar with the databases that the R.C.M.P. presently have for DNA typing?

A. Yes, I am.

Q. Were you in fact tasked with looking at all aspects of the databases?

A. All of the statistical aspects as well as some practical aspects that I was curious about, yes.

Q. And the databases, how are they comprised, briefly, in terms of racial origin?

A. There are three samples that are taken from Caucasian populations and we have now three samples - I guess it's four samples from some native populations.

Q. When you say Caucasian, the person in the yellow

shirt between the two police officers in the accused's docket, what racial group would he belong to?

A. I would classify him as Caucasian.

Q. With respect to the Caucasian database, first of all, Doctor, perhaps we'll deal with this aspect and move on, were you in court this morning when Dr. Fourney testified with respect to the five duplicates in the R.C.M.P. Caucasian database?

A. Yes, I was.

Q. Were you aware of this phenomena prior to that time?

A. Yes, I was. This was in fact a discovery made when the databases were specifically and consciously searched to see if there were any duplicates in them.

Q. It was actually searched for that purpose?

A. Yes, it was deliberately looked for.

Q. In the manner in which the R.C.M.P. Forensic Lab are permitted to obtain samples, that is, the method they obtain samples by not having technicians go out into the Red Cross Clinics themselves, what if any expectation would you have as a population geneticist as to finding duplicates?

A. It's not entirely unexpected given the limitations of the fact that we are obligated, or the R.C.M.P. is obligated, to the Red Cross or in the case of the Vancouver sample to a hospital, to provide those samples anonymously. The forensic labs do not have control and are not able to go into those blood donor clinics and in fact specify the way the samples are collected. They are obligated to

work within the limitations of confidentiality and so forth that are required by the Red Cross.

Q. Were these duplicates found accidentally or looked at for that purpose?

A. They were found when a program was used that had been produced by the FBI that would search specifically a database to see if there were duplicates in there, and that was done to see, in fact to convince ourselves that there weren't any duplicates in there.

Q. And who is aware of this phenomena of the duplicates?

A. Well, virtually everybody in the forensic labs are aware of it. The people specifically involved in this case, Doctors Waye, Bowen, Fourney, Dr. Kidd, Dr. Shields and myself, were aware of these duplicates in the database.

Q. You were in court this morning when Dr. Fourney testified with respect to the enquiries and the technical tests that they did with those duplicates?

A. Yes.

Q. To actually confirm they were in fact duplicates?

A. Yes.

Q. From a population geneticist aspect and based on the technical tests that the R.C.M.P. did or ran on these particular duplicates, have you looked at the probability of those not being duplicates but in fact from different individuals?

A. Yes, I have. We've addressed that specific question quite directly in the same way that when duplicates were found in other databases they were addressed, namely that they went back to the

original samples of DNA that were still in the refrigerators and tested them again for a number of other genetic probes, and they were able to show that on something like 20 bands the duplicates matched. The probability of that occurring when the samples originated really from two different individuals is less than one in a trillion, so one would conclude that in fact these were duplicates and not from two different individuals, or if they were from two different individuals the individuals had to be identical twins.

Q. Just so we can udnerstand what a trillion is, how does that one in a trillion apply to the population of the world right now?

A. The population of the world, the human population of the world right now, is something a little bit less than six billion. A trillion is something on the order close to 200 times greater than the population of the world at the present time. That number of a trillion is in fact greater than the number of humans who have ever lived on the earth.

Q. That is the probability that those five duplicates came from different individuals?

A. Any one of those duplicates, that's right. It's the probability of less than one in a trillion that any two of those came from different individuals other than identical twins.

Q. What if any effect do the finding of the duplicates in the database have on the frequency calculations generated by the R.C.M.P.?

A. They would have quite insignificant effects on it when you keep in mind that the databases we're

talking about constitute some 970-odd individuals. Whether you have five individuals in that who happen to duplicate exactly the DNA profiles of five other individuals or not is going to have a quite insignificant influence on the frequencies that are used to make these calculations that we'll be talking about subsequently, so in terms of that I'm not worried at all or have any concern that these duplicates were in there when calculations were done or if you took those duplicates out to do the calculations. They would have a very insignificant influence on the calculations.

Q. In regard to the formulation of the Caucasian database, R.C.M.P. database, what is being attempted when you form a database for forensic purposes?

A. Well, one would like to be assured first of all that it represents the Canadian Caucasian population, and that means we would want to have samples in that database that derive from different geographic areas of Canada. We would want it to represent as much as possible a random sample taken from throughout the country.

Q. I understand, Doctor, that you have a number of slides and you want to provide evidence to the jury with respect to the R.C.M.P. Caucasian database and the population of Canada and the provinces and the ethnic origins?

A. That's right, I thought it would be best to just put it in context in terms of the composition of the Canadian population, how these databases were derived, where the smaples came from, and to do this in a graphical way I think it's probably most

efficient to do that.

MR. WALSH: My Lord, with your permission we'd like to operate the - perhaps, Doctor, if you would, we've found that if you stand between these two desks it's the best place in this court room. That way you don't turn your back to anybody other than the public.

A. This first pie chart and this data is taken from the Canadian census of 1986 -

MR. WALSH: For the record, this is a "Profile of Canadian Ethnic Groups - Percentage Representation by Single Ethnic Origin"

A. - and shows a very coarse breakdown of the Canadian population. You'll see that the main point I'm trying to make here is that the Canadian population is over 93% Caucasian. This gives you a little sense of the proportions of the other ethnic groups in Canada. Within this Caucasian group these are made up of British, French, other European, Arab, south and west Asian, mainly India and Middle East, Latin and South America and Central America.

The next slide shows, in fact, the breakdown of the Canadian Caucasian population, so of that 93% you could break that down into what is predominantly if people were to identify their origins - is predominantly British ancestry and French ancestry with a number of other groups in there as well. Keep in mind that this is derived from information where people would be able to say that they had single geographical origins. Many of us, including myself, have mixed European ancestry. In my own case it's Irish, German and

English and a couple of other things thrown in there if I went a few generations back, and that I suspect is not uncommon, indeed, amongst Caucasian population, and means that in fact the composition in Canada in terms of the freguencies of various genetic types is in fact likely to be some average of many of these ethnic groups that derive predominantly from Europe.

Now, to break that down geographically - we've looked at the ethnic composition. To break that down in terms of its geographic distribution this is by province. In terms of numbers as of the 1986 census the estimate of the Canadian population was 25 million odd there, it's now known to be bigger, but these numbers derived from that census.

The next slide shows this same pie chart -

Q. Before you leave that, you've said 25 million is the total population. That's total of all races?

A. All races in Canada, yes, that's the total population.

Q. And the numbers beside what appear are obviously provinces. What is the population of New Brunswick?

A. The population of New Brunswick in 1986 was 710,000.

Q. And how does that break down either in Canada or in the Province of New Brunswick in relation to sex?

A. Typically there are somewhat more females than males. Alas, males have a higher mortality rate and so you find that the typical composition in most areas of Canada or in North America is

roughly something like 51% or 52% female, so about half that number are male in Canada, so you'd say roughly 305 - let's say 300,000.

Q. You're talking about New Brunswick?

A. About New Brunswick, there, O.K., which is the green, perhaps appropriate to New Brunswick.

Q. That would be all age groups?

A. That would be all age groups, correct. This is the same pie chart broken down by percentages of the population that are found in different areas, different provinces and areas of Canada, and you will see that New Brunswick constitutes almost 3% of the population of Canada.

The next slide shows the ethnic composition, again from Canadian census data of 1986, comparing the ethnic composition in Canada versus New Brunswick. New Brunswick here are in the red bars, the blue bars are averaged over all of Canada, and you'll see there again of probably not great surprise that in fact the origins of people living in New Brunswick have a higher British and French component to them than in fact the general Canadian population averaged over all provinces, so there's an enriched composition here in New Brunswick of genes that derived originally from the British Isles and from France. You'll see that in the case of most other ethnic groups here, German, Italian, Ukrainian, aboriginal, Chinese, and so on, that in fact they are under-represented in New Brunswick. Again it's probably corroborating your general impression of people that you see and people that you know.

Now, in the databases that have been used in

the calculations by the R.C.M.P. and the databases that I've been involved with in analyzing, they are made up of 356 individuals from the Vancouver area, 92 individuals from the Ottawa area, and 526 individuals from the Canadian Forces Base in Kingston, for a total of 974 individuals here, so you see they span a good geographic area throughout Canada, and particularly I want to spend some time talking about this Kingston database which is the largest of the three, and that database of 526 people derived from personnel at the Canadian Forces Base in Kingston and represent individuals that come from different parts of the country. To try and give you an impression of how representative that is and how geographically widespread the origins of that database are, this next slide shows in chart 4 more - actually in summary number form, the percentage of people, of military personnel at the Kingston Base, that derive from various provinces and from the Northwest Territories, and there's an 8% component from outside Canada.

The next slide shows these same numbers in graphical form in a pie chart, namely that this is the birthplace of the Kingston military personnel and their dependents. This database was derived from a blood donor clinic held on the base and military personnel contributed to that as well as some dependents. To just look at this, one of the things to observe and an important part of my presenting this, is that you'll see that amongst military personnel in the Kingston database 5% of them derive from New Brunswick or had a birthplace

in New Brunswick.

Q. Why is that important?

A. If you remember in a previous slide that New Brunswick constitutes a bit less than 3% of the overall Canadian population, so this means that in fact at the Kingston Military Base there is a higher percentage of personnel present on that base from New Brunswick or whose birthplace is in New Brunswick than amongst the general Canadian population, so that this database likely, although we can't say with 100% certainty - likely represents a goodly number of people from the New Brunswick area, and unless people from New Brunswick, which I from my experience would think highly unlikely, were unlikely to donate their blood at a blood donor clinic, I would expect that in fact there would be more people from New Brunswick in this particular database than in fact there are proportionately people from New Brunswick overall in Canada, so the next slide attempts to compare these percentages, the percentages deriving from the different provinces as their birthplace in the Kingston - amongst the Kingston military personnel compared to overall in Canada in terms of number of people and provinces, so again here overall in Canada this histogram represents the number in percentages in Canada overall and in red you have the representation of people in the Kingston Military Base, and you'll see that in fact New Brunswick here, there are in fact more people present in the New Brunswick database than there are proportionately in Canada. You'll see the reverse is true, and in general,

in fact, an interesting thing to observe here is that the Maritime Provinces here, which are all on the left, in fact are all over-represented in that military database, again perhaps corroborating general impressions that in the military, particularly in the eastern part of the country in a military base, you would expect to see an over-representation of people there deriving from the eastern provinces. You'll see that Quebec is under-represented, Ontario is under-represented, and then as you go out west, again all of the western provinces are under-represented in this database, too. That is that the red part of the bar here is lower than the blue part of the bar. This is to establish the fact that in a database derived from the military in Kingston that we're likely to have a good representation from the Maritimes and certainly a good representation from New Brunswick.

Q. Now, in terms of Quebec you mentioned the under-representation in Quebec, but in terms of the actual percentages, in terms of the percentage of Quebecers in Canada and compared with the percentage on CFB Kingston, what if any opinion do you have with respect to how well they're represented on the CFB Kingston?

A. Well, while they're under-represented proportionately in terms of their proportion of Canadians, they are certainly not in small absolute numbers. You would expect that there would be a healthy representation in terms of absolute numbers in that database deriving from both the Province of Quebec and the Province of Ontario, but in fact

one would expect just looking at this kind of histogram that a percentage of roughly 30 - well, in the case - let's take Quebec first, that roughly something like 21% of the people in that Kingston database are likely to derive and say that their birthplace was in Quebec, and in Ontario perhaps a third of the people would have derived from Ontario as their birthplace.

Q. So the Province of Quebec would be represented in the -

A. The Province of Quebec would be represented almost certainly. Again one can never say with 100% certainty because there are always potentially sampling biasses but in taking a sample of - what was it, 526 people, from this base, the chance that you would not include people that constituted 20% or 33% of that population is highly, highly unlikely, so it's almost certain that there are a significant number of people from both Quebec, Ontario, and New Brunswick in that database.

MR. FURLOTTE: My Lord, maybe the Crown could set the basis for this witness giving opinions of this type of evidence. I've been hearing absolute certainty, highly, highly likely, and -

MR. WALSH: Well, I think that's something that the doctor is entitled to give his opinion of. Mr. Furlotte may not like what he's saying and he can do that in cross-examination.

MR. FURLOTTE: My Lord, only expert witnesses can give their opinions and the doctor has not been declared an expert witness in this field.

MR. WALSH: I think it might be appropriate - this is

kind of a surprise to me since Mr. Furlotte has had this information for many, many months. I think that perhaps it might be important, My Lord, if we could argue the issue in the absence of the jury, then.

THE COURT: Mr. Furlotte, you're going to have a chance to cross-examine on these - these are sort of -

MR. FURLOTTE: My Lord, I have no problem with the doctor presenting this kind of evidence as being a factual basis for their findings of the different representations, both in numbers or in percentage-wise. but as to forming opinions that New Brunswick is well represented into the R.C.M.P. database or that Quebec is well represented into the R.C.M.P. database, I do not believe that this witness has the expertise to give that opinion because his opinion in this area is no better than mine.

THE COURT: I wonder if we could get over this hurdle by the witness saying it would be - I would assume that. Would that express your -

A. If I might hopefully clarify things here, the opinions that I'm giving in fact fall directly within my area of expertise, contrary to what defence counsel is claiming. I have experience in demography, I am a statistician of sorts, and these opinions are based on statistical ideas, that the chance that you would not have representation in this database deriving from Quebec or Ontario or New Brunswick is based on statistical information that I have.

THE COURT: Yes. Well, I think we'll permit the witness to continue, Mr. Furlotte, and he's subject, of

course, to cross-examination by yourself.

MR. FURLOTTE: Well, I think before any witness, expert, can give an opinion in court he must also present the factual situation for the basis of that opinion. If he's prepared to do that, then I guess I won't have any complaint.

A. I could calculate for the Court the probability that you had 5% of a population that derived from a province and that if you took 500 samples that there were no individuals that constituted 5% from that province, and I would argue that that is less than a probability of one in a million.

THE COURT: Well, continue on in the present fashion.

MR. WALSH: Thank you, My Lord. Continue, Doctor, please.

A. Well, this pretty much summarizes what I had to say about the database and the origins of the database is, in my opinion, representative, and in fact very representative of certainly the eastern part of the country and that it's highly, highly unlikely, based on statistical knowledge, that in fact these samples would have omitted people from the Province of Quebec, Ontario, or New Brunswick.

Q. Thank you. Would you continue?

A. What I next have to say actually gets on a slightly different topic and it has to do with the binning approach of how we take the data that is derived from the samples and obtain the bin frequencies.

Q. Before we get to that, Doctor, if we could just shut the projector off I'll have a number of questions and then we could get into the binning method of frequency calculation. The DNA sites

that we're studying here with the forensic RFLP typing, does that have a factor in considering how representative your database must be?

A. These are random sites chosen along the DNA, chosen specifically because they show a great amount of genetic variation. These represent seven sites that are representative as far as we know of the human genome and are chosen to be on different chromosomes, are chosen to be from places where we know they are not genetically linked to one another in any physical way. We know that they represent a random choice of sites along the genome, sites that are highly variable, and we would expect that if we could use more probes and look at more sites that ultimately we would be able to show that every individual was completely unique genetically. With this number of sites we can't show that there's absolutely no two people that would ever have the identical pattern of these sites. Nevertheless, we can give some probability estimates of the likelihood that two people were the same and the conclusion about that is that they're very, very low, that it's unlikely that you have two genotypes chosen at random, looked at for these sites, that are identical.

Q. Because of these sites how representative must your database actually be because you're actually looking at these kind of questions, geographically?

A. Geographically we have looked at these sites in those three populations, the Vancouver, the Ottawa, the Canadian Forces Base at Kingston, and

when we analyze these sites and look at the frequencies of the different patterns that occur at all of these sites we see that in fact there is no statistically significant and no practically significant difference between Vancouver, Canadian Forces Base in Kingston, or in Ottawa; furthermore that there are very few differences between any of these samples and other Caucasian populations from around North America and in fact from Europe as well.

Q. How adequate is the size of the combined database that the R.C.M.P. has, the numbers from Vancouver, Ottawa, and CFB Kingston? How adequate a size is that for what we're doing?

A. The adequacy of a database can be determined by how precisely you want to know the answer. If I could give you the analogy again of taking a political poll, I think you would have the sense that if you sampled ten people from throughout Canada your extrapolation from that sample of ten is likely to be quite misleading. It could well be that they could all say they were in favour of one political party, and in fact, when you try to extrapolate that to the Canadian population it would not be very accurate. On the other hand, as you take larger samples you get more confidence, you get a greater precision in the extrapolation from a larger and larger sample to the total Canadian population or to the total population of the world, and so when you have a sample that is on the order of a thousand individuals which our total Caucasian database is - 974, if I remember the precise numbers - that in fact that sample

would allow us to put a measure of confidence around any of the estimates we have for any of the particular kinds of DNA profiles, and so long as you don't need that estimate below a certain amount, the size of 1,000 individuals or 500 individuals is large enough to be able to come up with estimates that are quite precise. They're never going to be exact no matter if you took a million. The only way you would have a completely exact sample would be to have sampled every single Canadian that way, and that would be a practical impossibility. We can't even do that for census data. We can never know that we've censused everybody in Canada in any census, a census is an estimate, and in the same way here we are estimating what the frequences of these particular types are throughout Canada from a sample of a thousand people, and necessarily when we do that there has to be some imprecision in that estimate.

Q. What if any statistical tests did you use to compare the Vancouver with Ottawa with CFB Kingston?

A. I use a test that is a likelihood ratio test. That is, it looks at the various bin freguencies that we use to calculate these numbers, and it compares the overall profile. It was as though you had two of those histograms only now for the different bin categories and compared Ottawa to Vancouver, Ottawa to Kingston, Kingston to Vancouver. You make all those comparisons, you can even compare all three at once, to see whether there is any difference between those that would not be the result of just a random

sampling process, a simple random sampling process, where again if you went into a population and took two samples from Ottawa the actual numbers are going to be a little bit different. If you took 84 people I think it was from Ottawa and you took one sample and compared it to another sample there's going to be some slight differences. Those would be simply sampling differences, O.K.? Well, when you compare Vancouver to Kingston, Vancouver to Ottawa, Ottawa to Kingston, you find that the differences between any of those samples can be strictly attributed to the sampling process, to the fact that there could be a randomness that is the result of sampling, so that there is no evidence of any geographic distinction in terms of the frequencies of this type from one part of the country to the next.

Q. Does the fact that individual communities in each province, particularly in New Brunswick, have not been sampled have any effect with respect to the validity of the estimates the R.C.M.P. are giving in the R.C.M.P. Caucasian database?

A. In my opinion they don't, and my opinion derives not just from these particular three samples, but we - and I'll show later that I have done calculations on various Caucasian samples that were obtained from the United States and that were obtained from Montreal, in fact, and you'll see that in fact there are no statistically significant differences in the inferences that you would draw, namely that any particular genotype and the probability of a match is going to be rare.

MR. WALSH: My Lord, it's five after three. I'm going to

move into the area of method of frequency calculation. I can continue or you could have a break.

THE COURT: I think we'll have a break now. Do you envisage finishing with this witness, your direct testimony, this afternoon?

MR. WALSH: Yes, My Lord.

THE COURT: Well, we'll still have a break.

(BRIEF RECESS - RESUMED AT 3:30 p.m.)

(ACCUSED IN DOCK.)

(JURY CALLED - ALL PRESENT.)

DIRECT EXAMINATION OF DR. CARMODY CONTINUED:

Q. Dr. Carmody, you had mentioned that you had looked at the Caucasian data in other places in North America, is that correct?

A. That's correct.

Q. We'll be getting into the results of that work later, is my understanding correct there?

A. Yes.

Q. Based on the statistical work, the experimental work, that you've done with respect to the R.C.M.P. Caucasian database, if there was no one - assume for a moment there was no one from New Brunswick in the R.C.M.P. Caucasian database, what if any effect would that have on your opinion as to how representative it is of Caucasians in Canada generally?

A. From just my knowledge and from just analyzing populations in other parts of Canada and throughout North America and knowing that virtually all of us derive from the same Caucasian populations in Europe predominantly, one would not expect a

great amount of difference in doing any of these calculations even if there was nobody in that sample that had derived from New Brunswick, which is highly unlikely, but given that hypothetical scenario I would expect it would make virtually no difference.

Q. I'm going to ask you, Doctor, to take us and the jury through the method of frequency calculation one last time in this particular trial. How is the frequency - we have evidence before that the frequency of one band is determined by a method called the fixed bin method.

A. That's correct.

Q. The frequency of having two bands together is determined by the Hardy-Weinberg equation?

A. Correct.

Q. And that's your probe frequency, and then the frequency from probe to probe, the total frequency of all the probes that match, is a product of each of those frequencies?

A. That's correct, the product rule is used to derive across different loci.

Q. Would you explain, please, and I understand you have a slide projector here, what we mean by binning or the fixed bin method of determining the frequency calculation for an individual band?

A. Right. I just have two slides to, I think, probably reiterate again what the fixed bin approach entails.

Q. Now, these two slides, My Lord, I don't have a schematic of those so I'm going to ask that they be marked as an exhibit.

THE COURT: Yes, we'll call - you're aware of these, Mr.

Furlotte?

MR. FURLOTTE: I haven't seen them yet but I -

MR. WALSH: I described them to Mr. Furlotte.

MR. FURLOTTE: I have no objections to their admission.

THE COURT: Incidentally, the last exhibit or the nine components of the exhibit, we called it P-164. It should have been P-165, I believe, so we'll renumber that to be P-165, 1 to 9, and the slides would be P-166(1) and P-166(2).

MR. WALSH: That's fine, My Lord. I'll just leave them in the slide projector and the Clerk could mark them later. Now, just take your time, Doctor, on this one.

A. Right. This first slide, don't be distracted that you're not seeing something there, have bad eyesight, it's just an attempt to show that when you look at an autorad you could divide the areas in that autorad up into arbitrary horizontal bins, we would call them. These are the so-called fixed bins and each of these lines would be drawn across at a particular size standard that we would derive from the size standard lanes on that gel, so the fixed bin approach is to say that if you then took and ran each of those 974 individuals in the database and produced autorads from each one of those you would then look at the place that the particular band in that lane fell within those bins. Now, here is a slide that shows the bins drawn on top of a typical autorad. This could be an autorad that was used in collecting the information for the database. You'll see that there are some individuals that have a band up in this first bin, another one that has a band down in

this, perhaps tenth bin, whatever, here. There are some lanes where occasionally you'll have individuals that have a single bin. For example, this lane right here there is only one single band so that individual we would say is a single band pattern, is likely to contain two bands that in fact are superimposed on one another, O.K., but now, what's done in order to obtain data in the database - you also see, by the way, that there are lanes here where the standard sizes are run to allow you to in fact decide where these lines should go across on that gel, so you can derive, then, by looking at a number of gels like this, in fact dozens of gels like this, exactly how many times you have for each individual along here a band that falls within, let's say, this first bin, a band that falls in the second bin. Now, you'll see on some of these this blot is a bit over-exposed, so some of these bands are quite broad and it would be somewhat difficult to see from this exposed autorad exactly which of the two bins this one would be assigned to, but it would be assigned to one or the other. Typically in this case it would be assigned to one bin or the other based on the computer scanning of that gel that would allow you to, from its size estimate, place it in one bin or the other bin, so this would be done for each of those 974 individuals for each of the five probe loci that are used to do these determinations, so this describes, then, how you would derive this database, and these are called fixed bins because those lines are always drawn at the same sizes. There is an alternative type of

technique that's used in the U.K. where you have floating bins where in fact you draw an interval on either side of any particular band and then score how many other bands fall within that, and so it's called a floating bin because you don't have fixed values like this, but another point I want to make on here is that you can see that in these two instances here you have two bands in those two separate individuals that clearly fall in that same bin. Unambiguously they would be assigned to this same bin here. However, you can see visually that they don't match, and that's part of the conservative nature of this technique, namely that there can be a number of actual different sizes that would be present in different individuals that would really not be a visual match, so if you saw them adjacent to each other they would not be called a match visually. Nevertheless, they are placed in that same bin and it means that the frequency of that bin is not just for bands that are exactly and precisely this size or precisely and exactly that size, but in fact are an amalgamation of a number of size bands, so it means the frequency of that bin, that fixed bin, is actually higher than it really would be if we used bins that were narrower in size and in fact would separate this band from that band and put those in separate bins, so that's part of the conservative nature of this process of fixed binning, and also keep in mind that the width of these bins, these fixed bins, averages close to 10% in terms of the size of the bands that are in them. That is that the width of that fixed bin is

considerably wider, in fact on average about twice as wide as the match criteria. That is that two bands to be called the same have to be much closer than in fact the two bin boundaries here. If you had - as I indicated for these two examples here, these would not be called a match even though they fell in the same bin, so the bin sizes are considerably wider, and is a part of the conservative nature of this process.

In using the floating bin approach, which is not being used in this case and which is used in the U.K., you would come up with numbers, in fact, that are smaller than the numbers you come up with in the fixed bin approach, and when you start with smaller numbers which means when you multiply those together the net product of all those is going to be still smaller, and that would lead to, in fact, a smaller and rarer number than you would get with this fixed bin approach, so the fixed bin approach has built into it this conservative quality to it that you're always and you're knowingly and consciously using numbers that you know are larger than the numbers really would be if you were able to use a finer scale fixed binning.

Q. When you say conservative in whose favour are you talking?

A. By conservative I mean that you're going to come up with numbers that are not as rare, so that that would work in the interests of the accused in these cases, generating a number which would not be as rare as it would be if you used a finer scale bins or used the floating bin approach.

Once you have that database now that's been derived from those 974 individuals, and in fact, that the first instance those separate three populations are kept separate like that, statistical tests can be done, and you can test, for example, whether the occurrence and frequency that you observe a band in this category is correlated in any way with the presence of a band in any other category; that is, whether in fact the occurrence of a band in this first bin is statistically independent of where the other band would fall, and those tests are really tests of what - you've heard the term and what seems to be a complex term, this Hardy-Weinberg equilibrium, is really a notion that goes back to the question of whether in fact the occurrence of bands in these various bins are like a random process where you just sprinkle two bands down in bins at random which would be independent and would be in Hardy-Weinberg equilibrium, or whether in fact there's some correlation where certain bands that fall in one bin tend to be correlated with a band falling in another bin. When you do those statistical tests, and I've done those on each of the three databases, you find that in fact there is absolutely no statistical evidence that the bands fall into categories in these fixed bins that is anything other than random. The tests have a limitation in how powerful they are because you only have a sample size of less than a thousand, 974, so they're not as good as if you had a sample of a million, for example. You couldn't detect very slight correlations. There could be very,

very slight correlations that you could only detect if you had massive sized databases, but there is no really strong deviation from random expectations and so we can say statistically that these - a presence of these bands in different bins is in fact meeting statistical randomness and therefore congruent with some idea of the Hardy-Weinberg equilibrium generating these frequencies in the proportions that we would expect.

Q. That permits you to use what equation?

A. That permits us to use the equation where we in fact can calculate from knowing the frequency of - for example, in this lane, the frequency of that bin in the Canadian population to that bin in the Canadian population, and therefore generate an estimate of the time that we would expect to see that particular combination of bands, one in that category and one in that category, and we can calculate that by using the 2p times q, or the Hardy-Weinberg prediction, where we have to multiply that prediction by two because when you see this there is no way of knowing which of these two bands derive from the mother and which derive from the father, so that if this band derived from the mother and then this one from the father the probability of that would be p times q, but the reverse situation would have equal probability of occurring, that is that this band derived from the mother and that band derived from the father, and so you have p times q plus p times q, and when you put those together it's just two times p times q, which is the Hardy-Weinberg prediction of the genotype frequency, the genotype being the two

bands that you see here versus the individual bands that would be the product and the result of probing one particular copy of that in the individual.

Q. For our purposes, Doctor, correct me if I'm wrong, what that permits you to do is calculate the probe frequency for each - for each match you have at each probe you can calculate the individual probe frequency, is that correct?

A. That's correct. This would be for one particular probe. In fact, this is an illustrative gel done on D1S7. I believe that this is just a gel that was used in a database, I'm not sure what the origins of this particular gel are -

Q. You're using it to -

A. I'm using it for illustration purposes, it is not a gel that has any other bearing on the case specifics in this trial.

Q. O.K.

A. When, in addition to being able to get that information on each of the probes that you've been able to probe in your DNA samples to be able to establish whether two individuals match and what the frequency of that match is, you then look at another probe site and do the same thing, 2pq for that probe, 2pq for the third, 2pq for the fourth, 2pq for the fifth, and the net result is that you can then say, well, if there is statistical independence between what you expect at one probe site and what you expect at another probe site you should be able to multiply those two estimates together because they're statistically independent of each other. Now, I have done statistical tests

on the database to attempt to answer that question on whether what you see at this particular locus, at this particular probe site for that individual, shows any correlation with what would be shown for another probe site. That is to say whether when you found a band in this bin here and a band in that bin there, whether when you looked at another probe site that tended to show correlation with where the bands were for the other probe, and that if it did show correlation you would say that there would be linkage disequilibrium, that is that they wouldn't be independent of each other. The tests that I have run show quite clearly that in fact there is statistical independence of what is happening at one probe site across to another probe site, which is what we theoretically would expect given the fact that we have populations that have come from various places, have mixed together for several generations, and that derive from populations where even if you went back to Europe you don't find very great differences in our historical ancestral populations, so that the lack of that linkage disequilibrium and therefore the linkage equilibrium that we see by these statistical tests allows us to apply this product rule and be able to multiply the results of the Hardy-Weinberg calculation on each probe site by one another in this product rule to be able to generate an estimate of the probability of the combined genotype, what was present at this locus with what's present at the second locus, the third locus, the fourth locus, and so on, and that's the way the calculations in fact are

generated that we'll be using later on in the discussion.

Q. So to understand, Doctor, just correct me if I'm wrong, what you've described here, the binning process, is for the purposes of determining the freguency of each band that you see, then you - to test for Hardy-Weinberg equilibrium to see if each band that you see is independent of each other so that you can multiply them together using the Hardy-Weinberg equation?

A. That's correct.

Q. And that gives you your probe frequency?

A. The frequency of that particular combination of two bands, the genotype frequency at that locus.

Q. And then you did a test for linkage disequilibrium which is really a test to see if one probe frequency is independent of the other probe frequency, and so on, to permit you to multiply them across?

A. Right.

Q. These tests that you did, Doctor, are they things that just sprung out of your mind or were they recommended in the scientific literature?

A. They are recommended in the scientific literature. A statistician in particular at the University of Minnesota, Dr. Seymour Geiser, has suggested using the kind of test that I've used, it's called a likelihood ratio test, it's a non-parametric test that allows us to see if there is any great amount of statistical deviation from either of these assumptions, and when I applied that to the data for these probe sites for these populations I did not see any evidence that there was deviation,

strong deviation. The tests are not all that powerful, as I described earlier, really only having a sample of a thousand here, and when you consider all the possible combinations there are more combinations possible, in fact, than you actually have in your sample, so that you have to make some inferences again and they're not going to detect all weak amounts of deviation, but given that limitation and the lack of power in the tests they nevertheless showed that there was no strong deviation from what you would expect if everything were independent, and so it justified in my mind, and I think to the mind of anybody with statistical background, that in fact what we were doing was a valid procedure with this data, that is to multiply the probabilities within loci by using the Hardy-Weinberg equation and then multiplying that number across loci to give the product and the net estimate of the frequency of that genotype.

Q. You were saying that the formulas you use will detect strong correlations, strong deviations?

A. That's right.

Q. What if any effect would slight deviations that you can't pick up have on what we're doing here?

A. Well, slight deviations could work in either way; that is, that they could make your estimates more common than they should be, they could make your estimates less common than they should be. That is, that they would add an imprecision to your estimates.

Q. And what if any way do you compensate for that?

A. Well, the main way that that is compensated for is

by using that fixed bin approach where we know that there can be several different sizes that we would put together in that bin, and we know that that's being conservative so we start off with a number that is going to be larger than the number that we know really should be used in these calculations if one wanted to be meticulous about it, so we have that conservative element right at the beginning where the fixed bin is being generous in the frequency estimate and that would tend to propagate through the calculations so that when you multiply one by the other, multiply that by two, do that for every probe site, multiply then all those five numbers together, because you're starting off with a number that is deliberately larger than you actually know is the case, that in fact the number that you generate is not going to be as rare as the number really should be if you were more meticulous and used finer scale bins. So that's an attempt to be conservative and to in some way compensate for the fact that there could be slight amounts of deviation statistically that could make the imprecision such that in fact they should be more common or more rare, so we go on the side of making it more common.

Q. Doctor, I understand you did some calculations with respect to the - first of all, did you do any calculations with respect to the best estimate frequencies that the R.C.M.P. generated in relation to particularly the four and five-probe match in this case?

A. Yes, I have. I was given John Bowen's data.

I was not involved in calling the matches or determining which bins except I was given the information in terms of the estimates of the size of the bands that were derived from John Bowen's work and I then did independently the same kinds of calculations and, in fact, the identical calculations that he did, and found and corroborated indeed that there was no arithmetic mistake in his calculations and that in fact he was using the protocol that was part of the R.C.M.P. protocol where if a band fell very close to a bin boundary, that is if it fell within a 2.5% size of a bin boundary, you looked at the frequency of both bins, not only the one that the band fell in but the adjacent one that it was close to the boundary of, and if that other frequency in the other bin were larger than the one it actually fell in you actually take and give the benefit of the doubt and take the larger of those two, so that's a second conservative element, and that was done, as I remember, in the case of Mr. Legere's genotype, for one of the probes. It fell close to a bin boundary and we used a more generous estimate of the frequency of that bin of the adjacent bin. I corroborated that in fact that was indeed done and it was done properly and I came up with estimates for the combined genotype where in some specimens you had only four probes that could be looked at because of the amount of DNA that was present, and in the case of the five probes I calculated the frequency of that as well.

In addition, as a statistician I'm aware, and perhaps more aware of the fact that when we

generate this number at the end that number has an imprecision in it. It not only has a deliberate imprecision in it because we've started off with a number that is greater than we know it really should be, but we also know that based on a sample of close to a thousand individuals there is going to be an imprecision that results from that, a sampling error that results from that, and that can be very well inculcated into these results by calculating what we would call this confidence interval, this 99% spread around that estimate that we've made. That 99% spread says that well, if we were to go back and take another sample of the same size that we use to generate these frequencies and go through all the gyrations and do the calculations, if we generated another set of estimates and did the same calculations again we'd be able to say with that 99% confidence interval that 99.7% of the time, in fact, we would come up with a number that fell within that range, so it conveys a sense of what we call statistically the robustness of that estimate; that is, how sensitive that estimate is to going in and taking another sample. If that were to bounce around, if that confidence interval were very, very wide, which would be the result of having a smaller sample, we would then have less - would be able to have less confidence in that particular value. In these particular cases I did that calculation and I have it summarized in tabular form if we wanted to get into that at this point, or I leave it up to you.

Q. That's fine. I understand that you have it on

the overhead projector, you have it on an overlay?

A. That's right, I have it in an overlay and I have it in a Xerox copy to submit as an exhibit.

MR. WALSH: My Lord, I have shown this to Mr. Furlotte. Dr. Kidd testified with respect to these. I have a Xerox copy of the overlay that the doctor is going to show to the Court and I would submit the Xerox copy as an exhibit. I understand that the Xerox is an exact duplicate of the overhead you're going to be showing the Court?

A. Yes, it is.

THE COURT: So this would be P-167. How would this actually be described on the exhibit list?

MR. WALSH: My understanding, My Lord, it's a summary of the four and five-probe match, a statistical summary of the four and five-probe match generated in this case, as well as a comparison to other Caucasian populations that Dr. Carmody compared these statistics to. That's not very much of a summary, unfortunately.

THE COURT: In three words.

WITNESS: I have a title on the table, in fact, if you want to use that.

THE COURT: Is there a title? What is the title?

MR. WALSH: It just says Mr. Legere's statistics, and that's not much of a help either. It's just a summary of statistics associated with this case.

THE COURT: Yes, frequency statistics, would that do it?

WITNESS: And then I have the two slides that were used that we did not have copies of.

THE COURT: Those are P-166(1) and (2).

WITNESS: These are for all five probe sites. You'll recognize these numbers, the D1S7 and so on

through the D17S79. This column called R.C.M.P. here in fact represents the estimates in the middle that John Bowen had generated and that I was able to corroborate. Around them I've indicated what the 99.7% confidence interval is. That is that that's the interval and that's the span that we can be 99.7% confident in that if we were to take other samples of the Canadian Caucasian population of the same size that we would derive numbers that would fall within that interval 99.7% of the time. We can never be - well, we could have wider intervals and it would give us a higher confidence, but this is a convenient one to calculate it, it's three times the standard deviation on either side, and it's one that's commonly used in statistics to give a sense of the precision or the imprecision in that estimate. A point that I'd like to make here is that when we say things like one in 78 for the freguency estimate of that genotype it doesn't mean that we know it's exactly one in 78 and not one in 77 and not one in 79, but in fact it really is somewhere between one in 56 and one in 129, so that gives a sense of the imprecision, and in the same way for the other four probes I have the best estimate and I call that the best estimate because in fact given the information that we have that is the best number that we can generate but that gives a sense of the fact that we don't know that with complete precision, and in order to get that more precise we would have to do larger and larger samples, and what happens is that you need to basically quadruple the sample

every time so we'd have to go to 4,000 in order to make this confidence interval roughly half of what it is here, and it becomes a question of diminishing returns. How accurately do you really need to know that when in fact the calculation tells you when you multiply these centre ones together to generate this either for four loci one in 5.2 million, or for five loci, one in 310 million, that in fact you're saying anything other than the frequency of that particular genotype is rare.

Down here I've indicated again, and one can do a similar type of calculation - based on knowing what these confidence intervals are, you can do a similar statistical calculation to see what the confidence interval is on this number that's generated from multiplying those together, and you'd have the sense that when you take numbers that are imprecise and you multiply them together, indeed the product of those is going to have a wider confidence and imprecision on it than any of them individually, because it can magnify like that.

Now, what Dr. Kidd did, in fact, to do a very conservative calculation, you can take the most frequent, O.K., that is one in 56 is less rare than one in 129. You could do that for each of these confidence intervals on each of the separate loci and multiply those together and you come up with a number here that in fact is more common than one in 3.7, and I think if you did that - I actually haven't done that calculation but I think he indicated that if you do that you come up with

in this case something like one in 17 million. You could propagate that through by multiplying. What I've done here is the statistically correct, meticulous way of doing it, where in fact you wouldn't expect always for these estimates to be off in the same direction. That is that statis-tistically it is highly unlikely that if these were in error that you would always be down on this end, that is that sometimes you might be down on this side, sometimes you might be up on that side, if the estimate were wrong, and the confidence intervals on the four-probe match and on the five-probe match here are what you would expect to see if you propagated that kind of error through the multiplications, and so down in these lower parts of this column in the next to last cell and in the last cell here you'll see that the one in 5.2 million has a confidence interval on that is anywhere from one in three million to one in 17 million here, and in the same way here for five probes it's one in 175 million through one in 1.3 billion, that is. I didn't write billion in there but in fact it's 1,300 million, which is 1.3 billion, O.K. So I think, and what I wanted to convey with this information, is that indeed we don't know that this number is bang-on and exact, and in fact, we know it's likely not to be precise and exact, but we can give some sense of the fact that even if we allow for some error in the sampling that in fact we're still talking about a one in three million for the four-probe match or a one in 175 million for the five-probe match. I think it leaves you with the impression that

indeed the calculation and statistically the interpretation would be that the probability of those four loci matching is pretty rare. The probability of the five-probe match is even more rare, and they're both pretty rare, so that this is saying we can have pretty good confidence that this is not happening by chance; that is, the frequency of this particular genotype we would estimate to be, you know, one in five million, one in 300 million - pretty rare.

I want to move on to the right side of that table because what I've done here is to give you a sense of if you did those same calculations for different databases, with databases that I personally have not been involved with collecting and verifying and doing anything with, in fact. Well, I have been a little bit with the old data-base but it's quite premature to say much about it, but you could take the information that we had from the autorads that were run in this particular case and do the same calculations from a sample of some - I think it was about 800 individuals derived from a blood donor clinic in the City of Montreal. It was taken, I'm told, from a specifically French-speaking area. Although it's not verified that indeed all the individuals that contributed here are Francophone it nevertheless is highly likely that most of them are, that these numbers you would calculate in the same way as I did on the R.C.M.P. database. Rather than one in 78 you get one in 83, rather than one in 59 you get one in 58, rather than one in 68, here you get a more rare occurrence, you see, whereas in the

R.C.M.P. database it's one in 68, here it becomes one in 87. Where it was more rare for this locus at the R.C.M.P. database, one in 108, it's now one in 71. The one-eighth becomes more rare here one-twelfth, and you then multiply those through and you come up with the four-probe estimate of one in 6.1 million compared to one in 5.2, of the one in 310 it's one in 356.

You'll see that these are not really different from one another. Indeed, one in five million is different from one in six million, but at this level and given the imprecision in this estimate you're getting numbers that fall well within the confidence interval here. This could well be numbers that derive from a separate sample of Caucasians from virtually any place in Canada, so it suggests very strongly that we're not going to find any significant differences, forensically significant differences, when we sampled populations in French-speaking Canada versus English-speaking Canada.

Again I had access to some other databases from North America. These were provided to me by members of TWGDAM from various places. We have a sample from Minnesota here where again you can look at the numbers. Indeed, they differ numerically, but the net upshot is that rather than one in five million we get an estimate of one in eight million - not statistically anything to really get excited about. Here the one in 310 becomes one in 402. I had a composite sample that the FBI has put together from taking 100 individuals from about five geographic areas in the United States

and is their database that they use for their calculations for Caucasian database and you come up with these numbers. You can look across and you'll see that they jump around, there are differences. The net results are, in fact, you come up with still rarer estimates. Are these estimates really significantly different from that estimate? The answer is no.

In the case of a Florida sample, unfortunately I did not have information on one of the probes. In their particular protocols they don't typically do D10 and so I wasn't able to get that but I included it just to give you a sense of the variation you're likely to find when you take and apply these samples to different Caucasian databases. The net result is that you don't all of a sudden when you do that come up with a number that is remarkably more common; that is that it's one in a thousand or even one in 5,000. You still stay in very much the same range of your estimates here. That gives us a further corroboration that in fact these numbers have a robustness to them that if we were to take samples from twenty other places throughout North America, twenty other places throughout Canada, look at Caucasian databases, we are almost certainly going to come up with numbers that are very rare, as these would indicate, and so I attempted to pull this together in this kind of table form to give you a sense of the imprecision and yet the precision and the robustness of the conclusion that in fact these are a rare occurrence to have two different individuals show that same identical pattern.

I think we could get the lights back on. Do we have some questions about the overhead, further questions?

Q. No, that's fine. Do you know Dr. William Shields?

A. Yes, I have met him on two occasions and have spoken with him, yes.

Q. Are you familiar with testimony or evidence that he's given with respect to the evidence in this particular case?

A. Yes, I am. I was present at the voir dire when he testified and have read the transcript of that testimony.

Q. Are you familiar with any tests he has done comparing the R.C.M.P. and the FBI Caucasian data?

A. Yes, he has. He's done some statistical tests, in fact, similar tests. They're Chi square tests, they're called, similar tests to the ones that I did, and he did find, as I found, that for some loci when you compared the bin frequencies, when you just compared the profiles over the bins at certain loci from our Canadian database to the database that the FBI uses, you found that were some statistically significant differences.

Q. What if any bearing does that have forensically, in your opinion?

A. Well, I think as I've demonstrated by this chart, certainly in this particular case it leads to no forensically significant difference; that is, that some of the bin estimates are going to be lower in one database, higher in another, and vice versa, that the two databases are quite similar though statistically different, that is that you would not say statistically that they derive from just

taking two samples from the same place. You can see some differences but when you do the calculations, because some bins are higher, some bins are slightly lower in the two databases, when you multiply them together and you do the multiplications across different loci, some loci of which are completely identical, the net result is that the database estimates that you derive are really not different, as I've indicated in that table, whether you use the FBI database, whether you use the R.C.M.P. database, whether you use a database from Montreal or Minnesota.

Q. What if anything is your understanding or your interpretation of Dr. Shields's opinion on that aspect?

A. Dr. Shields, my understanding is, feels that when you find statistical differences in the bin freguencies that that is an indication that there is some what we would call substructure; that is, that there is some geographic differentiation, or that there is some pattern of matings going on within populations that would not be consistent with them completely being randomly mixed.

Q. Now, so we're clear, this is with respect to comparing the R.C.M.P. to the FBI database?

A. That's correct.

Q. You did the same kind of tests comparing Vancouver with CFB Kingston with Ottawa, and what conclusion did you find there?

A. I found no statistical differences for any of - in fact, I looked at six probe sites, one probe of which is not used in these calculations, and for all six probe sites there was no statistical

significance between any of those combinations of Vancouver to Ottawa, Vancouver to Kingston, or Kingston to Ottawa.

Q. But when you compare R.C.M.P. to the FBI there is some statistical difference, significant difference?

A. As I remember best for something like two of the six probes there is a statistically significant difference, I don't remember the exact number.

Q. O.K., now, if you could just finish that up, I think I had interrupted you. Your interpretation of Dr. Shields's opinions on that?

A. My interpretation of Dr. Shields's interpretation of that is that that would indicate that there is some substructuring: that is, that there are some differences detectable genetically between the two samples, between the two populations that those samples derived from. My sense is that though there is some statistically significant difference there it does not lead to any difference in your forensic conclusion and -

Q. Which is?

A. And the forensic conclusion is that individual genotypes, regardless of how you do the calculations, are rare.

Q. What if any other aspects of Dr. Shields's opinions in this particular case, if any, have you addressed? I'm particularly interested in background band sharing. That term came up earlier.

A. Yes, Dr. Shields looked at the autorads and found that, I guess it's indicated on this particular summary chart, instances where some individuals

actually shared similar band patterns, or in fact, virtually shared bands, between individuals that were unrelated to each other. He did a calculation and from that drew the conclusion that because of the coincidence of getting band sharing to the degree that you see in this chart amongst people who you could say were a random set of - in this case what is it, I guess four people, I believe, two of these specimens derived from the same individual so that they would not be used twice, you could only use one of those two.

Q. So we're clear, Doctor, without the chart, what are you referring to in terms of what individuals would he have used for his sample?

A. He had used individuals for his sample people that had been run on the autorads. In most cases they were a victim and the accused, or in one case I believe it was somebody who was an alternate suspect at one point or whatever, but he was suggesting that because of the amount of shared bands that you saw in this sample of people -

Q. That's single bands?

A. That's single bands, that that was inconsistent with this population that they were drawn from, being the same as the Canadian Caucasian sample that we used to generate numbers in our database. I did some further analysis, and in fact in conjunction with Dr. Kidd, whose testimony you heard earlier this week, I did some calculations based on what you would expect to see in a sample of nine unrelated individuals taken from the Caucasian database that we had to work with, and in fact I was able to show that the amount of band

sharing that you actually see when you compare this group of nine people and look at them in all the pair-wise combinations of one with two, one with three, two with six, whatever, when you made all those comparisons for all five loci, which Dr. Bowen did for me, the number of times that you saw bands being shared was not statistically greater than the number you would expect if the population that these nine individuals came from were nine random individuals drawn from our database that we used for the calculations at the R.C.M.P.

Q. And what conclusion can you draw from that?

A. I would draw the conclusion from that is that there is no enhanced degree of either inbreeding or population subdivision, population sub-structuring, present in the area from where these nine individuals were drawn than there is in the remaining part of the Canadian population in general, and in fact, the numbers were completely consistent with there being no evidence at all in this data of there being any inbreeding or there being any difference between this population that the nine were drawn from and the population that we had put together for the R.C.M.P. database, and so I feel that from that analysis of band sharing where we took into account all the possible combinations, and unlike what Dr. Shields had done where he looked through the autorads and picked out a few instances where there was band sharing, indeed if you do the calculations just on those isolated pre-selected cases where they were seen to be shared and look at those as though they were a random sample when they were not because

they were selected because they shared bands, indeed the probability is very low that you would get that exact observation, but when you put it in the context of all the comparisons that can be made in the total set of nine unrelated individuals and you consider all the ways and what the expectation is for the number of times you would share bands, the number of times you would share bands is not statistically unusually high at all, and it's perfectly consistent with that group of nine individuals and indeed with this group of four individuals having been chosen from the Canadian Caucasian database that was used to generate the probabilities that we use in the chart that I had up on -

Q. When you were looking at how to calculate the incidents of single bands matching did you consult with anyone in that regard?

A. Yes, I did, and it was only through, in fact, the collaboration between Dr. Kidd and myself in quite a dramatic way while he was here, and we did it partly by fax this morning, there were a couple of faxes that went back and forth, and indeed, we were able to come up with the proper algebraic formula which I -

MR. FURLOTTE: My Lord, I'm going to object to any hearsay evidence in relation to case specific evidence. I will not have any opportunity to cross-examine anybody that this witness has maybe consulted with or conferred with in relation to his case specific evidence, and if he's going to give his opinion in relation to Dr. Shields's testimony, then I would submit, My Lord, that he

gives his opinion and nobody else's.

THE COURT: Well, isn't he talking now about something he's done himself today?

MR. WALSH: Yes. My Lord, it's four-thirty, I have a little bit more to go, we'll never finish it within a reasonable time of four-thirty. It might be an opportune time to break for the day and we can discuss this particular matter and we could start afresh in the morning.

THE COURT: Yes, well, let's do that, and if there is any new material here, Mr. Walsh, perhaps you could - have you any new material that you could provide to Mr. Furlotte?

MR. WALSH: Well, other than a formula, I can provide that. It wouldn't make any sense to Mr. Furlotte or me, but I'm certainly going to provide it to him - I will.

MR. FURLOTTE: O.K., we'll discuss this in the absence of the jury.

THE COURT: Yes, all right, we'll let the jury go home. We'll see you in the morning at nine-thirty. Just before the jury goes, the Crown will be finishing its end of the -

MR. WALSH: Yes, I expect to be finished very early in the morning. I don't expect to be very long in the morning.

THE COURT: And tomorrow is Thursday, isn't it? You wouldn't be going into Friday? I mean you're -

MR. FURLOTTE: I was hoping to be able to finish with this witness tomorrow.

THE COURT: Yes, well, we could assume safely, I would think, that the Crown's case would conclude tomorrow? Mr. Allman or Mr. Walsh, is that -

MR. ALLMAN: If Mr. Furlotte finishes. We've got one other matter that I need to discuss with Mr. Furlotte but it will be very brief.

THE COURT: Yes, but that means that then we'd be finished on Thursday evening and then of course when the Crown's case is finished I'll be asking the defence if they're calling evidence. There's nothing likely to happen on Friday, as I take it. We'll probably be adjourning from Thursday until Monday morning, is that the - I've discussed this earlier with counsel a couple of weeks ago in chambers. We seem to be fitting into that pattern. What I want to do is just let the jury know that probably when you leave here tomorrow you won't be coming back until Monday morning. I'm not going to forecast beyond that at the present time but that will - you will be on call on Friday the same as you have been.

MR. FURLOTTE: I was just going to say hopefully you're not setting them up so I can disappoint them.

THE COURT: Oh, well, they will always be prepared to work on Friday this week if you need them, Mr. Furlotte. O.K., we'll see you in the morning at nine-thirty, please.

(JURY WITHDRAWS.)

THE COURT: You don't want to discuss anything now?

MR. WALSH: No, My Lord, what we could do is I could just so we have an understanding of Dr. Carmody's evidence and we can put it in the context of Mr. Furlotte's objection and we can see where we're going to go tomorrow on that, I could perhaps ask

a few more questions to try and flesh out this particular area to see what we're dealing with.

THE COURT: You'd appreciate that, Mr. Furlotte? I mean it would give you some idea - this is on a voir dire?

MR. WALSH: Voir dire, yes, My Lord.

THE COURT: We'll have to have the witness sworn on the voir dire.

MR. FURLOTTE: First of all, My Lord, my understanding ofthe voir dire in this case was to see what evidence would be admissible before this Court and if this type of evidence would be admissible before the Court, O.K.? Now, because of the evidence we went through in the voir dire and because of the disclosure by the Crown I felt that I was prepared for trial in order to answer the evidence that was coming before this Court. Now all of a sudden I find out that these witnesses are coming to court and bringing into evidence something that I was totally unaware of, totally unprepared for. Not only is he attempting to bring in hearsay evidence with this witness, he's attempting to bring in new evidence, and I don't appreciate being taken by surprise. If the Crown was aware that this was the type of evidence Dr. Carmody was going to come to court with today, then I think I should have been advised as soon as the Crown was aware of it and as soon as Dr. Carmody was aware of it.

MR. WALSH: I could ask a few questions of Dr. Carmody to perhaps help us out, My Lord.

THE COURT: Let's hear this witness now on the voir dire. This is not being admitted at this stage and it

will give Mr. Furlotte an idea.

DR. GEORGE CARMODY, being duly sworn on the voir dire, testified as follows:

DIRECT EXAMINATION BY MR. WALSH:

Q. Dr. Carmody, with respect to your calculations in regard to whether or not there's a high incidence of background band sharing, single band sharing, on the sample population, when did you first become aware that there were calculations like that being made in relation to this case specific evidence? When was your first - you first became aware of that?

A. I first became aware of that during Dr. Shields's testimony at the voir dire, and I guess that was in the end of May.

Q. Did you have any inclination of the fact that that was in fact what he was going to testify about?

A. No, I did not.

Q. And single background band sharing, what normally does that - what system does that apply to, what type of typing system does that normally apply to?

A. Where I've seen it previously was in the multi-locus probe situation that had been used in the U.K., and that was originally developed by Alec Jeffreys. I had never seen it, in fact, applied to the single locus VNTR situation until I heard Dr. Shields testifying.

Q. The Crown would have had opportunity for rebuttal on that particular issue. Would you have been able, based on what you heard that particular day, to testify on that particular aspect five minutes after the defence -

A. No, I would not have been, and indeed, it has taken me several months of pondering the situation and analyzing it before - and in fact, as I testified a few moments ago, it was only this morning that we were able to resolve it into a formula that would give the correct estimate.

Q. Before, actually, this morning in actually getting a formula to arrive at the correct estimate you had said you had given some thought to the problem that Dr. Shields had presented, or his calculations?

A. Yes, I had, and I had come up with some approximations and some formulae that I knew were not completely accurate but that I thought maybe could be used but I was not sure until I had time to confer with Dr. Kidd that we could actually arrive at something that was a definitive way of approaching it.

Q. You mean definitive meaning -

A. That it would be the scientifically correct, mathematically correct, way of looking at this particular problem which is an element in probability theory called, as I think Dr. Kidd testified, the birthday problem. I had alluded to that situation in my testimony in the voir dire where I was making some metaphorical comparisons to what Mr. Furlotte had had me calculate in my cross-examination at the voir dire, and I tried to convey the fact that what he was having me calculate was not what in fact needed to be calculated, but at that time and until, in fact, just this morning, I was not able to resolve exactly how that should be calculated.

Q. The exact method of calculation, but before that did you have any opinions, tentative opinions, with respect to whether Dr. Shields was correct in his -

A. Yes, I did have tentative opinions and I was quite convinced that the approach that Dr. Shields was taking was incorrect and that what he had calculated was not what he was interpreting to have been calculated, but yet I could not come up - and though I knew it was incorrect and the numbers that were being generated by that were not correct I nevertheless was not able to come up with a reliable alternative calculation that I felt confident in being able to show to the Court.

Q. Are you confident in the calculations -

A. I am confident in the calculations. They were a collaboration between Dr. Kidd and myself and I think they are of great enough importance that they're likely to lead to a publication between the two of us.

Q. Collaboration between two scientists, is that something that is normal in scientific work?

A. Very much. If you look at both Dr. Kidd's list of publications and my own list of publications, I know in my own case over 90% of them are done with various co-authors. I believe the same would probably hold for Dr. Kidd's. I've never seen Dr. Kidd's entire list but I would suspect the majority of them are jointly co-authored.

Q. Do you have a copy of the formula that you've derived with respect to this background band sharing?

A. It is here.

Q. If you would, please - do you have it on an overhead?

A. I have it on an overhead.

Q. Would you put it on the overhead projector, please?

A. I know this is going to smack of some atomic scientist or whatever coming up here and giving you a formula but -

Q. What if any benefit do you think that formula would be to me or Mr. Furlotte?

A. It allows the calculation of the probability of band sharing between two individuals where the P, subscript i, in these cases down here indicate the frequency of a particular bin. These capital sigma letters on the front of this expression here indicates that you have to sum this algebraic expression over all of the bin categories. You then have to add the expression for these other categories, again now sum over two different subscripts here where you take one bin, multiply it by the frequency of every other bin but itself, O.K., so it's the P, subscript i, times all of the other P's in the frequency of those bins, multiply this formula, that's squared up there, whatever, and that gives the frequency of the time when you took two individuals and looked at them at a locus how often you would expect to see them sharing bands, and if you do calculations where - and I have not had the opportunity to actually put in the bin frequencies in the actual database because these calculations cannot be done easily on a hand calculator, I would have to write a computer program to do that, but if I do it for

some values that are known to be close to the bin frequencies that we do have and that we make an assumption that all the bins are equally frequent, you get estimates for this probability that show that for various loci that we've looked at the freguency that you'd expect to see individuals sharing bands are often in the case of one locus as often as a third of the time, so that the frequency that you expect to see band sharing even in a random database that we have for the Caucasian sample that we used for our calculations is considerably higher than one would have perhaps intuitively or naively expected, that this formula in fact is the way to do the calculation and is - I could go through the derivation of that algebraically, it gets a little bit extensive and you'd have to know some probability -

MR. WALSH: O.K., that's fine, Doctor. I won't trouble you on that particular aspect. You can shut that off right now.

THE COURT: Just while we have that in front of us, though, may I ask the witness this question? Would that sheet there - it wouldn't, without having a key on it, I take it, have any significance for Dr. Shields if it were to be faxed to him by Mr. Furlotte this evening? What would you have to do to fix it up?

A. That is correct, I would have to define what the P sub i and the P sub j refer to. We'd just need to add that they refer to the bin frequency and that what you're summing there, the one to n, is over all of the bins.

THE COURT; Yes, but you could do that on the balance of

the sheet very simply?

A. I could do that on that overhead, Xerox it, and give it to Mr. Furlotte.

THE COURT: If that were done and if that were faxed to Dr. Shields it would give him an opportunity to, what, analyze it in the context of what his views are or -

A. Yes, it would. Yes, it would.

THE COURT: Well, I just wanted to ask that question. You carry on, Mr. Walsh.

Q. Dr. Carmody, with respect to Dr. Shields, what if any intentions did you have to discuss this matter with Dr. Shields?

A. I'd be fully happy to discuss it with Dr. Shields. I understand that you've asked me to be here during his testimony and I would be happy to share the derivation of that formula and I would think by Monday I could have further calculations done that would support and show the conclusions that I'm drawing from this formula.

Q. Would you consider the problem that you were faced with a complicated problem?

A. It is surprisingly complicated. I thought at first that it was going to be easy to crack but it's more subtle than I had thought and it eluded my probability theory abilities for a while, and it was only actually in - it was a very interesting collaboration that - I feel it's really a shared solution between Dr. Kidd and myself because we were constantly correcting each other.

THE COURT: You mean Mr. Furlotte and Mr. Walsh and I are not going to get any credit if this is published?

A. We'll have to acknowledge you in a footnote.

THE COURT: As co-author.

MR. WALSH: My Lord, this here - we'd have to mark that on the voir dire and enter it as an exhibit on the voir dire. I could arrange to have a photostatic copy of that made. I'll give back the overhead to the doctor.

THE COURT: I think that would be the way to do it. This would be 5D, I think. Let's give it that number tentatively, anyway, VD-5D.

MR. WALSH: My Lord, I have no further questions on the voir dire subject to cross-examination by Mr. Furlotte, and I would ask that I be permitted to address the Court following that.

THE COURT: Just before Mr. Furlotte does cross-examine, though, may I just make a few observations, and one is, I suppose, that if you were to let - if Dr. Shields - I don't know what the intention is, I am assuming here that perhaps Shields is being called as a witness. If he were to expound the theories he did earlier on the voir dire I suppose the Crown then could as one form seek leave to call rebuttal evidence to deal with that particular aspect of the thing and presumably call Dr. Carmody in that. I would think it would be preferable from the defendant's point of view to have the witness deal with this matter in anticipation - I don't see the - we'll come back to this in a minute but I don't see the hearsay aspect to it.

MR. FURLOTTE: Well, I just don't want this witness saying that him and Dr. Kidd come to this type of a formula because I don't have the ability to

cross-examine Dr. Kidd like I'm going to have to cross-examine Dr. Carmody.

THE COURT: Well, he can say it's his own done in collaboration with Dr. Kidd.

MR. FURLOTTE: Well, I think I'm almost - I don't know, the whole thing is stupid as far as I'm concerned and it's a poor way to discuss things when you're taken by surprise like this, but I don't even know if I can get a hold of Dr. Kidd until -

THE COURT: Shields.

MR. FURLOTTE: - he's scheduled to come in Sunday night and I don't know if I can get this information to him or discuss it with him.

MR. WALSH: From a practical point of view, My Lord, if I may, I would like Mr. Furlotte, if he would, to tell me how else I can do it. From purely trial strategy point of view the Crown could take the risk of not eliciting this particular evidence, wait for Dr. Shields to testify as to his conclusions on background band sharing, and ask the Court to call Dr. Carmody to put these formulas into evidence. I thought by actually doing it in advance I was in fact being fair or attempting to be fair as commensurate with my obligations.

THE COURT: I feel this is the preferable way to do it. I think my main concern is how can Dr. Shields be advised of this in advance so that he has a little time for preparation on the thing and so that Mr. Furlotte has a little time for preparation. Now, I wonder if the best idea isn't to proceed tomorrow with this evidence before the jury on the understanding that this evening, Doctor, you would complete your formula here with your key and put

it in a form that might be intelligible to Dr. Shields - well, I'm sure it would be, and copies of that would be made available to Mr. Furlotte. He can choose when he wants to send that or give that to Shields. At the same time, when you have concluded your evidence tomorrow we would ask the court reporter to type up your evidence on this aspect of the interrogation as soon as possible, say on Friday, and that would be made available to Mr. Furlotte either to communicate by fax to Dr. Shields or to have - presumably he'd be coming -

MR. FURLOTTE: My Lord, the problem I have with that, and I'm sure Dr. Shields might have with that and I'm sure Dr. Carmody can appreciate, this voir dire ended in June - actually, it ended in May of this year. It took Dr. Carmody all that time with the assistance, I suppose, yesterday of Dr. Kidd who had all kinds of time to consult with anybody else in the meantime to, I suppose, shoot down Dr. Shields's testimony, or his assessment of band sharing. It may take Dr. Shields just as long to assess this problem and to see where Dr. Carmody is wrong. This has taken the defence totally by surprise after 240-some witnesses. On the last witness at the eleventh hour we come in with some kind of miracle drug that is going to cure all the problems that Dr. Shields may have been able to throw at them.

THE COURT: The alternative would have been, as Mr. Walsh described earlier, to have let Dr. Shields testify and then seek leave to call rebuttal evidence to shoot down that theory that he expounds in his evidence, in his direct evidence,

and take him by surprise, would take him by total, utter surprise. This way he has an opportunity to consider. He may abandon - I don't know, is there any likelihood of your convincing him that he's wrong in that particular regard or will it confirm that he's more right than -

MR. FURLOTTE: I think out of professional courtesy I would expect that - I sure as heck can't explain this to Dr. Carmody (sic). No matter how much Dr. Carmody would explain that here to me today or to the court tomorrow there's no way I can explain his position to Dr. Shields, and -

THE COURT: Oh, I quite agree. Mind you, how much impact this is going to have on a jury of twelve peers I'm not sure anyway. You know, we're perhaps talking more academically here than anything. It's just a question, I suppose, of whether this should go on the record.

MR. FURLOTTE: I want to go on the record right now as -

THE COURT: Do you want to cross-examine this witness now on any aspect?

MR. FURLOTTE: I wouldn't know how to cross-examine this witness on this type of thing.

THE COURT: I don't know how you would.

MR. WALSH: Mr. Furlotte finds himself in the same position, I expect, that I found myself when I got the words background band sharing and Nichols and Balding correction factor jumped on me in this court room. I have attempted to be forthright and I can't understand how Mr. Furlotte could be surprised by this. We have a defence expert come in and generate some kind of a background band sharing and come up with the conclusion that the

coefficient of inbreeding in the Miramichi was somewhere close to the highest ever seen in the world, and I don't think that he would be surprised by the fact that the Crown would take a directly frontal assault on that kind of conclusion.

MR. FURLOTTE: I think Mr. Furlotte is surprised by this because on cross-examination of Dr. Carmody at the voir dire he agreed that the calculations of probability of Mr. Legere sharing certain bands with the Daughney sisters were what Dr. Shields had actually calculated them out to be.

MR. WALSH: I think you better ask that question of Dr. Carmody.

THE COURT: Yes, well, I don't want to get into that just at this point, but - oh, I don't know that I can say anything more useful here. You don't want to cross-examine this witness now?

MR. FURLOTTE: I wouldn't know how, My Lord.

THE COURT: Do you have anything more to say, Mr. Walsh? I think I'll reflect on this overnight and deal with this in the morning.

MR. WALSH: The suggestion Mr. Allman makes is that we could start on Tuesday instead of Monday, give Dr. Shields and Dr. Carmody a chance to consult on the matter, if Dr. Shields is coming in on Sunday.

MR. FURLOTTE: Dr. Shields is coming in on Sunday. Well, if the Crown wants to pay for the extra time that Dr. Shields has to put on this I could -

MR. WALSH: The Crown is paying for it one way or another anyway, My Lord.

THE COURT: Well, I'm not anxious to delay the timing next week or to change the timing from our

original timing.

MR. FURLOTTE: My Lord, maybe under the circumstances, in the light of this new testimony that's going to be proposed by the Crown, the Court could appoint an expert witness to assist it.

THE COURT: To assist whom?

MR. FURLOTTE: To assist the Court. Maybe we could have Seymour Geiser called in as an expert to assist the Court.

THE COURT: Oh, I'm not going to have any more assistance than I've got now. I'm confused.

MR. WALSH: My Lord, I have no intentions of getting into the formula. Dr. Carmody's opinions are directly related to whether he agrees with Dr. Shields on his formula for calculating background band sharing. Dr. Shields will have an opportunity to dispute it or not. Then it's, unfortunately, an issue for the jury.

THE COURT: Yes. Well, we'll adjourn now, and I will think about this overnight and I will come up with some sort of a direction tomorrow morning on what we're going to do. I would ask you, Doctor, in the meantime, would you prepare your key and do that so that it would be available in any event?

A. Yes, I will.

THE COURT: And did you have something, Mr. Allman?

MR. ALLMAN: Just hold on one second, My Lord, I think they may have come up with another idea. No, Mr. Walsh doesn't think it's a good idea.

THE COURT: What I would like to do, I wonder if in the morning perhaps I could meet briefly in chambers with counsel at 9:30, say, and I'd like to just review again timing, the matter of timing of the

trial, and this might have a little bearing on this thing and perhaps we can see where we're going. I don't want to discuss this in open court. It will be a very brief discussion.

MR. ALLMAN: Mr. Furlotte already indicated he wanted to meet with you in chambers to do just that sometime tomorrow.

THE COURT: Well, if we could do that first thing in the morning perhaps we can go on from there, so the jury have gone, we'll retire now until 9:30 tomorrow morning.

(ADJOURNED TO 9:30, OCTOBER 24, 1991.)

(COURT RESUMED AT 9:30 a.m., OCTOBER 24, 1991.)

(ACCUSED IN DOCK.)

THE COURT: Now, we'll have the jury. There's nothing to discuss with counsel?

MR. ALLMAN: No, really. I'll tell Your Lordship now and I'll tell you in the presence of the jury two things. First of all, Louise Pineau, whose name is on the list, she was sick and we couldn't call her before. I've spoken to Mr. Furlotte, we don't need to call her so her name is being taken off.

THE COURT: Oh, yes, 237, yes.

MR. ALLMAN: We're not going to be calling her and we are going to be inserting Catherine Anne Lyons at 9:30 because she has a young child that she wants to get back to.

THE COURT: And I understand you propose to call her first?

MR. ALLMAN: Yes, Mr. Furlotte again has indicated he has no objection to that, and I'll repeat this for the benefit of the jury.

THE COURT: The other on the witness list, Alice Garner, she was the affidavit person, and then I have a name, Kathy MacKay, was that the other affidavit?

MR. SLEETH: My Lord, her affidavit accompanied that of Alice Garner for Section 30 of the Canada Evidence Act.

THE COURT: We'll have the jury, then, please.

(JURY CALLED - ALL PRESENT.)

MR. ALLMAN: My Lord, as you know, we were in the middle of the direct examination of Dr. Carmody, but I have a witness, Catherine Anne Lyons. We had intended to call her quite a long time ago, it

wasn't possible at that time. She has a young child, she wants to get back to that child, and Mr. Furlotte's been kind enough to indicate that we could insert her evidence at this time, and while I'm on my feet discussing the witness list I could also advise Your Lordship that there is one witness, Louise Pineau, who was on the list. She was sick last time I checked, her evidence is not of great importance and we don't propose to call her, and Mr. Furlotte doesn't require that we do call her.

THE COURT: All right.

CATHERINE ANNE LYONS, called as a witness, being duly sworn, testified as follows:

DIRECT EXAMINATION BY MR. ALLMAN:

Q. Is your name Catherine Anne Lyons?

A. Yes.

Q. And what town or city do you reside in?

A. Halifax.

Q. And where are you employed in Halifax?

A. The R.C.M.P. Forensic Lab.

THE COURT: Pretty hard for those people at the end of the jury to hear what you're saying. Would you shout right out, Mrs. Lyons, please?

A. Sorry.

Q. You're employed with the R.C.M.P. Forensic Lab in Halifax?

A. Yes.

MR. ALLMAN: My Lord, with Your Lordship's permission I'll lead her through her curriculum vitae. It won't be as long as Dr. Kidd's.

THE COURT: All right.

Q. I understand that between 1975 and 1976 you took part in a B. Sc. program at the University of Prince Edward Island?

A. Yes.

Q. From 1976 to 1978 you continued your B. Sc. program, this time at Queen's University?

A. Yes.

Q. And in 1979 you switched from the B. Sc. program into a lab science technology program and you graduated with a diploma in lab science technology from St. Lawrence College?

A. That's right.

Q. Where is St. Lawrence College?

A. In Kingston, Ontario.

Q. After that you were employed from 1979 to 1981 as a - or in the Technical University of Nova Scotia, and then from 1981 to 1985 with the Department of National Defence Materials Chemistry Section?

A. Yes.

Q. And then from 1985 to the present day, some six years, you've been in your present position with the R.C.M.P. Forensic Lab in Halifax?

A. That's right.

Q. And what in fact is your position with the R.C.M.P. Forensic Lab?

A. I'm a scanning electron microscopist.

Q. Could you just tell the jury what a scanning electron microscopist does?

A. I look at very small samples using a scanning electron microscope. I view them and do chemical analysis on them.

Q. To see what they are?

A. To see what they are.

Q. I understand you attended a number of courses, special courses and training; 1982 a course on energy dispersive X-Ray analysis, Princeton, New Jersey?

A. Yes.

Q. 1983, scanning electron microscopy and X-Ray microanalysis at Lehigh University, Bethlehem, Pennsylvania?

A. Yes.

Q. 1984 a course in advanced organic chemistry at Dalhousie?

A. Yes.

Q. 1986, service and troubleshooting course in Kebec's Instruments in California?

A. Yes.

Q. I take it a Kebec's instrument is one kind of the ones that you use?

A. Yes, that's what we have.

Q. And in 1986 an energy dispersive X-Ray analysis course at Kebec's Instruments again?

A. Yes.

Q. And you're professionally affiliated as a member of the Microscopy Society of Canada?

A. Yes.

MR. ALLMAN: My Lord, subject to any objection, and if she's declared an expert I'll have her go into more detail on what it is but I'd have her declared an expert in microscopy.

THE COURT: And you're a microscopologist?

A. Microscopist.

THE COURT: Do you have questions you want to ask?

MR. FURLOTTE: I have no questions.

THE COURT: Well, I would declare you an expert for the

light source, it's electromagnetic lenses instead of light lenses. It reaches very, very high magnifications. Most of the samples cannot be seen with the naked eye when you put them in.

Q. As I understand it, it works on the theory that the different chemical elements produce different

A. Yes.

Q. Do you remember the date upon which that occurred?

A. April 3, 1991.

Q. Did he leave the object with you for a while or was he present at all times while you performed your tests?

A. He was present at all times while I performed the tests.

Q. And I believe Sergeant Kennedy's evidence was that the object that he brought to you was what is now P-137. You didn't put any markings of your own on it, I take it?

A. No, I didn't.

Q. Does that appear to you to resemble what you looked at?

A. Yes.

Q. I'll leave it there just in case you want to make any reference to it.

THE COURT: Just to relate this to the case, this is -

Q. Yes, the evidence, I believe, from Sergeant Kennedy, I'll be corrected if I'm wrong, is that this is the left cast of Mr. Legere. Mr. Sleeth corrects me, I put that too shortly, it's the cast of the left foot. Whether that's the left cast or not I don't know. O.K., when that was brought to you, what was the purpose of bringing it to you? What were you to do with it?

A. There is a small rusty-coloured spot in the heel portion and Sergeant Kennedy was inquiring as to what it could possibly be.

Q. O.K., so just tell us in your own words what you proceeded to do.

A. I looked at it, I took samples of it under an

optical microscope, that's the bench type. I mounted them on what we call stubs, it's a sample holder that you put into the microscope. We examined it, I did the chemical analysis on it and gave him the results.

Q. Now, I understand that if we want to break it down there were in fact three samples that you analyzed?

A. Yes, there was the rusty-coloured spot, there was also a reddish spot just to the side of that, and a control sample of dental stone material or the mold material.

Q. What's a control sample?

A. That's a sample in a totally different area from the area you're looking at to make sure that the piece you're looking at is not - is different from the matrix material.

Q. So you'd take a piece from the toe or the heel or somewhere of that kind, not - sorry, the toe or the ball?

A. Yes.

Q. And when you analyzed that bit, the bit that didn't come from the spot, what did you find that to consist of?

A. When I - pardon me?

Q. When you analyzed the control sample, what was that? If you need to refer to your notes I take it there would be no objection, but if you can remember just go ahead.

A. I can't remember.

MR. ALLMAN: May she refer to her notes, My Lord?

THE COURT: Oh, yes, sure. These were notes you made at the time?

A. Yes. O.K., the dental stone material itself was made of sulphur, calcium and potassium, the elements of it.

Q. Now, the second test you indicated that you ran was on the red spot itself?

A. Yes.

Q. O.K., what did you do - first of all, what did you do to get the substance?

A. Picked it out with a probe.

Q. And then after you'd picked it out with a probe, had a look at it under a regular microscope, you put it in the electron microscope, and what was the result of that test?

A. It had an appearance of a fibrous material. The chemical analysis of it was mostly composed of iron, trace amounts - and by trace I mean less than one per cent of the whole make-up of the matrix was sulphur, calcium, potassium, chromium, titanium and silicon.

Q. Now, the sulphur, calcium and potassium, as I understand it, would be consistent with having scraped out some of the material of the mold itself?

A. Of the dental - yes.

Q. And you say it's basically iron but with trace amounts of other substances?

A. Yes.

Q. The other substances you mentioned, I think, were sulphur -

A. Yes, that would be part of the dental stone material.

Q. Calcium, potassium, chromium, titanium and silicon?

A. Yes.

Q. What are they, chromium, titanium and silicon?

A. Common to a lot of things.

Q. The last area that you dealt with was the rust-coloured area?

A. Mm-hmm.

Q. Where exactly was that in relation to the red spot?

A. It was in the little indentation in the heel part.

Q. And I take it you did the same process, extracted a little of that and -

A. Yes.

Q. When that got into your electron microscope what were the results of that analysis?

A. It was composed of iron, trace amounts of calcium, sulphur, chlorine and potassium.

Q. O.K., now, the calcium, sulphur and potassium, again that would be consistent with the mold material?

A. Yes.

Q. And the chlorine, what would that be consistent with?

A. That's very common, sweat -

Q. So apart from the sulphur, chlorine and potassium and calcium it consisted of iron?

A. Yes.

Q. Is there any way - you received this on the third of April, I believe?

A. Yes, I did.

Q. Is there any way of knowing how long that substance that you analyzed had been in that location?

A. Had been in the mold?

Q. Yes.

A. No, other than it was - it probably had been there when they took the mold. It was mixed in with the mold material.

Q. O.K., it was mixed in with the mold?

A. Yes.

Q. Is there any way of knowing from what original object specifically the iron came?

A. No.

MR. ALLMAN: I have no other questions.

THE COURT: Cross-examination, Mr. Furlotte?

CROSS-EXAMINATION BY MR. FURLOTTE:

Q. Now, Mrs. Lyons, just how big was this red spot that you analyzed?

A. It was on a micron level. I think it was in the range of around five microns.

Q. And just how big would that be, in layman's terms?

A. You couldn't see it with a naked eye.

Q. You wouldn't be able to see it with a naked eye?

A. No.

THE COURT: Like the angels on the head of the pin, I think.

A. Yes.

MR. FURLOTTE: We won't get into arguing how big the pinhead is either.

THE COURT: Or how big angels are. Have you seen an angel?

Q. Now, the spot on the heel here, is that what you would call a red spot or the rust-coloured spot?

A. That was the rust-coloured spot.

Q. Rust-coloured; what is the red spot? I've noticed you've used the term rust-coloured spot

and red spot. Would you distinguish between the two?

A. Well, the rust-coloured spot would be the area in the heel. The red spot was another dot that was on there that we were curious as to what it was.

Q. Now, when you say rust-coloured, does that mean there was rust in there or just rust-coloured?

A. Well, at the time I didn't know what it was so it was rust-coloured.

Q. So it's just a nice description?

A. Description of the colour.

Q. Now, you mentioned that this little microscopic spot was - or dot or - you wouldn't be able to see it with the naked eye?

A. The red spot?

Q. Yes, the red spot, you wouldn't be able to see it with the naked eye?

A. Not the red spot that I took, no.

Q. But through the microscope you could see the colour of it?

A. No, you can't see the colour of it.

Q. Well, how do you know it's a red spot if you can't see the colour of it?

A. Oh, sorry, through a bench microscope, through the optical microscope, yes, I could see the colour.

Q. Do you have any idea what would give it that colour?

A. No.

Q. What is the colour of iron, does iron have a particular colour?

A. Metallic or oxide?

Q. Darned if I know.

A. Well, metallic iron is - well, I suppose it's

black, or depending what it's mixed with or -

Q. What about chromium?

A. Well -

MR. ALLMAN: What's the question?

Q. Did it have a colour?

A. They're metals.

Q. Chromium is a metal also?

A. Yes.

Q. Titanium is a metal?

A. Yes, in its pure form.

Q. And silicone? Is it silicone or silica?

A. Silicon.

Q. Is that a metal also?

A. Mineral.

Q. And you have no idea what kind of item would contain these types of metals and -

A. Well, they're quite common. It could be -

Q. Quite common. Now, I noticed you received this on April 3, 1991?

A. Yes.

Q. And I believe these molds were taken on November 24, 1989?

A. I don't know.

Q. O.K. This length of time, could that have anything to do with the colour of the item, -

A. No.

Q. - colour might change over that length of time? How big a spot did you check as your control sample? You must have taken the control sample off the cast to see what materials were in the cast?

A. Mm-hmm.

Q. How big of a sample did you take off the control -

for the control?

A. It would be a small scraping, I didn't measure how big it was.

Q. Not much bigger than the red spot?

A. No.

Q. Be about the same size that you had taken?

A. Probably be about the same size as that spot right there. You could see it.

A. So what you found in this spot here, there could be a lot more of those red spots in the cast that you wouldn't know about?

A. Well, they weren't apparent on the surface of it.

Q. Right. Now, you mentioned that Robert Kennedy was there with you when you were doing the tests?

A. Yes.

Q. But you didn't receive this material, the red spot, from Robert Kennedy, did you, or the items?

A. He brought the foot mold in.

Q. In your ntoes do you say that you received the following samples from J. Buckle?

A. Yes, he's a colleague at the lab, he was present as well.

Q. And you state that you received it from him, the red spot embedded into the heel of the foot mold, "Sample from rust-coloured spot in heel of foot mold and control sample of dental stone material".

A. Well, he was present while I was taking them from -

Q. So he did tests on this before you?

A. No, he was present along with Sergeant Kennedy while I took the samples. He was there and it's written this way because technologists don't usually go to court and that's the flow of the

paperwork in the laboratory.

Q. What do you mean by technologists don't usually go to court, yourself?

A. Mm-hmm.

Q. But you state that you received these materials, items, from Buckle and that you gave them back to Buckle the next day - or not the next day -

A. No, same day.

Q. - on April 6th, three days later. Is that a six at the bottom?

A. I can't read it on my copy.

Q. What did you do with these items once you finished them?

A. They were handed back to Sergeant Kennedy.

Q. And why does your report say you received them from Buckle and you gave them back to Buckle maybe two days later when you -

A. No, I didn't give them back to Mr. Buckle two days later. The case came through the Chemistry Section in the laboratory, of which Mr. Buckle is a member.

Q. O.K., but at the bottom of your report under remarks you state: "The samples have been returned personally to J. Buckle on 91-04-and which looks like -6.

A. It's a zero and I think there's a three after it. I can't say that for sure.

Q. But it doesn't appear as if it's the same date, does it, that you state you gave it back to J. Buckle?

A. It was the same date.

MR. FURLOTTE: It was the same date. I have no further questions.

REDIRECT EXAMINATION BY MR. ALLMAN:

Q. I just want to try and clarify. You indicated there was one thing you couldn't see, one red thing you couldn't see?

A. With the naked eye?

Q. Yes.

A. Yes.

Q. O.K., what was it that you could see?

A. The rust spot.

Q. The rust spot, and the second question, why don't technologists go to court?

MR. FURLOTTE: Well, My Lord, maybe she should clarify that again and say it was a rust-coloured spot, not a rust spot.

A. All right, rust-coloured spot.

THE COURT: Yes, I'm confused. There was no rust spot that I know of, it's a rust-coloured spot.

MR. ALLMAN: No, you meant rust-coloured?

A. Rusty, rust-coloured.

Q. Which would be - is there any trace or element that that left on the P-137?

A. The spot right here.

MR. ALLMAN: She's pointing, My Lord, to the spot there.

THE COURT: Well, for the record indicating - that's what you call the indentation?

A. The indentation.

Q. Is there a problem or some reason why technologists don't normally go to court?

A. Well, if we went to court we wouldn't have much time to do the work.

Q. If you are asked to go to court by the Crown or defence I take it you will attend?

A. Yes.

MR. ALLMAN: Thank you.

THE COURT: Just one other question, the red spot that you speak of, that was visible to the naked eye?

A. No, it was visible under the optical microscope.

THE COURT: Yes, and it was located elsewhere than at the indentation. How far was it from the -

A. Oh, it was right beside it.

THE COURT: Yes, but what do you mean by right beside it, part of it, almost, or -

A. Yes.

THE COURT: Almost part of the indentation, but why do you differentiate between the two spots? Why weren't they all part of the -

A. Well, because I took - it looked different from the rusty-coloured spot, therefore we didn't know what it was so we sampled it.

THE COURT: But actually it had the same constituents, did it not? The items you listed were virtually the same or -

A. It had trace amounts of chromium and titanium and silicon in them which the rusty-coloured spot did not.

THE COURT: Didn't have them, so they seemed to have come from different sources?

A. Yes.

THE COURT: Any questions dealing with those?

MR. FURLOTTE: No, My Lord.

MR. ALLMAN: No, My Lord.

THE COURT: Thank you very much, Mrs. Lyons. You're excused. I'm not sure what that was all about but, anyway, go ahead, Mr. Walsh.

MR. WALSH: Pardon, My Lord?

THE COURT: Well, my remark was that I'm not sure what that last witness was all about, but you go ahead with your -

MR. WALSH: I recall Dr. Carmody, My Lord.

DR. GEORGE CARMODY RESUMES STAND:

DIRECT EXAMINATION BY MR. WALSH CONTINUES:

Q. Dr. Carmody, when we finished yesterday you had just gone through the concept of background band sharing, is that correct?

A. That's correct.

Q. Just to summarize, what if any abnormal background band sharing did you observe between the individuals tested in this case, either on any of the suspect gels or on the gel containing the females and the males?

A. I went back to the autorads and had Dr. Bowen look at the nine individuals that were unrelated on those autorads. I have the actual individuals' names or the the particular lanes in my notes, but there were nine people from the area of Miramichi that were unrelated to one another and I had him record all those instances where for all six blots that had been done there were bands that were shared between individuals, that is, where there were at least between an individual at least one band in common, called a shared band, and he recorded that and gave me the numbers. I used a formula that I had worked out with Dr. Kidd -

Q. O.K., but in doing that what if any conclusions did you draw with respect to -

A. The conclusions that I drew from that analysis is that sample of nine people showed no increased

amount of band sharing beyond what you would normally expect in taking any random sample of nine people from the Ottawa R.C.M.P. database or the Vancouver database or the Kingston database, so there was no information in that group of nine people or the people that were run for those autorads that would in any way support any notion that the people in that region either had genetic profiles that were different from the rest of Canada or that were more inbred or that, as we would say in population genetics, showed any substructure, showed a distinct kind of area in terms of mating patterns or anything else that one would expect to see if there was substructure there. In other words, that that sample of nine people, small as it is, and we would have to concede that a sample of nine is small, showed no evidence of a differentiation of that area from the rest of Canada.

Q. Doctor, have you heard the term or could you tell us what, if anything, the term Nichols and Balding correction factor means?

A. Yes, the term Nichols and Balding are actually the last names of two scientists who published a paper in a journal called, "Heredity", about six months ago where they did a mathematical derivation and derived a correction factor that would allow you to apply a correction factor to the probabilities that we normally calculate where we're assuming Hardy-Weinberg equilibrium that would take into account, they suggest, amounts of inbreeding that could be present in perhaps some isolated populations. They suggested that this could be used to

correct for not only what we would call genetic inbreeding as such but in fact to correct from slight biasses, perhaps, in the process that is normally done in the U. K. where they use the floating bin approach and where the numbers are considerably smaller than what we would derive with our fixed bin approach here in North America, and by applying that factor you could in a sense apply kind of a safety factor and say, well, we're not absolutely sure - as I've indicated yesterday, we're not absolutely certain that the number that we generate as our best estimate is exactly precisely that number, and that's why we put the confidence interval around it, but they suggested, these two scientists, Nichols and Balding, that you could correct that number in still another way with a mathematical formula that would take into account any hypothetical or imagined amount of inbreeding, and you could do that to the formulas as we calculated them.

Q. What if any aspect of the measurement imprecision does this correction factor take into consideration as well?

A. Well, in fact, it gives you again a number that is less rare, that is the number that - let's say one in 310 million - I've forgotten if you apply the one correction factor that they suggest that might come down, I in fact don't remember the actual number when you apply that, but suppose that would come down to one in 50 million or something like that. I think the net implication of that is that even being extremely generous, applying this correction factor which we in fact have no

evidence to suggest needs to be applied, but even if you were to apply that correction factor you would still get a result that says that that particular genotype is rare.

Q. This particular correction factor was developed for what kind of a system?

A. Well, it's derived specifically for a multi-locus system and a system where you use the floating bin approach.

Q. Doctor, considering that we use a fixed bin approach and that we use single locus probing, considering your findings on background band sharing and considering your conclusions that you've given with respect to the Canadian Caucasian population and taking into consideration all the statistical tests you did in regard to the Canadian Caucasian population, what if any application in your opinion does the Nichols and Balding correction factor have to this particular case?

A. In my opinion I don't feel that applying the correction factor is at all necessary. I have no objection to somebody applying that factor and generating the number because I feel it does not change the inference that one would draw from these numbers, so I don't have strong feelings about it. If one wants to apply it you can apply it and generate a number knowing that you're being safe, in the same way that when you build a bridge, as I understand it, engineers design that bridge so it will take several full times the normal weighting load that the bridge is expected to take. In the same way here you could say that

applying that correction factor you might say is a safety factor, if you will. You could apply it, it's being overly cautious, overly conservative. You still end up with a number and an estimate for the frequency of the particular genotype that says it is still rare.

Q. But in your opinion, Doctor, do you think the Nichols and Balding correction factor is necessary?

A. I don't feel that it's necessary in this particular instance. I would think it might be necessary in cases where you knew that there was a degree of inbreeding there. There are some remote populations, there have been populations reported in the literature, where there are very high degrees of inbreeding. The amount of inbreeding that's been estimated in the highest that I've seen in Canada is .007, I believe it is, and that's considerably lower than these correction factors would be applicable to.

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

THE COURT: Thank you, Mr. Walsh. Mr. Furlotte, cross-examination?

CROSS-EXAMINATION BY MR. FURLOTTE:

Q. Dr. Carmody, I believe you stated in your post-doctorate you worked with Dr. Richard Lewontin?

A. That's correct.

Q. And what do you know about Dr. Richard Lewontin?

A. Dr. Richard Lewontin is an outstanding population geneticist. At the time he was at the University of Chicago and I worked at his laboratory for two

years. I know Dr. Lewontin very well, had dinner with him a couple of years ago in Toronto, in fact, and he's now at Harvard University and he is a leading population geneticist.

Q. Probably the leading population geneticist?

A. I would say it's difficult to establish a hierarchy like that. I don't know as I could rank people strictly and simply as one, two, three, four, five. I'd say I would rank him amongst the top five in the world, yes.

Q. But basically everybody in your field knows Dr. Richard Lewontin and his reputation?

A. Yes, population geneticists would know of Richard Lewontin, yes.

Q. How many population geneticists would there be in North America?

A. Well, I'd have to do an estimate on that. I'm just guessing. We have an EMAIL network that has probably about 120 or so, and that's mostly theoretical people. I would say it would be on the order of 300 to 500.

Q. Do you know about Dr. Eric Lander?

A. Yes, I do.

Q. He's well-known in the scientific community also?

A. He is well-known in the scientific community. He's not known as a population geneticist and people don't think of him as a population geneticist, in my opinion.

Q. And I understood that - I believe it was Dr. Fourney, I could be mistaken, but mentioned that the National Academy of Science appointed Dr. Eric Lander on their panel as one of the population geneticists?

A. I don't know what the title of his designated position is. I believe he's on that committee but I don't actually know that for certain.

Q. And do you know whether or not Dr. Eric Lander is considered by many to be the brightest individual to come into population genetics or in micro-biology in the past 20 years?

THE COURT: I didn't catch the word, brightest?

Q. Either population geneticist or micro - or molecular biology?

THE COURT: No, but you said is the brightest, did I understand?

Q. Is considered to be the brightest prospect to come into this field in the past 20 years?

A. I haven't heard that or read that comment, no.

Q. But he is also highly respected in the scientific community?

A. He has a big reputation, yes.

Q. And they have many publications, both Dr. Richard Lewontin and Dr. Eric Lander?

A. They both have a number of publications, yes.

Q. In the area of DNA analysis?

A. No, only Dr. Lander does. Dr. Richard Lewontin has no publications that I've ever seen in any peer review journal on DNA and forensic analysis.

Q. No, Dr. Lewontin is more on the theoretical aspect of population genetics?

A. Both theory and experiment, actually, but he has nothing at all published on DNA use in forensic analysis.

Q. But he has lots published on the theoretical aspect of population genetics?

A. And on drosophila genetics. He is a drosophila

geneticist.

Q. And in comparison to them how are your publications on either - you're mostly in experimental?

A. That's right.

Q. And what are your - what's the extent of your publications on the theoretical aspect of DNA analysis?

A. I do not have any publications in that area. I am presently working on some papers with the people that I collaborate with.

Q. So the answer is - and you would not be as well-known as Dr. Lewontin and Dr. Lander?

A. That's correct, overall in population genetics, that's correct.

Q. As a matter of fact, as an experimental - as yourself in the experimental field you use the theories, the theoretical models, that are put out by people like Dr. Lewontin?

A. That's correct.

Q. And do I understand that Dr. Lewontin objects to your ability to use his theories the way the forensic fields are using them?

A. Well, in none of this are we using any of his theories, in fact. The theories that we were using he had no connection with. These are theories in population genetics that have been in population genetics for much longer than Richard Lewontin has been a scientist. He objects to drawing some of the inferences that we do. He feels that the numbers that we generate are not precise enough and he feels that there needs to be more information. He has never said that one cannot use DNA analysis for forensic purposes but

he feels that the - and in fact he has, as I understand and read in transcripts, said that it is a very powerful technique but that he feels that the numbers that are drawn from the information are less precise than the way they have been given in court rooms.

Q. Not only less precise but also could be way out of proportion?

A. Could be far out. He's never put any number on how far out they could be in his opinion.

Q. Dr. Lewontin believes that because of sub-structures exist within the different communities that it's improper to use the Hardy-Weinberg formula and the product rule?

A. Well, I would put him more in a category of agnostic where he says that he's not sure that there's a lot of substructuring but that he would say that we just don't know, and until we really know by having detailed information, particularly from European populations, we are not safe in going ahead and using any numbers.

Q. So basically what he's saying is that you're forming an opinion on facts which you have not proven?

A. That's what he is saying, yes.

Q. And in science - I believe you're a professor also?

A. Yes.

Q. Yes, and in science if your students come and put professional opinions before you and basing them on facts which they could not prove and you would probably give them a failure in their experiment or paper, would you not?

A. Well, I don't think I would give them a failure. I would try to enlighten them so they see the error of their ways and perhaps not necessarily failing them but they would be criticized if they were to do that, yes. I might hasten to add, in this particular area I feel that there is ample evidence to support the calculations as we're doing them.

Q. Yes, we'll get into that, Doctor. Now, as an experimental population geneticist you - in your experiments you are always looking to see if the theories correspond to the observations that you make?

A. That's typically what is being done, yes.

Q. Your empirical findings?

A. That's right.

Q. Yes, and what happens when your empirical findings are contrary to the theory?

A. Well, it makes us either look at the assumptions that the theory is based upon or perhaps try to develop a new theory or to try and understand why they don't correspond to that theory, so there's a number of ways that a disagreement between experimental results and theoretical predictions might be explained.

Q. Or if the theory and the experiment don't correspond, then there could be something wrong with the factual situation that you're relying on in order for you to rely on the theory?

A. There are two ways that you could get a disagreement. Either the information that you're using has been incorrectly obtained and is not what you think it is, or in fact the assumptions that the

theory is based upon don't really hold for that particular situation.

Q. I believe you said you teach the introduction to genetics population, introduction course?

A. I teach an introductory genetics course, I have for a number of years, and I teach an advanced course in population genetics, yes.

Q. And an advanced course in population genetics, and you state you work with statistics?

A. That's right?

Q. But you're not a statistician per se?

A. I'm not a statistician per se, no.

Q. I believe you also stated that the R.C.M.P. consulted you one time over some statistical evidence and found - if I can read my own writing here - found your consultations useful or -

A. That's right, that was back in the early 1980's. Barry Gaudette at the R.C.M.P. who was involved with the Hair and Fibre Section at the time had published a paper and he asked my advice on some criticisms of the paper.

Q. And what was that paper about?

A. That paper was about the probability that two random human hair samples would in fact match.

Q. And he went to you for statistical advice in order to be able to draw the probabilities of a match?

A. Actually it was to try and answer some of the criticisms of his paper that had been published that I had no connection with in his original publication.

Q. And I believe the figures were something like there was only one chance in 4,500 that somebody else would have the same hair sample?

A. That was the number that was derived from that experimental study, yes.

Q. And you agreed with the author of that paper, experiment, at that time?

A. No, in fact, I offered some advice, and indeed, if I had been in on the design of the experiment I would have given him very different advice than what was done in the experiment. The experiment had been done and the inferences that had been drawn from that were not strictly correct and I suggested some ways that - and I also found some of the criticisms of his paper incorrect and I gave him some advice at the time on how to answer the criticisms.

Q. Has anybody ever done a subsequent study that is now accepted?

A. To be honest, I have not kept up with that area and I can't comment on that. I am not knowledgeable in that area and I don't know what the state of that art is now.

Q. Doctor, would you agree with Mark Twain when he says that there's three kinds of lies; lies, damned lies, and statistics?

A. I wouldn't agree with him, no. I know it often seems that way. I know even in my experience in reading press articles and whatever that it would seem that one can take statistics to bend them in whatever direction your persuasion would lead you. I don't actually believe that, though. I believe that somebody who has some training in statistics can easily see a misapplication when it's been done.

Q. And there's even textbooks out on how to lie with

statistics?

A. That's right.

Q. And you've read them, at least one?

A. I read one, as I related in the voir dire, actually. It was an interesting memory that I had that I read a book by Darrell Huff, is the author, on how to lie with statistics when I was in my third year of high school and taking an economics course and I used it for a book report, and it's an excellent book. It's become a classic, now in paperback in about the 50th printing, whatever, and in fact despite its name of how to lie with statistics what it really does, it makes you very aware of how other people might be using statistics to deceive you in terms of graphical analysis and so forth.

Q. But basically what the book is pointing out is not necessarily how to lie with statistics but more so the misuse of statistics?

A. That's right. I mean, I think the title, I would say, is kind of an ironical choice of a title to, in fact, teach you the complete opposite, how not to lie with statistics, if you will.

Q. And the basic objection by most of the population geneticists in this field when they're criticizing the use of the Hardy-Weinberg formula and the product rule and the forensic databases is that the forensic field is misusing statistics?

A. I wouldn't say that. My view of it would be that what their criticism is is that it's not the misuse of statistics, it's that the statistics that are being given are given as being more precise than they actually are and that to people,

when they hear a number of one in three million, you think that that really means it's different from one in 2.9 million and one in 3.1 million. We've tried to convey now in this particular case some notion of the imprecision in that estimate, and the criticism would be further from Dr. Lewontin, Dr. Lander, that the confidence interval that we use is perhaps even wider than you could defend statistically because of some hypothetical potential biological situation that we can't be absolutely certain does not exist.

Q. But the criticisms go beyond the area of the numbers that you want to present to courts or to other scientists and the criticisms go right down to first principles, don't they?

A. I don't feel that, no.

Q. No, you don't feel that, but they do?

A. I wouldn't say that it goes down to first principles. They would say that we have to get more empirical data before we can use these formulae.

Q. Because you haven't proven your first principles?

A. Well, I feel that we have, and there are many population geneticists, and many population geneticists who have published on this, who feel that there is ample evidence that populations are for other loci, for hundreds of other loci that have been looked at, in Hardy-Weinberg equilibrium, that for hundreds of other loci that have been looked at there is no evidence of linkage diseguilibrium, and these are studies that have been done over decades, and so the conclusion from that would be that unless these particular loci

have some unique characteristic about them, of which we have no evidence either, that these should fall into a similar pattern with the hundreds of other loci that have been studied. Doctors Lander and Lewontin, as I say, are taking what I would describe as an agnostic position and saying well, we can't really extrapolate from everything else we know, we have to look only at these particular ones, and unless we have studies on every European population we just can't do anything, and I feel that that is, what would I say, an extremely sort of puristic approach. I think we're not intending these numbers, by any stretch of inference, to claim that these are very, very, very precise, we're just saying that the result is that our estimates are all leading in the same direction that a particular genotype is rare in human populations, that you're not going to get two genotypes that are occurring in a freguency of one in 500 or one in 1,000.

Q. O.K., the position, then, of the other population geneticists, that through the calculations that the forensic field is using is that yes, you're coming up with rare figures but you're coming up with ridiculously rare figures?

A. Well, they're rare figures, and I would say - I'm not sure they use the term ridiculous, but they would say that because we can't give a precise estimate when we use a number that's rare we should at best try to convey some notion of how imprecise it's likely to be and that often, and I think the criticisms were levelled very much in the past when it in fact in the first court room

cases that I'm aware of in the States, people were coming into courts and saying it was one in some extreme number, giving it down to the decimal point, virtually, when in fact as a statistician population geneticist we would know that you can't give that kind of precision to an estimate when you're basing it on a sample of a thousand people or two thousand people or four thousand people.

Q. And since the original court cases, I suppose in your studies of them, have you found that the expert witnesses by defence lawyers have caused the forensic labs to clean up their act in a lot of areas?

A. Well, I think particularly in population genetics my own sense is that in the very first early days of using DNA in court room proceedings that the people in that field were essentially coming from the molecular end. I mean all the technology and molecular biology in this is performed by people who were trained as molecular biologists, and I think many of them did not have an understanding, and I think to a certain extent that still holds. Many of them do not have a sense of the variation that is present in real populations of organisms, and they in many cases didn't even have the notion of what a confidence interval is or what kind of measures of imprecision one could apply to point estimates, and so I think it's a learning process in that sense. I think that most of the forensic labs that I'm aware of now are taking that into consideration and realize that they have to perhaps have larger databases, in the case of some labs, or they have to have databases on

different racial groups, different ethnic groups, different geographic areas, and it's that aspect of it that I think is being improved, with knowledge coming from people like myself in population genetics.

Q. So would you say that the forensic labs are moving closer and closer to Dr. Lewontin's position and Dr. Lander's position all the time?

A. Well, they're moving closer in the sense that yes, there's more information being gathered, and there's certainly more information being gathered, but they're not moving closer to their position in saying that well, we can't make any inferences until we have a complete ultimate set of data. They're still disagreeing with them and I know many population geneticists who disagreed with them in print that feel that they are dismissing decades of previous research that has been done on other genetic loci.

Q. Now, you mentioned something in your direct examination about the five duplicates in the R.C.M.P. database.

A. Yes.

Q. And there was a search to see if there was any duplicates for that purpose?

A. That's right, it was a deliberate attempt by the R.C.M.P. to screen that database to see if there were any duplicates in it.

Q. And I believe most forensic labs do the same thing, they search their database to see if there's any duplicates?

A. I believe so. I can only speak, really, from direct experience with the R.C.M.P. Lab and from

what I've read about at the FBI labs. I don't know about the private labs in the United States or the paternity labs.

Q. O.K. Now, is the search - the purpose to see if there is any duplicates, or is there a search to see how common band sharing is amongst the population, how many people might by accident or by chance share five probes?

A. Right. I know it was done specifically at the R.C.M.P. to search to see if there were duplicates. On the other hand, we're also interested in knowing the answer if there are people there who share the bands and what the frequency of that is. From my knowledge, the R.C.M.P. motivation for doing this was to ensure that there were not duplicates, and that was because they did not have complete control over how the samples were obtained. They were relying on the Red Cross to supply them with these samples, or in the case of the Vancouver sample, from the hospital there, and to preserve confidentiality and for other reasons the Red Cross has their own operating procedures and would not let an organization like the R.C.M.P. come in and say well, we need to know the identity of every one of these individuals that's in these samples of blood that you've given us, and because of that and because you can't control whether in fact the same person could have given blood at two different times and two different blood donor clinics one has to try and eliminate any duplicates that might occur, whether they're for identical twins, people giving blood more than once, people giving blood in different blood donor

places, or for laboratory mix-ups at the Red Cross where they might have two vials of blood having come from one individual and having labelled them differently.

Q. Well, we wouldn't have mix-ups in laboratories, now, would we, Doctor?

A. It has been known to occur. I detect a note of sarcasm in the question.

Q. Doctor, the people that the R.C.M.P. got their blood samples from were instructed what the R.C.M.P. wanted and they were also instructed what the R.C.M.P. didn't want?

A. I believe so, and I haven't seen the actual written instructions. I can relate an anecdote that I know happened in the very first samples that were provided by the Red Cross, and when they were told that the R.C.M.P. wanted some 600 samples, a couple of days later two vials appeared, of blood, and when the R.C.M.P. said, well, where are the remaining 598 samples, they said, "Oh, well, we thought you wanted 600 samples and we put them all in two vials", and they mixed 300 in one and 300 in the other, thinking that well, you wanted 600 samples of blood, you've got 600 samples of blood. They had forgotten to realize that in fact they meant to be kept separately and you need 600 separate vials, so that's just an example. It's an anecdotal one that I've heard where there was perhaps imperfect communication, shall we call it, whatever, where in fact it was sort of implicitly understood on one side that when you ask for 600 samples of blood, indeed the person responding to that would

have absolutely realized that they had to be kept in separate vials and not just all mixed together.

Q. And I believe you stated that you run statistical tests as to what would be the probabilities that those would not have been duplicate samples?

A. That's right, because I know that once the duplicates were found on the five probes -

Q. Well, let's for instance just say two samples with similar profiles.

A. Right, similar profiles. Let's say they matched the similar profiles. There was then additional work done where in fact the lab went back to the original vials of DNA that had been extracted from the original vials of blood that had been obtained from the Red Cross so that they could ascertain, for example, that those two separate DNA extractions had not been done mistakenly or mislabelled, that in fact you could show that they went back to two different vials of blood that had come in from the Red Cross and then additional probings were done, and one can do probings, the molecular biological term is to do it at low stringency, so that when you probe you get a number of bands coming up, it's something like the multi-locus approach that used to be used in the U. K., and you can score then this genetic fingerprint on a multi-locus probing and look at these same samples to see if they match on, my understanding is, over 20 bands, and so my analysis of that was to use the approach that would be used in the U. K. for a multi-locus probe and say if the chance of any two bands being shared in a multi-locus system is .25, to say

well, the chance that two individuals matched on 20 would be .25 raised to the 20th power, and that number becomes less than one in a trillion, so that's how I arrived at my conclusion that for those two samples to match on that many bands would only happen in less than one in a trillion cases.

Q. O.K., so we have samples now up to freguencies less than one in a trillion?

A. In the case of the duplicates, and that's the question of whether these duplicates could have arisen from two separate individuals, that's what that calculation is based upon, because there are many more bands.

Q. And to keep things in proper prospect or - that is one chance or less than one in a trillion of coming from an unrelated individual?

A. Yes, two unrelated individuals, yes. Yes.

Q. And the chance of maybe those two samples coming from siblings would be one in 1,000?

A. No, in fact, when you run the 20 sites it would be less than one in 1,000. I'd have to think of the calculation but let's say for 20 sites you're talking about one-half raised to the 20th power. That is going to give you quite a low number. I don't have that number in my head right now but it's a very low number. It would certainly be less, very significantly less, than one in 1,000, even for siblings.

Q. O.K., I believe you mentioned that there was a lot of people knew about these duplicates in there?

A. That's right.

Q. And I believe you mentioned Dr. Shields as being

one of them?

A. That's right.

Q. So I suppose the lab was very concerned about that and wanted to make sure that it didn't come from somebody else?

A. That's right. If these were indeed coming from separate individuals that would be a remarkable finding.

Q. So you wanted to extinguish that possibility?

A. We would want to be able to know that that was not the reality, yes, because if that was the reality it would make a very significant impact into the way we're using this technique, yes.

Q. So if you can use these extra probes and get up to less than one in a trillion for five probes, but yet for court cases you don't have to be so sure so you just come in with the much less standard test and come in with one in 300 million?

A. These were done on individual single locus probes and that is done, and I would support the rationale behind doing that, the rationale being that we know exactly what we're looking at. When you use a multi-locus probe you're not sure what the bands mean exactly, and it's always, I feel as a scientist, much more reliable to know precisely what you're looking at and to be able to analyze that in stricter, more rigorous genetic sense than basically saying when you're using a multiple locus situation it's, if I were to draw the analogy, almost like taking a photograph of two people and saying, well, look, we can superimpose them so it must be the same person. We don't know the biology behind that, we don't know the basis

for why one person's nose is a certain shape and another person's another shape and how similar noses have to be to be called identical and so forth, and so the single locus probe situation, we know the molecular biology behind that. We know that we're looking at two specific sites in an individual and we can distinguish the differences unequivocably. When you do the multi-locus situation things get much more hazy and you're comparing apples, oranges, and at least pineapples if not potatoes as well.

Q. O.K., my position, Doctor, is that whenever you want to guess as to whether or not the evidence sample come from a particular individual analyzing five probes is good enough, but when you want to be sure, then you'll try and match up on about 20 bands?

A. Well, as a consideration in these comparisons that make the situation of trying to establish whether two samples in the database are duplicates, and it's very different from comparing a forensic specimen to a known body standard, in the database samples one can always go back to the DNA. You have ample amounts of DNA to be able to go back to, you can rerun tests, whatever. Often in the forensic context, when you have a sample of the DNA that's been obtained from a crime or victim, the amount of DNA that you have is quite limiting and you can't just go back to that. You often have used it all up in your initial probing and so you can't go back, and so you want to be able to get the most reliable information you can out of that forensic specimen. That's unlike the

situation in the database where you have samples of DNA that are virtually unlimited. You can go back to them, you can reprobe them, if you make a mistake with one you can always go back to the original. In the case of forensic specimens you just do not have that luxury and you have to be very cautious with how you treat that specimen, so there's a distinction there about the nature of the specimens themselves that has to be taken into account and it's not that a forensic specimen, you can go back and probe it and if it doesn't work you can go back and extract some more and do another technique. You have to be able to make sure you're going to get the best possible results on that one shot that you have at the sample, so I would say that that makes a significant difference in how the two approaches are done.

Q. You're only allowed one mistake?

A. Typically, from what I know, in the case of some forensic specimens there is enough DNA and you can go back to it, but it can be frustrating if you've used up all the specimen and you can't go back and something has gone wrong.

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

THE COURT: Yes, it would, so the jury will go out for 15 minutes.

(BRIEF RECESS - RESUMED AT 11:35 a.m.)

(ACCUSED IN DOCK.)

(JURY CALLED - ALL PRESENT.)

Q. Now, Dr. Carmody, when you were explaining the ethnic diversity throughout Canada you stated that 93% of the people in Canada are Caucasian?

A. Are classified as Caucasian, yes.

Q. And it was a very small percentage that are Indian descent?

A. Yes, I don't remember the figures exactly. I think it's something like 1.8%, 2%, something of that nature.

Q. That's throughout Canada?

A. Well, they're not evenly distributed throughout Canada, but in Canada, yes.

Q. Did you inquire as to the Miramichi area, say around Newcastle, what the Indian population is?

A. I personally don't know, no.

Q. So you don't know what ratio there would be there?

A. I don't know what there would be there, no.

Q. Do you know the ratio of criminal offences committed in the Newcastle area between Caucasians and Indians?

A. No, I don't.

Q. I believe some witnesses testified that in a criminal case that it would be beneficial since you don't know the ethnic group of the person who committed the offences, then it would be good to bring before the Court the probabilities in all ethnic groups which there may be possibilities of the criminal coming from?

A. That has been suggested. I know that John Bowen -

I haven't personally done it but John Bowen did a calculation of Mr. Legere's genotype using the same techniques as we've used for the Caucasian database using the Northern Ontario Indian sample that we have, and I just know - again this will be hearsay, I suppose, but he told me that the number came out to be rarer.

Q. No, I don't want to know what the results are, Dr. Bowen would have had the chance to put that into evidence, but that has not been put into evidence?

A. That's not been put into evidence.

Q. No. And mentioning the group of Indians from Northern Ontario, I believe there's been calculations done on Indians from B. C. also?

A. That's right, the R.C.M.P. has at the present time, actually, three samples from three areas of native Canadian Indians, one from British Columbia, one from Saskatchewan, one from Northern Ontario.

Q. And the findings of the bin frequencies between those three groups of Indians, they would be all statistically significantly different?

A. They are statistically different from one another. I've been involved in that analysis. In fact, it was a paper that I presented with Doctors Fourney, Bowen and Kirby at the International Congress of Human Genetics two weeks ago in Washington where in fact those three samples of native Canadian Indians showed that they had very different genetic profiles.

Q. And if a crime was committed in B. C. and the accused was from Northern Ontario it wouldn't be

proper to run his profile through the B. C. database?

A. Well, it depends on the question that you're asking. Again I think Dr. Kidd made the point, and I would support the point, that there are two questions there, that if you feel that you want to estimate what the frequency of that genotype is amongst alternative suspects one would use the database that represented the population in general in that geographic area or for which there was some information for the police or whoever investigated it to suspect that it was in a certain area. You'd use the general database for that. If you want to come up with an estimate that is most favourable to the accused one would use a database that had the same ethnic background and the same geographic background, the same in the case of native Indian, the same tribal background as the accused, and that would give you an estimate that is most favourable to the accused, but that does not mean that that's the frequency of that genotype in the general population. It would be in the sub-population, and if there was some information suggesting that the alternative suspect had to come from that particular native group, then in fact that would be the proper number to give.

In the absence of that in general it's often, I know in the United States, becoming more routine now to give an estimate where they have a Hispanic database, they have a black database, I believe they have an Asian database but I'm not sure of that, and they have a Caucasian database, so you

run those calculations through all four databases and you give the numbers. I can just say that I've seen that done and I know cases where I've done it myself. The inference is very much the same, that no matter what database you run it through you come up with numbers that indicate that a particular genotype in whatever database you have is going to be rare. The numbers will vary, sometimes they'll be statistically different from one another, but they still will give you numbers where the genotype is rare.

Q. Now, when you checked within the R.C.M.P. database you checked the geographic area of Vancouver and you compared Vancouver to Kingston and to Ottawa?

A. That's correct.

Q. And you found no statistical significant difference?

A. That's correct.

Q. So based on that you, I believe last time in court, assumed that there would be no statistical significant differences through Canada?

A. That's correct.

Q. Was there any statistical significant difference with the group, database, from Montreal?

A. Yes, I have not finished the analysis there and I was not fully given the information till quite recently. There are, if my memory serves me, two loci out of the six that were statistically different in the Montreal sample from the overall amalgamated total Caucasian sample that we're calling it at the R.C.M.P. However, in the same way as with this particular case, if you run a particular genotype through that database in

Montreal you typically come up with a number that is insignificantly different from the number you would get if you used the R.C.M.P. database.

Q. Yes, I realize that's your finding, Doctor, but in May of this year you didn't think there would be a statistical significant difference within any groups in Canada and Dr. Shields disagreed with you, he thought that there would be a difference between French and English?

A. I don't remember if he specifically said that but he could well have. I don't remember specifically.

Q. So your opinion in May was wrong?

A. I wouldn't say it was wrong, I'd say for those two loci, two out of - we have six loci there - there were some statistically significant differences. One could say that if you do enough tests the nature of these tests is such as that sometimes you're going to find statistical difference when in fact there really is not statistical difference. It's in the nature of the process where you have to use some level where you decide two things are different or not, and you can't always be 100% certain.

Q. Even when you get statistical significant differences? How can you rely on statistics when they are not reliable?

A. Because statistics are always based on a finite sample. The larger the sample the less risk you have that in fact you will be misled by the inferences that you draw from those samples. Statistics by its very nature of analysis, some people have described it, is a process of making

inference under uncertainty. We don't have complete information in these situations so we're trying to draw the best conclusions we can and extract the maximum amount of information from the data that we do. We can't, however, be absolutely 100% certain in the types of inferences and statements that we're making, so typically in statistical tests that we do we might be using a 5% level of significance, as it's called, in which case if you did 19 tests on two things that really were the same, you did 20 tests, 19 times out of 20 you would expect to get them not being different, but once out of 20 you would expect to see them different even though they were not really different. On the other hand, if you use a one per cent significance level you would only see a bogus difference one time in 100, so depending on the size of your sample and the inference you're trying to draw, you have to make that decision ahead of time as to what kind of level of significance you're going to accept, because if you set that level too stringently, then you can make the other false conclusion, and that is that you won't find real differences when they really are there, so it's always a trade-off in these situations when you're comparing two things. You either are so stringent that you won't detect many differences when they really there and as a consequence make the mistake of calling things different when they're really not different, or in fact, using more stringent criteria, in which case you'll commonly be making the mistake that things are called different when they're really

not. I know that gets complicated and I don't know a simpler way to put it.

Q. When we get to calculating the odds of probabilities I believe you can have a scientific based opinion and you can have a generally based opinion without any scientific background, I suppose, to support your opinion?

A. There are opinions that are not based on specific explicit facts, I suppose, and people have opinions that are drawn from general knowledge and intuition and experience, life experience and whatever, and there are opinions that are based on hard factual data that you can go back to and re-challenge or be able to re-examine or be able to see if there is any mistake in that original factual data, so there are at least two different kinds of opinions that I can think of in that case, yes.

Q. Did you ever play poker, Doctor?

A. I have; not in many years, but I have.

Q. Blackjack?

A. Again not in many years, but I have played blackjack.

Q. But you know the principles?

A. Yes, I do, yes.

Q. And could the odds of drawing to an inside straight be calculated scientifically?

A. Yes, they could. You'd have to - if you're just dealing me five cards I could calculate that probability. That could be calculated scientifically and would not just be an opinion, yes.

Q. And even after so many hands are dealt out, say there's four or five players, the hands are dealt

out and then you're drawing cards, calculating as to how many cards are left and the chances of the card that you need being already out, scientifically you could calculate as to what the odds are of drawing to an inside straight?

A. That could be done. The calculation becomes more complicated, but it could be done. It could be done. There's imprecision in it but you can calculate a probability, yes, if you know how many cards have been dealt out and you have some information about what other people have bid and so forth. You could take that into account.

Q. And generally, too, as in poker or blackjack or any card game sometimes you find a player unusually lucky?

A. It seems people can have winning streaks, yes, or losing streaks.

Q. Seems to defy all odds?

A. In fact, when they're analyzed they actually don't. It's remarkable how - my rendition of it would be that I think the human mind is always trying to fit structures onto the world, and in the same way, when you have a winning streak or losing streak it is a way of pulling together a lot of experience and information that is simple to convey and say, well, they've won an unusually greater number of times than I would have expected, but in fact when you actually calculate them it's surprising how often you expect things like that.

Q. So let's bring ourselves down to the game of blackjack where you're playing just against one other player, the dealer.

A. Right.

Q. And basically your odds are usually, whether you're the dealer - I believe the odds are a little in favour of the dealer than the other individual?

A. I believe so. I'm not an expert on blackjack, I know that there are books written on it and there are people that claim if you count cards and you get towards the end of the deck you can adjust your bidding so that you can exploit the fact that you have a greater probability, if certain cards are out, to win versus the dealer and so forth. To be honest, I'm not that expert at that particular game.

Q. But generally your odds are almost 50 to 50 that you're going to beat the dealer?

A. I think in blackjack it's - from what I've heard of casino games, it's probably the one where you have the best shot, yes, but I think it still is - well, depending on how good a card counter you are and whatever and how many decks are in the stack and so forth, you can have better or lesser chances. I don't know how close it is in terms of the two sides.

Q. But depending on luck again a person can sit there and can double his money thinking that, well, I've got to beat the dealer one of these times, you know, the odds are in my favour, I haven't beat him the last seven, eight times, I'll beat him this time. That happens?

A. That does happen and it can happen in a situation like blackjack where in fact the odds are changing with each hand if you keep using that same deck.

If you have a freshly shuffled deck for each hand the odds are going to be staying the same. I think it's easier to analyze something - if you want to draw an analogy, it would be something like roulette where, in fact, if you kept betting on red and red hadn't come up your chance of winning on the next bet is the same as on the first bet, there's no maturity of the odds happening there.

Q. Yes, but it's much like the Lotto 6/49, your odds are the same on every ticket?

A. That's correct.

Q. And how would you calculate the odds in a 6/49 draw of winning, as a statistician?

A. I'd have to think about that because as I understand it, I'm not that familiar with the rules of Lotto 6/49, that you - I don't think there has to be a winner, if I'm not mistaken?

Q. No, that's right.

A. So it would just go for another week?

Q. That's right.

A. And so it would depend on how many tickets were sold that week, for example, as to -

Q. As to what the prize is.

A. What the prize is.

Q. That doesn't change the odds of winning?

A. It doesn't change the odds of winning because any particular combination of numbers has an equal probability of coming up, and what are there, six numbers?

Q. Six numbers, you pick out six numbers out of 49 and you'll see if those six numbers will come out of the big round ball.

A. Right, so that the number of possible combinations is going to be 49 factorial divided by six factorial divided by 43 factorial. That would be the total number of possible combinations. That would be in the denominator. In the numerator you would have the number - so that's the number of combinations, and you presumably have one of those combinations, so you have one over that number in the denominator.

Q. Could you calculate that out for me?

THE COURT: Oh, now, aren't we really - say a trillion, over a trillion?

A. Well, it's some number. It's admittedly a low number.

MR. FURLOTTE: My Lord, I would ask -

THE COURT: I did it in my head, it's one over a trillion.

A. It's a number that is very low -

MR. FURLOTTE: Well, My Lord, you're wrong.

A. - and yet very many weeks somebody wins the lottery, as I understand it, again not being a lottery player but -

Q. No, but being as sort of a population geneticist and using statistics you should be able to figure out what the number would be?

A. Well, I just gave you the formula. If you want me to sit and work it out, I think that, for example, my calculator does not allow me to easily calculate 49 factorial.

Q. Would you give the formula again?

A. It is 49 factorial, that is 49 times 48 times 47 times 46 times 45 times 43 all the way down to one, O.K., that's 49 factorial, divided by six

factorial, that's six times five times four times three times two times one, divided again - and that multiplied and divided again into 49 minus 643 factorial, which is 43 times 42 times 41, all the way down to one, so that gives you the number of potential combinations of taking six things out of 49 things, and that's the number of combinations because you don't pay attention to the order of the numbers, as far as I know, in the Lotto - lottery of 6/49. It doesn't matter if you have a 45 before a 43 or whatever, the order doesn't matter, so you're talking about combinations, you're talking about the number of ways that you can choose six numbers out of 49 numbers, and the formula that I just gave you would give you the number of combinations of six things taken out of 49.

Q. So it would take you quite a while to figure that out?

A. If I had the right calculator I could just punch that in. In fact, there are some calculators where you can just put that number in there and hit a button and an electronic marble gives you the number. It's going to be, obviously, a very large number, and so when you say it's one over that number the possibility of that occurring and of your winning is going to be quite low. On the other hand, I believe in Lotto 6/49 there are other winning combinations where you don't need to get all six, there are sort of partial winners, isn't there?

Q. Well, those are partial winners, yes. We don't have to get into that.

A. And so you can get into very complex considerations there.

Q. O.K., Doctor, I did a rough estimate last night in my hotel room and you can tell me whether or not this method would be right. There's six numbers out of 49, I divided six into 49 and I come up with one in 8.16.

A. Well, six divided into 49?

Q. Six into 49 is 8.16, 6666, but we'll just use 6, O.K.?

A. O.K.

Q. Then that left because you have a chance - you pick six numbers so you got any one of those six numbers could come out on the first ball, so you've got six chances out of the 49, so that brings it to one chance in eight, right?

A. O.K.

Q. So that leaves 48 balls left in the drum and you've got five numbers left, so you divide five into 48 which gives you 9.6, then four balls left out of 47, you divide four into 47 and it gives you 11.75. You've got 46 balls left in the drum, you've got three chances left, and that gives you once chance in 15.3, with two balls left it gives you one chance in 22.5, and one ball left out of 44 balls left in the drum gives you one chance in 44, so what you would do is you would multiply 8.16 by 9.6 by 11.75 by 15.3 by 22.5 and by 44. Would that be appropriate?

A. No, it would be wrong.

Q. That would be wrong?

A. Yes.

Q. Why?

A. Because you've assumed the specific order that you had to get.

Q. No, I haven't.

A. As I understand what you were doing you were assuming that you had to get a specific order that the balls were coming out.

Q. No, as long as the balls come out with one of the ones you picked.

A. Well, I'd have to go through that calculation because - let's say for the sake of argument, and I don't know what the point is that you're trying to derive from this line of questioning, but it is a large number, is that not right? Or maybe I shouldn't be asking the questions?

THE COURT: One over a trillion. May I just intervene for a minute here? Where is this leading us? Aren't we wasting the time of the jury and of the Court and of everyone involved here in pursuing this thing? We've talked about blackjack, we've gone from there to 6/49 Lotto, what is the purpose of this, Mr. Furlotte? Are you seeking free advice here from this -

MR. FURLOTTE: I want to show that regardless of how high the odds are, My Lord, there's always possibilities.

THE COURT: Well, what relationship has this got to the question of population genetics with which we're concerned in this trial?

MR. FURLOTTE: My Lord, I'm following up to another area of questioning here.

THE COURT: Well, tell me what it is. I mean tell me what the significance of all of this is.

MR. FURLOTTE: The chances that somebody from New Brunswick is in the R.C.M.P. database.

THE COURT: Why don't you take my figure of one over a trillion? That's way, way out, I'm sure.

MR. FURLOTTE: Oh, it's way out.

THE COURT: Yes, but give us the bottom line there of your figure.

MR. FURLOTTE: The figure, one in 13,942,000.

THE COURT: O.K., let's take that as an example.

A. I agree that that's a large number and if you put it in a denominator you get a very small number.

Q. Regardless of how high the odds are of winning the lottery it's won often?

A. Not every week, though.

Q. Not every week, no. Sometimes there's -

A. Sometimes you go for a number of weeks without it being won.

Q. Sometimes there's five and six winners.

A. That's right, and there are many millions of people who play the lotto.

Q. Now, when you said that it would - I believe you said there might be one chance in a million that there isn't somebody from New Brunswick in the R.C.M.P. database?

A. That was a seat of the pants estimate. I can calculate it for you if you like.

Q. Yes, please.

A. The way you do that calculation is to say that let's say you were to draw 500 people at random from the Kingston area that could have contributed to the database, O.K., 500 people. To have nobody from New Brunswick represented in that sample of 500, if we knew that the military personnel, and we did know, that 5% of the military personnel there were from New Brunswick, O.K., and assuming

that everybody had equal probability of donating blood. You know, you can argue about that but it's a simple, I think probably correct, assumption that there's equal representation in proportion to the numbers that are there. The probability of you choosing a person at random from there and they did not come from New Brunswick is .95. There's a 95% chance that you would not have somebody from New Brunswick when you chose one person.

Q. I can't understand that. How many people at the Kingston -

A. I'm just saying when you're choosing, you're choosing from an area where you know 95% of the people do not come from New Brunswick. Five per cent of them do, 95% of them don't, so when you choose a person at random from there, the chances of not getting a New Brunswicker are .95. You have a 95% chance when you choose one person, O.K.?

Q. Right.

A. O.K., you've chosen one person, they didn't come from New Brunswick. Most of the time they're not, 95% of the time they're not. You chose a second person, the chance the second person didn't come from New Brunswick is .95. The third person, .95, fourth person, .95. You would have to multiply .95 times itself 500 times, O.K.? That gives you a number that is very, very small. I can't tell you right off what it is, I can do it on my calculator, but that's the way you would calculate the probability of having 95 samples taken independently from that database where there was

a 95% chance that each one of those samples were not from New Brunswick, so the chance that all 500 of them were not from New Brunswick is .95 multiplied times itself, so when you keep multiplying .95, which is close to one, but you keep multiplying by itself, it keeps getting smaller, it gets down to 80, whatever. I can do that calculation for you, it's a fairly simple calculation.

Q. Didn't you say the odds, to begin with, would be 95% chance you're not going to pick somebody from New Brunswick? Is that right?

A. On any single sample like that, yes.

Q. If you put 100 balls in a big drum, you've got 95 blue ones for people who are not from New Brunswick, you've got five people who are from New Brunswick, and you spin that and your chance of getting, say, a red ball out for New Brunswick rather than a blue one - your chances of getting a red ball out is only a 5% chance?

A. Right.

Q. And those odds would remain the same every time?

A. Every time if you have a large enough group of people and we call it sampling with replacement. That is, by taking a sample out you don't change the odds, that's right. You could do the calculation that way, it's much more complicated. I did the calculation and I could tell you that in fact the probability of getting a sample of 500 from that database where we know 5% of the military personnel were from New Brunswick is less than one in 1.2 trillion. Just did the calculation, .95 raised to the 500th power, that is .95 multiplied by itself 500 times, which is what

would have had to have happened in order to not have any New Brunswicker in a sample of 500 from the Kingston Base.

Q. What was your calculation?

A. I had one in - sorry, one in 7.27 trillion. 7.274492 times 10 to the minus 12th, which is a trillion.

Q. That there isn't anybody from New Brunswick in that -

A. That's the probability you would calculate to have a sample of 500 from that area where you knew that there were 5% of the people from New Brunswick, of the probability of not having any New Brunswicker in that sample of 500, so my estimate of one in a million, alas, was wrong.

THE COURT: I was closer.

A. You won the bet.

Q. Now, that's based on pure chance, if we were using the ball method?

A. That's right.

Q. Of course, since we're dealing with populations and human characteristics those odds could change, if New Brunswick was full of a bunch of wimps that wouldn't give blood?

A. That could possibly be. From my experience I would doubt that assumption but - I think if anything, from my experience, they're likely to be over-represented but -

Q. Would there be other factors that you could take into consideration except that -

A. It could be that a particular regiment was there from New Brunswick that was out on maneuvers during the time of the blood sampling. It could

influence those odds slightly because they included people not only in the military but their dependents, so if they were based there you would think they would have equal chance. Five per cent, I don't know what the actual size of the total military personnel was, but there are several thousand people there. I think it's a low probability that there were no New Brunswickers represented. I would also say from our knowledge of the samples through Canada that we don't see significant differences, that if there were no New Brunswickers there, let's take that hypothesis, from the information that we do have on distribution of blood group frequencies in Caucasians and other genes in Caucasian populations it would be quite extraordinary to find that the numbers would be different in our database. In the same way, if I could go back to just those duplicates in the samples that were in the original R.C.M.P. database -

Q. Maybe, Doctor, you won't have to. In order to calculate the way you did the probabilities of nobody from New Brunswick in that database, there cannot be any unknown factors to be able to use that mathematical formula, for it to be reliable?

A. No, there's lots of unknown factors but -

Q. No, I know there's lots of unknown factors, but in order to use the mathematical formula there cannot be any unknown factors; that's the first principle?

A. Well, I would say that the simplistic model that I used of sampling with replacement for that size of a sample, you could expect that there would be

slight deviations. Suppose, for example, that there were many younger people there from New Brunswick than from other provinces and they were less likely to give blood or something like this. You can use your experience and intuition to say some things about military databases that you don't have to have hard factual data on. You could say, for example, that there were no known movements of people in or out of that database in the two-week period that the sample was derived and so forth, so I'm trying to think of some realistic situation that would cause me to have some doubts about that calculation, and to be honest, I'm pressed to come up with something in terms of an explanation that would suggest that that calculation is not likely to be right, and I'm coming up short. I can't think of one except if there was some oath that people from New Brunswick had signed not to donate blood, suppose they were all Jehovah's Witnesses or something from New Brunswick. I would suggest that that would be getting into science fiction.

Q. Now, you mentioned you did a statistical likelihood test between the groups from Vancouver, Ottawa and Kingston?

A. That's right.

Q. And I believe you consulted with a statistician?

A. It was not a consultation. I read something that he had written in a journal called, "Chance", and it was an issue that was devoted to forensic issues around estimating probabilities of DNA. He had an article in there where he suggested one of the tests to be done to see whether there was

any statistical deviation from randomness was this non-parametric test, this median test that I used to see if there was any deviations. I did not and I've never spoken with Seymour Geiser. I know he is an eminent statistician at the University of Minnesota, I've seen reference to other of his publications. I was following his suggestion in the sense of it being out in literature as one way of testing.

Q. But before you read that article you didn't know that this test could be made?

A. No. I knew it could be made, I hadn't actually thought of applying that test to this data. Sometimes I'm a little bit slow that way.

Q. But the thought of applying that test to that data, did that come about because Dr. Shields had applied that same test between the R.C.M.P. data-base and the FBI database?

A. No, in fact, now we're talking of a different issue. In fact, the test that I used - and now we're talking about comparing bin frequencies, and that was not suggested by Seymour Geiser at all. That was in fact a test and a way of applying a particular test, a contingency table test, likelihood ratio test, a Chi square test, that I had done at least a year, or at least six months before I even knew the name of William Shields, and I had in fact developed a computer program that would do that test in a very rigorous way for samples where in fact you have very low numbers in some of the cells, as we call them, which is a problem statistically, and it is a program that in fact I've written and

distributed to a number of people, and I did that much before William Shields ever brought that out in any testimony.

Q. Had you ever tested in court before you heard the name William Shields?

A. It's a little bit close. I'm trying to remember now because my first testimony in court was just last January, and he testified in the same voir dire, and I'm trying to remember if it was before or after me that he testified, and I can't remember because it was in Ottawa, and I believe that I testified before he did and I had no knowledge of him at that point.

Q. And in that case did you recommend confidence intervals?

A. In that case I did use confidence intervals, yes, and I recommended that confidence intervals - actually, I didn't make a recommendation. I used confidence intervals and I'm used to using confidence intervals, and to me they've always seemed a very convenient tool to communicate the imprecision in numbers, and I think often we can be deceived by just hearing numbers that a certain poll gives 19.2% to something, and unless you have some sense of the imprecision of that number it really is not communicating what it should statistically.

Q. O.K., but maybe just to clarify matters, when you testified in that case although you may have used confidence intervals for your own purposes, did you just come into court and substantiate the findings by Dr. Waye, or did you come into court and change the figures?

A. As I recall, they were substantiating Dr. Waye's figures. I redid the calculations and I presented confidence intervals in my oral testimony. In fact, as I look back upon it now, I'd like to correct. I know definitely now that I testified before Dr. Shields in that particular voir dire, and at the time, at the point of my testimony, I did not know of Dr. Shields.

Q. O.K., back to the test that you did after reading Dr. Seymour Geiser's article. You said you didn't see any strong deviation?

A. That's right.

Q. And that was to check for linkage disequilibrium?

A. There were two tests there. There was a test for the assumption of Hardy-Weinberg equilibrium, and that is for randomness within bands at one locus, at one probe, and I found no indication there of deviation from statistical independence within one probe. Then I did another test which essentially is the same thing only applying it across two probes, and there I found no statistical evidence of a deviation from the independence of what was happening at each of those two probe sites.

Q. Now, when you say no statistical evidence that means you didn't find a rate of deviation which would have statistical significance?

A. That's correct, and I would be -

Q. And what do you mean by statistical significance in this particular event?

A. I mean that there would have to be correlations occurring between certain bands at one locus and they're always occurring, or almost always occurring, with bands at another locus that would

be a great enough correlation that you would pick it up when you did this test.

Q. But for statistical significance in this test would you have had to find that there was enough variation to show that there was linkage disequilibrium?

A. That's correct, if there were small amounts of it the test is not powerful enough to have picked them up.

Q. Because you didn't have enough samples?

A. That's right, that in a sample of even a thousand individuals the number of combinations between bands at two loci is so great that you don't get enough occurring in every of the possible combinations.

Q. But in the small samples that you did have you found there was a small deviation?

A. No, in the samples that I did have I found no evidence of deviation, but if there were some small amounts I would not have been able to see it, that's the point of those tests, that they are going to pick up strong deviations but not slight deviations.

Q. O.K. I copied from my notes, and I may have misunderstood but I thought you said, when I did the test I didn't see any strong deviations, there was a weak amount of deviation.

A. No, if I said that I would retract it. There was no even weak deviation. They fit the expectations of what you would expect if there was independence between bands at one locus and bands at another locus.

Q. And what samples were you using for that test?

A. I was using the Caucasian database for that test.

Q. That the R.C.M.P. have?

A. That the R.C.M.P. have, yes. That's the only -

Q. Did you test all of them? Did you make your tests with all of the R.C.M.P. Caucasian database, use all the samples, or did you just pick a few out of it?

A. No, I took the whole database because you need as many samples as you can to run these tests. The larger the number that you have, the more powerful the test. That is to say that because of all the different combinations you want to have the possibility of having as many of those combinations occur as often as they can, and if you have a sample of ten there are perhaps 10,000 combinations. Well, you're certainly not going to get all of the combinations represented, so if you have a sample of ten it's going to be a very sparse table that you have, and you're not going to be able to do - if you even have a sample of a hundred you're not going to be able to fill up all the cells in that table, and you don't know if you don't have an observation in a cell whether that would never occur at a larger sample or whether it just didn't occur in your sample of a hundred, so you have to have a large sample.

Q. O.K., as I understand the databases from Vancouver, the combination from Vancouver, Ottawa and Kingston, there was no statistical significant difference in binning frequencies?

A. Between them, no.

Q. Now, where Montreal has a statistical significant difference in binning frequencies -

A. For two of the six, yes.

Q. Two of the six. If you did that same test with the Montreal database, comparing them, would you find a - are you more likely to find a small deviation?

A. Looking within the Montreal database I don't think there's any higher or lower chance of there being a deviation.

Q. What about when you're comparing them?

A. When I combined it with the other? If I combined it with the other -

Q. You haven't done that test?

A. I haven't done that test, and in fact the Montreal sample is a quite preliminary sample, I just received it very shortly ago, and in fact, one of the loci has not been completely finished yet, and it is a sort of early sample, so to speak, from the Montreal area so - and I haven't done the tests on that sample, and I haven't personally done tests on the FBI sample or the Minnesota sample which are other samples that I've included in that chart. I've not done tests on those. The purpose of giving those calculations were not to show that all of those particular populations are in Hardy-Weinberg equilibrium or linkage equilibrium, but merely the fact that if you run the same genotype through those other databases you come up with a number and you come up with the same inference. That was the only purpose of that, but I can't verify those other databases, I have not done the studies on those. I know that Dr. Bruce Weir at the University of North Carolina has been analyzing and has analyzed the

FBI database in a number of ways and has found no evidence that there is either deviation from Hardy-Weinberg equilibrium or linkage disequilibrium in the FBI database.

Q. I understand Leo Lavergne was also doing a test of a small community in northern Quebec to compare it with the Montreal -

A. He has two other samples that I have not seen and I'm not even sure are finished yet, one from Abitibi and one from Chicoutimi, which should be very interesting, and I'm very interested in seeing those ultimately because if there is likely to be any population substructuring, knowing historically the origins of those areas and the fact that there were a relatively small number of founders, and by relatively I mean several hundreds of people, and then there were a number of generations where there was not a lot of migration into those communities and there were very large family sizes for a number of generations, that would be in my opinion, if there is going to be any evidence of substructuring, any evidence of populations in North America that show difference from other populations, Caucasian populations, they're likely to be found there. I can't think of a better biological situation to find differences, and that's why I'm really interested in looking at those. He at the present time has not finished them, to my knowledge, and I last saw him a month ago and he had not finished those yet. I know he's making some comparisons and collaborating with some people from France on those as well, but I don't

know those results and I have not seen those results, and so far as he's told me, they are not available yet.

Q. Did he give you an indication that there was a significant difference between two probes?

A. He didn't. He didn't have any information to give me on those at all. He didn't give me any information.

Q. O.K., you mentioned he's interested in getting data from France?

A. Yes.

Q. I believe you also checked the database from France?

A. I have and I had and I presented in the voir dire information on two probes that I'd received through the FBI that came from France, yes.

Q. And there seems to be a radical difference in the bin frequencies between France and the R.C.M.P. database?

A. I would not use the term radical. In fact, as I recall them, I have them back in my notes, for one of the two it fell outside the range of the confidence interval on that probe. That was not a radical difference, whereas I remember it was - our estimate was one in 78 with some confidence intervals going down to, let's say, 60, and France gave you one in 57 or something like that, it was outside the confidence range, and that would suggest that perhaps when you looked at the total bin profile at that locus in France versus North America you might find a statistical difference overall. Looking at that particular one it looked like there was, others might not

necessarily be different, and so overall you may not find statistical difference in the bin frequencies. I don't know and I haven't seen those comparisons done yet. I'm very interested in doing some of those.

Q. But you had that information back in May?

A. I had the two probes from France, yes.

Q. Yes, and even though you had that information back in May you told the Court that you didn't think that there would be any statistical significant difference in some groups across Canada, geographical areas?

A. That's right, and I still think that. I still think it's unlikely that there will be differences and I still feel it's unlikely that when we have more samples from Quebec that we will find forensically significant differences. Perhaps there'll be some slight statistical differences but -

Q. Let's stay out of forensically significant differences here and stay with -

A. Well, I thought that was what was important for the purposes of this case.

Q. Let's stay with -

MR. WALSH: Well, I think Dr. Carmody is entitled to give his answer and -

MR. FURLOTTE: And I'm entitled to ask questions.

MR. WALSH: Well, I think he has the courtesy to let him finish his answer before he can continue with another question.

MR. FURLOTTE: There are statistical significant differences between the R.C.M.P. database and the database in Montreal?

A. For two of the six probes.

Q. Right, and at the May hearing you told the Court that you didn't think there would be any difference even though you had that data from France?

A. That's correct.

Q. And after Leo Lavergne completed his database he proved that you were wrong?

A. For two of the probes.

Q. For two of the probes, that's all we were talking about.

A. Yes, and we're also talking about forensically significant differences, and for forensically significant differences there were none.

Q. For forensically significant differences, if you run your profile through the R.C.M.P. database, five probes -

A. Right.

Q. - you would find it extremely rare and maybe the same figures, one in 300 million?

A. Quite likely.

Q. It's quite likely, possible. If you compiled a database from the Carmody family and you run your profiles through that you would expect to come out with what kind of a -

A. A number that would be less rare, a number that would be more common.

Q. But even though that number would be less rare and more common, you would probably say that there is no forensically significant difference, isn't that right?

A. Well, if it were rare, which it's likely to be even in the Carmody database, I would say that

there was no forensically significant difference, yes.

Q. So why are we bothering with population databases?

A. Well, it seems that defence counsel can sometimes become preoccupied with the difference between one in five million and one in 300 million, and we've been trying to, rather, perhaps, ineffectually, convince them that forensically it doesn't make any difference whether it's one in five million or one in 100 million. That is still a rare occurrence and the chance that two people happen to have coincided like that or two people had donated different specimens is very rare.

Q. But it's only once defence counsel was able to get expert witnesses to come to court and testify that there was statistical significant differences that the forensic labs come up - sit down, Mr. Walsh - that the forensic labs come up with the new term, "no forensic significant difference"? Is that right?

THE COURT: Well, before that question is answered we're going to recess and we'll come back at two o'clock.

MR. WALSH: Thank you, My Lord. Your caution yesterday has stopped me from saying anything.

THE COURT: If you were going to say anything you were going to say it very mildly.

MR. WALSH: Very loudly, I would have.

THE COURT: No, mildly.

MR. WALSH; Mildly, yes, My Lord.

MR. FURLOTTE: Sign of weakness, My Lord, sign of weakness.

THE COURT: Two o'clock.

(LUNCH RECESS - RESUMED AT 2:10 p.m.)

(ACCUSED IN DOCK.)

(JURY CALLED - ALL PRESENT.)

THE COURT: Now, you had further questions, Mr. Furlotte?

MR. FURLOTTE: Yes, My Lord. Doctor, I believe when we left off I had asked you the question, but it's only once defence counsel was able to get expert witnesses to come to court and testify that there was statistical significant differences that the forensic labs come up with the new term, "no forensic significant difference", is that right?

A. I am not sure of that. I have not read all the previous transcripts and cannot comment as to whether that's true or not.

Q. But in some of the transcripts that you've read the experts for the forensic labs were saying all along that there was no statistical significant differences between any groups within the Caucasians; would that be about right?

A. Not even positive about that. I think that - I'd have to say that was the likely belief. I don't know if the tests had actually been done and whether there was anybody who had actually said that.

Q. And Dr. Lander and Dr. Lewontin was saying all along that -

MR. WALSH: My Lord, at this time - I've been patient in the way Mr. Furlotte has been questioning this witness. Mr. Furlotte is well aware of the law, that he cannot by phrasing questions in that fashion put the evidence of others who are not testifying in this court before the Court in that

particular fashion. Now, he's done it throughout the morning and I haven't said anything, but now he's starting to actually testify through the mouth of these experts, or so-called testify through the mouth of these experts. Dr. Carmody has given his answer as to his knowledge and I don't think it's fair under these circumstances to have him phrase the question in that fashion.

THE COURT: Well, I think, Mr. Furlotte, as Mr. Walsh says, you have been given quite a bit of liberty, and I've given, perhaps, both sides some liberty in that regard, but you are suggesting things here that Lewontin and Lander are purported to have said which they may not have said, I don't know.

MR. FURLOTTE: My Lord, the Crown's expert witnesses have been coming to court and giving their opinion and stating that they based their opinions and their opinions are supported because of articles they have read by other experts -

THE COURT: Those are the Crown witnesses, but the Crown lawyers haven't been putting words in the mouth of these two gentlemen, Lander and the other man, but you are. You're putting words in their mouth and you're putting them in the position of testifying here at this trial, in effect. It may be right, what you're quoting, or it may be wrong.

MR. FURLOTTE: As defence counsel and on cross-examination, whether cross-examination is from defence counsel or from Crown counsel, I can ask leading questions and put the answers in their mouth and ask them if they agree with it. That's what a leading question is.

THE COURT: You can, but you cannot give testimony for

other witnesses who aren't called. You can ask leading questions on relevant topics of evidence, and if you want to put up a certain theory to this witness and say do you agree with that or don't you agree, would you agree, for instance, that the population geneticists have become more conservative in their outlook in the last two or three or four years while DNA cases have been being tried in the United States, what is your opinion of that, and you can ask the question in that way, but - I suppose if you want to ask him have these two gentlemen, Lander and the other chap - have they taken more conservative views than you have of a certain question.

MR. FURLOTTE: I believe that's already been established anyway, My Lord. Doctor, would you agree that the position of the forensic labs - population geneticists in support of the forensic labs at one time believed that there was no significant differences between - with Caucasians in different geographical areas?

A. Well, if you meant worldwide, I don't think that was the case. Perhaps within North America they would have felt that there was not going to be any significant frequency differences, yes.

Q. And since that assumption was made experts on behalf of defence counsel have proven otherwise?

A. Well, there have been some statistical differences shown in some of the bin frequencies between different areas as I've shown in the case of the Montreal sample compared to the composite R.C.M.P. sample. Again, as a statistician, as a population geneticist, one has to keep this in perspective

that these differences in frequency, while they may well be statistically real, really don't have a significant bearing on changing the inferences that we're drawing from these numbers. To just reiterate a statement that I made earlier, it's not that you sample a population that hadn't been looked at before and you find that, gosh, that frequency of that genotype is now only one in a thousand. It still turns out to be in some cases rarer, and in fact, in many cases rarer than it was in your original estimate, and in some cases it's a slight bit more common, but I haven't seen examples where in fact there have been remarkable surprises, and indeed, there have been studies done where you deliberately take data, and I know of a case in the U. K. where this was done, where they took data and they took the Caucasian data-base from the U. K. and they ran every one of those genotypes through their Afro-Caribbean database where it was known that there was statistically significant differences and where any population geneticist would have expected there to be differences. Nevertheless, when you do that and you deliberately and with malice, so to speak, run it through an obviously erroneous database, the conclusions are that those genotypes that were rare still remain rare, and you don't get any surprises where something that was one in 300 million is now all of a sudden one in a thousand. They remain rare, they remain within our, I think, just intuitive notion that genotypes are rare, and so the slight differences, though they could be statistically real between

geographic populations of Caucasians, are having even less of an impact in changing the forensic numbers that are generated by this technique.

Q. But, Doctor, we should be attempting to give the Court a clear picture as to exactly what the forensic laboratories' position is and exactly what the position of the people opposing the position of the forensic laboraties is? Would you agree with that?

A. I would agree, yes.

Q. So we'll try to get everything as clear as possible.

A. Right.

Q. Right, so in doing that - again, to distinguish the difference between what is forensically significantly different and what is statistically significantly different, exactly what are we looking at?

A. Well, in the case of statistical significance it's very much more completely objective and decidable ahead of time, one can set some limits.

Q. And is scientifically based?

A. And scientifically based, and I would hope that legal decisions are not strictly just based on scientific laws, that in fact there are a lot of elements in making any legal decision, making any decision about human behaviour or whatever, that we can't rely strictly on science. I mean one could imagine some kind of encephalograph test or whatever that you could tell something about a person or something about their history. Perhaps that is some possibility in the future but I would think that still the nature of the law, the nature

of the legal process, the very reason for having a trial before your peers, is that there are human subjective elements that can never be squeezed out of these decisions entirely and that I would hope that that would always be the case, that even in the example of this DNA, I would hope very much that a jury is not concluding from this that what I'm saying is that this is the probability that this person committed that crime. What these are probabilities about are the probabilities that in fact the evidence at the scene of these crimes were left there by this particular person. There could be alternative explanations as to how that happened. There can be many cases where you have data that are difficult to resolve scientifically strictly in isolation. That's where a person with their life experience, their background, their intuition, their judgment has to be called into play, and that's not - and I think happily, is not strictly a scientific process.

Q. Right, so it's very important not to rely solely upon the DNA evidence to convict any individual?

MR. WALSH: My Lord, that again is a legal question. Mr. Furlotte is attempting to delve into the whole legal aspect, that's something you will have to address the jury on and the court on, not Mr. Furlotte, and not through any evidence.

THE COURT: What was the question again? You had just got started on it, but what was it?

MR. FURLOTTE: I believe I stated something that as a result of that it would be very important, then, not to rely solely on DNA evidence in order to -

THE COURT: Well, that's a legal question, as Mr. Walsh

says. I'll be instructing the jury, you know, very much along the line of what the witness has just said when it comes to all this DNA evidence. It will be an instruction that this is a circumstance, this is circumstantial evidence that will have to be considered, they will have to attach their weight to it. If they say yes, that semen belonged to the accused, if that is their determination, they've got to go beyond that and say, as the witness points out, are there other explanations. You know, that doesn't mean that he is guilty of the crime in itself. They look to other circumstances, presumably, or other evidence to see if -

MR. FURLOTTE: I believe this witness said there may be other explanations to explain the statistical - the chance.

THE COURT: No, I think the existence of the semen in that particular circumstance was what I took.

A. Yes, that was my -

THE COURT: Yes, I understood you correctly.

Q. O.K., Doctor, when we're talking again the difference between what is statistically significantly different and what is forensically significantly different, one is based in science and the other is based on pure human subjectivity?

A. Yes, it is.

Q. So when you say there is no forensic significant difference you're not giving your opinion as a scientist, are you?

A. Well, I'm using my background as a scientist, my background in statistics, my background in knowledge of population variation, to inform me

and partially inform me about that decision, and I'm making some subjective threshold or boundary and saying, well, if I had a number that said the chances of this being left by another person were perhaps one in a hundred, I would put considerably less weight on that kind of evidence than I would if the evidence suggested it was one in 100,000. Now, I know we're going to get into the argument about where do you make that threshold. I would say that there's probably not a clear-cut, simple threshold, that this is a measure of what kind of weight I would give to that evidence. If it was only one in a hundred, if it was only one in ten, I would say gosh, I'd want to have other corroboratory evidence that was stronger to make me feel that - I guess the legal term is beyond a reasonable doubt, this didn't just happen coincidentally. If it were one in 100,000, if it were one in 10,000, I would be persuaded more and feel that the weight of the evidence were greater than it were if it were one in ten. I'm not going to say that at some point, one in 497, automatically you cross a threshold and the person is guilty if it's below one in 497 and not guilty if it's less than 197. That's what I mean by there not being a clear-cut scientific threshold that one could establish ahead of time. One has to somehow, in some very non-scientific way, factor into your decision in this as much of the evidence as you feel is worthy of being given weight, and the weight that you attach to it is going to come from your own private experience.

Q. O.K., so when I gave you the example before of if

you took your DNA profile on the five probes and run it through the R.C.M.P. database you might come out with the chances being similar to what they've come out for Mr. Legere?

A. Yes.

Q. And if we run your DNA profile through the Carmody family or clan the numbers would still come out as being rare?

A. They would come out being rare, probably not as rare, although I'm not absolutely sure of that because -

Q. And again there would be no forensically significant difference because as far as you're concerned they're rare on either occasion?

A. That's right.

Q. But if we run your DNA profile through the Carmody clan the figures might come out definitely as low as one in 1,070 or maybe it might come out as one in four or five thousand?

A. I would think it would be less than that because in fact the accidental fact that I have the last name Carmody is really only an indication of where my Y chromosome came from, and my other chromosomes are a mixture of all kinds of other places. I contain perhaps one-eighth Irish ancestry. It doesn't mean that my genes - on average one-eighth of my genes have derived from a Carmody ancestor in Ireland, in County Clare in Ireland, in fact, but indeed half of my genes derive from the Rhine River Valley in Germany, and the fact that I have the name Carmody is a very poor indicator of what my genetic composition is.

Q. O.K., so maybe you're a bad example.

THE COURT: There's a salmon fishing pool on the Miramichi River called the Carmody Pool.

A. My goodness. I knew there were a lot of inbred people up there.

Q. The fact is, Doctor, that if you used a general Canadian population database as used by the R.C.M.P. or you used something from a small inbred population or you used something from just a family, a big large family who are all descended from the same two individuals or just maybe from four different individuals, you're going to get a much wider range than what your upper confidence interval is showing?

A. That's correct. This is based on taking random samples from a large population.

Q. And basically the position of the scientists who oppose your position and the other forensic laboratories' position is that the fact that there are substructures and now they have proven that there are statistically significant substructures out there, that only tells you that there are substructures and it does not tell you any way whatsoever as to what degree substructure exists?

A. Well, it allows us to put some limits on how much substructuring there could be, and in addition to the amount of substructure we know from decades of human genetic studies on populations that while there are some statistically significant differences, let's say, from on average between France and, I don't know, Albania, to take just an example, that those differences for very many loci are likely - are in fact quite small, and if you looked at adjacent and averaged over all of

Europe, you're probably unlikely to make erroneous forensic decisions based on a database that was just thrown together by taking ten people from various countries in the European Common Market and from other places around the world, that the forensic differences are going to be very, very slight from what we know already of the differences between populations, because you could have the situation where, let's say, in the City of Toronto you may have certain ethnic neighbourhoods where there's a majority of people who are of Italian extraction, another neighbourhood might be Greek, another neighbourhood might be Portuguese, whatever, and we know from sociological studies that indeed there tends to be a phenomenon that we recognize, endogamy, that is that people of similar ethnic background tend to marry, tend to have children with spouses from that same ethnic background; not a hundred per cent, but you can show a correlation, and so there is definitely substructure present in human populations, we know that. Nevertheless, when you look at the genetic differences between people, of Greek people, of Italian people, of Portuguese descent, the differences are small enough that they're not going to change whether you calculated this frequency - significantly change whether you calculated that freguency on a Greek database, on a Portuguese database, on an Italian database, despite the fact that we could document very much that there is this phenomenon that is called officially endogamy, that is a non-random mating that goes on. There's non-random mating of all

sorts that goes on in human populations. Nevertheless, when you see that substructuring it's not necessarily, and in fact most genetic loci that have been looked at do not reflect that kind of substructure. Virtually all genetic loci that have been looked at in exhaustive detail turn out to be in Hardy-Weinberg equilibrium, no correlation within a locus, turn out to be between them in linkage equilibrium between loci like that, and so it would be quite remarkable and really quite dramatically surprising if when looking at these loci through further and further and further studies throughout all European populations that you found something that was dramatically different, you found an area that was dramatically different so that when we ran the numbers, you ran a particular DNA profile through that, you came up with a number that all of a sudden was only one in 5,000, something like that. I mean I'm giving an example, I could have said one in 500. We know already from, as I say, decades of studies of other genetic information, that you don't find that kind of difference. On the other hand, if you were comparing Caucasian populations to native aboriginal populations, I'd say yes, there could be quite significant differences. In some native aboriginal populations you can get up to fairly common frequencies because there are certain genotypes that are very much more common in certain native populations than they are in Caucasian populations which are the result of great mixtures.

Q. All right, because in your native populations -

what would a three-probe match - I know we have a five-probe match here as being one in 310 million, a four-probe match being one in 5.2 million. In the average, say, in the R.C.M.P. Caucasian database what would a three-probe match figure out to be, about?

A. In the native -

Q. No, in the R.C.M.P.

A. In fact I don't have that number readily in mind. I would say to take three of these genotype estimates of let's say one in 75 would be a kind of average that I remember per locus and multiply that by itself three times.

Q. Do you have your calculator on you?

A. Yes, I do.

Q. Please do it.

A. Then that would be - if for a three-probe match if for each of those probes there was an estimate of one in 75 for that genotype it comes up to be one in 421,875 individuals. Whether I said it was one in 60, I don't know what the average genotype frequency is for each of the probes.

Q. But we're just taking a rough estimate?

A. Yes, I'm taking a rough estimate, so it's one in let's say 400,000 for three probes.

Q. And are you familiar with the Baptiste case from B. C.?

A. I'm familiar with that case, I did not have any testimony in that case and was not connected and never did any calculations in that case.

Q. But in the Baptiste case with an Indian there was a three-probe match and the probabilities was one in 9,000.

A. That does not surprise me. I know that there are probabilities in native populations where they're much lower, but much more frequent.

Q. So depending on the database for the different sub-populations you can come up with a wide variety of numbers and great differences?

A. Except that in those native databases they are remarkably unlike Caucasian profiles. They show extreme cases of what we would call founder effect; that is, that these populations were probably the result of a rather small group of people that immigrated to North America across the Bering Straits at some point, that these populations often have been further fractionated during historical time where they form small tribal groups, and it would be similar to the data that Dr. Kidd was referring to in terms of Amazonian tribes and so forth, that there are many instances of smaller aboriginal bands in North America that show quite strong profile differences from Caucasians. The differences that we see between any Caucasian populations that have been looked at are quite, quite smaller than any of the differences we see in the Amerindians.

Q. O.K., but if you take your Amerindians, for instance, and I believe Dr. Kidd also testified about one small island, he gave the dimensions which I forget just now but I think he said something like there was about 26 different tribes and all different languages on there, and to calculate the frequency for each different one they were, well, quite different?

A. Yes, they could be.

Q. Now, if you were going to form a general database for all those tribes for that island, take a couple out of each tribe and have a general database for all of them, it wouldn't be proper to run any one of those individuals through the general database, would it?

A. It would depend again on the question you're asking. If you were unsure of who the alternative suspect might be in a particular crime and you had no prior notion of which particular tribal group or linguistic group that that individual may have come from, could have come from any of them, in fact the proper calculation would be to run it through all of them, or a composite of all of them. If, however, you had information that the person you were looking for indeed spoke a particular language and you knew that he or she had to therefore have come from a specific linguistic group it would be best to run your calculations through that particular sub-group's database, or to obtain that database.

Q. Do you know why it is that a doctor, I suppose Dr. Kidd must have been working off of some kind of grant to go out and do that study - why is it that he can go out to some foreign country or island and do a nice population study on that island to test all the little different groups but in Canada or even North America we can't even single out one isolated community so that we can compare it with the general population database?

MR. WALSH: That's not correct. That's not a correct statement, My Lord.

MR. FURLOTTE: Will you let the witness answer the question?

MR. WALSH: Well, I don't want Mr. Furlotte to testify as to his understanding of what the evidence is because it's been shown to be notoriously incorrect. That is not a true statement. In fact, there have been, my understanding of the evidence from Dr. Kidd - there have been studies of isolated populations. In fact, in Canada, you remember the Mennonites and people of that particular part, so that's an incorrect statement.

THE COURT: Yes, you're putting this as a statement. Would you rephrase your question?

MR. FURLOTTE: I'll rephrase the question, then. Leo Lavergne from Quebec who is doing one in Montreal?

A. Right.

Q. And he finds it necessary or very appropriate to test a small community in northern Quebec?

A. He is getting samples from these two areas where in fact we know there are higher frequencies for certain genetically based diseases, which would indicate that at least for those disease-causing genes are higher than in other Caucasian populations.

Q. That's an appropriate method?

A. In that case, keeping in mind the fact that what we're looking at here are areas of the human genetic information that have a lot of variation, whereas in the case of these disease regions, that cause disease, there you basically have one alternative form that causes the disease and then all of the other forms that are present are the so-called normal, and so there you have what we

call a two-allele system. This is a multi-allelic system and most of the alleles at these VNTR loci are going to be pretty much the same frequency, sometimes you find skewness in the distribution but you don't find the kind of phenomena that you would get if you had just two possibilities at a particular region, a kind of plus or minus where you had the disease or didn't have the disease, and so it's not at all sure that what he would find when he looks at these genes at these loci in these remote populations, that they would necessarily - and it would surprise me if, certainly, all of them reflected the high incidence of certain alleles that would seem to parallel the high incidence of certain diseases.

Q. To get back to the Baptiste case or the question of the Indians in B. C., there seemed to be a big difference between, say, one in 9,000 for three probes and one in 400,000 for the R.C.M.P. data-base. That's because that sub-group has a high degree of band sharing?

A. It has certain bin frequencies that are very much higher than the bin frequencies in Caucasian populations. One that I just remember is that there is at least one locus where one of the bins has a frequency of 40%. A frequency of 40% in one particular bin means that there are going to be a lot of people that have a band coming from that bin, so that means that when you compare people at that VNTR probe, for that VNTR probe, that you're going to find that a number of people share that particular band from that very frequent bin, yes.

Q. And they probably share a lot of other different

band sizes?

A. Well, not necessarily. You see, you can have a situation where -

Q. Just the one -

THE COURT: No, well, let him finish.

A. You see, you can have a situation which is in fact the case for the native Indian sample that I've seen where there is one particular bin that is very high in frequency and most of the other bins are about the same low frequency, and so while they will often share this particular one that's in high frequency the chance of sharing any of the others is no higher than in a Caucasian population. There are some other differences that are found in American Indian populations as well in terms of certain variants that are present that are found in very low frequency in Caucasian populations, namely so-called three-band patterns and so forth.

Q. So just the high rate of sharing that one band frequency could change the figures from one in 400,000 to one in 9,000?

A. It could do that, yes, it could, because rather than at each of these loci it being one in 75, which is the number that gave us the one in 400,000, if that were to change to one in 25 or in the case of a 40% bin that would change to one in 2.5, you could see how going from one in 75 to one in 2.5 could very strongly influence your calculation.

Q. So if a community was sharing a lot of bands it could drop the probability -

A. It could make that frequency estimate more common,

it could generate a number that was less rare.

Q. Now, you mentioned about testimony of Dr. Shields, that he did some statistical tests similar to the ones you did in relation to comparing the different databases?

A. Yes.

Q. Between the R.C.M.P. and the FBI?

A. And the FBI, he's made a comparison for one locus, I've forgotten which locus, that he found a statistically significant difference.

Q. And actually he did those comparisons before yourself and you did them to verify his findings?

A. He did them before I did them, yes.

Q. And you did them because he did them?

A. No.

Q. Why did you do them?

A. I did them because I was interested in the very questions that he was interested in, in seeing whether in fact there were differences. I did them as soon as that FBI database and other U. S. databases were made available to me, and they were not made available to me until I had been consulting with the R.C.M.P. for several months and in fact was interested in using the program that I had developed, that is the computer program, in fact to do exactly these kinds of tests, and I'm still interested in getting data and I still am sent some data from places in the U. S. and from different ethnic groups in the U. S. to see what kinds of differences are going to be present.

Q. But you knew he was going to come to court in this case and testify that he found a statistical significant difference between the R.C.M.P. and

the FBI?

A. I don't recall when I spoke at the voir dire whether in fact I knew that or not. I must say I'm not sure that I knew that at the time, and I really would say that that was insignificant, to use that -

Q. Is that a statistical insignificant thing?

A. Statistically insignificant factor in my decision to actually do any of these comparisons.

THE COURT: You'll have to start using the expression, meaningful.

A. Meaningful, a word which I don't like, Your Honour.

THE COURT: It's like point in time. I got Mr. Walsh cured of using that.

MR. WALSH: I noticed, My Lord, I was keeping track through the voir dire and the trial and more people use that phrase, point in time, than I realized.

MR. FURLOTTE: I like it myself, My Lord. My Lord, I think this might be an appropriate time for a break, and during the break I can maybe shorten up some of my time that I'll be before the jury.

THE COURT: All right, yes. We're not departing, I can assure the jury, from the plan that you will go home this afternoon and come back on Monday. I think I can safely say that?

MR. FURLOTTE: Oh, you can safely say that, yes.

(BRIEF RECESS - RESUMED AT 3:10 p.m.)

(ACCUSED IN DOCK.)

(JURY CALLED - ALL PRESENT.)

CROSS-EXAMINATION OF DR. CARMODY CONTINUES:

Q. Doctor, when we're dealing with difference in numbers, say between one in five million and one in ten million -

A. Yes.

Q. - would there be any statistically based test that you could rely on to say whether or not there is a statistical difference between these two numbers?

A. If you just have two numbers in isolation like that all you can say is that they're arithmetically different. If those two numbers represent some kind of summary statistic that results from some sampling process or is a mean that's derived from some set of individuals or whatever that number comes from, then you can statistically determine based on the amount of variation that is present amongst the individual components that make up that summary statistic, you can then draw some conclusion as to whether they are statistically different from each other. That is to say, if you have two numbers and you said something was six feet tall and another thing was six and a half feet tall, you could say whether they were different or not, and indeed they are different. If, however, this six-foot number derived from a sample of ten people and their average was six feet and you took another sample and the average was 6.9 feet, you could not just by being given those numbers decide whether they

were statistically significant. It would depend on the variation in the individuals in the sample that gave that mean, so whenever you're dealing in isolation with just two arithmetic values that are not identical, they are different, but it's not a statistical question. The only time you could answer a statistical question is when you have numbers that are based on some sampling process where you've taken a sample, where you have a measure of the variation in that sample that will allow you to decide whether two different samples or two different numbers that you're comparing are statistically different from each other. If the difference within each of these units is very small, then in fact the means are going to be different, but if in fact there is great variation in the individual populations that these two samples were drawn from calculating a mean, while it may be arithmetically different, does not necessarily mean it's statistically different, so when you say one in five million versus one in ten million, I would say the only way you can decide whether that is statistically different is by giving me a number that would indicate the variation amongst those numbers that contributed to that five million and the variation amongst those numbers that gave me the ten million. Then I could tell you whether they're statistically different.

Q. O.K., in Exhibit P-167 where you give - titled "Legere's Statistics", and you basically run his profile through the R.C.M.P. database, Montreal, Minnesota, the FBI, and the Florida database, I

believe you found there was no statistical difference in the final product?

A. That is correct, yes. Given the confidence interval that is around those numbers, since any of the other numbers for the four-probe locus, for the four loci, for the five loci, they fall within that confidence interval, I would say they are statistically insignificant.

Q. Right, but even if you didn't give it the confidence interval and you just relied on the best estimate that Dr. Bowen come up with, there would have been statistical significant differences in the end product?

A. I couldn't tell unless I knew something about the confidence intervals on those estimates to be able to make that decision. They would be arithmetically different, there's no question that if you said one in whatever it was, 310, versus one in 600 million, they are without question arithmetically different.

Q. Normally you'd want them within 95% of each other?

A. Typically, I don't have a simple rule of thumb there. It would depend actually on some more complicated things or the amount of variation in each of the two and so forth. In general if it fell within that 95% confidence interval you would not find any statistical difference when you did the proper statistical tests.

Q. And when you used the intervals would you say that often when you have an estimate of one in five million you could not exclude, in fact, all the way up to one in ten billion on the low side or that one in five billion could be as small as one

in two million?

A. I'd have to see the sample sizes because that interval on the confidence interval is going to depend on the sample size. Again the larger the sample size the narrower and more precise your knowledge of the real value. The smaller the sample size the much wider that confidence interval is going to be, so I'd have to have information on the size of the sample. If we want to make some assumptions that it's based on a sample of a thousand you could do the calculations and decide whether in fact that's likely to be a statistically significant difference if you were assuming that it was based on a sample size of a thousand.

Q. I believe in direct evidence you mentioned that you used an upper confidence interval to allow for sampling error?

A. That's right.

Q. And maybe you could describe what you mean by sampling error?

A. Sampling error is a statistical term that means that when you take a sample from the same population, from the same group that you're trying to get some information about, and you calculate some number based on that first sample and you take another sample, and you would compare the number that you had calculated, whether it was the mean or other statistic, you want a - the sampling error is the amount of difference that in general you would expect to see by repeating that process again and again, and it gives you a notion of the reliability and robustness of that estimate,

robustness being used in a very strict statistical sense meaning how much is that going to vary when I take another sample and I take another sample, and I think your intuition would say to you that if I took a sample of ten from the Canadian population and I calculated the percentage that were going to vote for a certain electoral party in the next election and I took another sample of ten and another sample of ten, that there's likely to be differences in the percentage that you would get from those different samples of ten. If, on the other hand, I took samples of a thousand people and I repeated that and took another sample of a thousand and another sample of a thousand, the difference from one sample to the next is likely to be much less because it's averaged over more people, it's likely to be more representative in terms of being a thousand, so you get the idea that the larger the sample the less the differences are going to be between the samples, and that's what we mean by sampling error and sampling variation, that the fact that we've not looked at the entire population and we're taking a sample of that population and trying to extrapolate what is really that value in the entire population is going to vary from sample to sample. If I flip a coin ten times, sometimes I get four heads, sometimes I get seven heads, sometimes I get five heads, sometimes I might get nine heads, very rarely, but nine heads. That difference from one set of ten to the next set of ten is what's called sampling variation, and it's a well-defined statistical phenomena that we can

handle statistically if the samples have been obtained randomly, so that's what we mean by sampling error. Any sample is going to have some chance of deviating from what the actual population value would be. When we calculate and estimate the frequencies in these bins we haven't sampled everybody in Canada. It would be impossible, to start off with. We based this on a sample of a thousand, and we can put some precison and those confidence intervals are saying that if we took another sample, and another sample, the same size, a thousand, did the same frequency calculations, another sample, a thousand, did the same frequency calculation, another sample, and continued that process very, very many times, we would get estimates that fall within - well, I guess this is not the chart, but the one I had above there that showed the confidence intervals - that we would get values that fell within that range, that sampling error, would give us values falling within that range 99% of the time. It means some percentage of the time, some small percentage of the time, we're going to be a little bit further out than that, but it gives us a notion that, well, you know, that's a pretty good idea of where the mean is likely to be, really. Some samples are going to give a little bit different, though.

Q. How did you come to the conclusion to use the upper confidence interval of 99.7%?

A. It's a very simple pragmatic level that's used. A number that's calculated to measure the amount of variation in a sample is called the standard

deviation, and that 99.7 limit is three times that standard deviation. It's a number that is used, rule of thumb kind of approach. There's nothing absolutely written in stone about using that, some people use 95% intervals, you could use whatever interval you like. It's a partly historical tradition in the statistical literature to use that level for confidence limits and typical statistics. There's nothing magical about that. You would not be wrong if you wanted to do a 98% confidence interval, you could calculate that. You'd have to multiply the standard deviation. Rather than by three you'd have to multiply it by two-point - I don't know, nine-one, or something like that, and it's just as simple to remember as rule of thumb that if you calculate the standard deviation in a sample you multiply it by three and that gives you this 99.7% interval. It's nothing more, nothing less than that.

Q. So if you were using, say, the 95% upper confidence interval, what would you be saying then, well, 95% of the time I'd be right?

A. 99% of the time if I took further samples I would get a number that would fall within that interval, and that interval would be a bit narrower.

Q. And if you used a 95% interval you would be saying 95% of the time I'd find numbers that would fall within that?

A. Yes, and in fact that 95% interval is the interval that is actually calculated on various political polls that you hear reported on CBC and othewise where they say a certain percentage is 37 plus or minus three per cent 19 times out of 20. What

they're saying when they say 19 times out of 20 is a 95% confidence interval because 19 out of 20 is 95%, and that's what it means.

Q. And you used the 99.7% upper confidence interval before you were aware of the bin frequencies from the Montreal database?

A. Yes, I did.

Q. And before you were aware of the bin frequencies of the Montreal database you thought that you could demonstrate quite conclusively that the R.C.M.P. database represented very well and very accurately and very precisely the Canadian Caucasian population?

A. Yes, I would say that. I don't recall testifying to that effect but I would say that, yes - and I still do feel, in fact, that it is a good reflection and there is not any different inference I would draw from running the sample through an FBI database, R.C.M.P. database, Montreal database.

Q. O.K., but the fact that the Montreal database is statistically significntly different than the R.C.M.P. database, what does that do for your upper confidence intervals? Any reason why you should change that, or are you just as confident?

A. Well, that confidence interval is really reflecting a sampling. I would say that, to be honest, based on just one comparison like this and the fact that it's just two probes out of six in Montreal's database that are different it could well be it was a statistical fluke, it could well be that I'd want to do further sampling to really corroborate that it was, but the fact that it fell

outside that 99.7% interval when I did one of the calculations there I think is quite beside the point.

Q. What if we kept checking all different areas of the country, Halifax, Moncton, other areas out west, western provinces, and we kept getting bin frequencies which had statistical significant differences? What would that do for your confidence?

A. Well, we could take that into account and we could readjust the confidence intervals, and we could say that they would be wider in that case, probably, although not necessarily, because the differences in the bin frequencies in general are not leading to very grave differences and very great differences in the numbers that we ultimately calculate there.

Q. For forensic differences?

A. Well, not only for forensic difference but for genotypic frequencies, because what's going to happen is that some of those bins are going to be higher, some of those bins are going to be lower.

Q. When you take a sample of bands from those bands, some of them are higher, some of them are lower, you'll find in fact that one locus tends to cancel out another locus and you end up with a number that's not too different, even though this individual locus might be more different, so that if one particular locus is quite different it would depend on that particular genotype, the particular sample. In general when you do this, though, you find that there are very, very strong correlations in the genotype frequency when you

run it through one database and run it through a second database. It's one of the projects I have in mind for the future and that I'm suggesting to the R.C.M.P. is that what we do is we take, in fact, a random set of genotypes and run them through different databases and see what kinds of correlations we get. That, believe it or not, has not been done.

Q. If you run an individual through a database other than his own population which he belongs in, substructure, sub-group, whatever you want to call it, is the calculations likely to prejudice him?

A. On average they are likely to prejudice him, yes.

Q. That was the position of Dr. Shields in an affidavit that he had made in another case?

A. That is correct.

Q. And you disagreed with that at the hearing here in May?

A. I disagreed because the interpretation, perhaps it was my error in making that interpretation, was that he was not using the term, expectation, that as I understood it he was saying that they would always be prejudicial, and that is not the case, and I would continue to disagree if the statement was that they are always prejudicial. They are not always prejudicial. There are going to be some genotypes that are rare in, let's say, the proper database, that are going to be more common in another database, but on average, and the mathematical expectation taking an average individual from this database and putting it through the wrong database - on average, and the expectation, the mathematical and statistical

expectation, is going to be that it would be lower in the wrong database, so it gets into a question of what we mean by expectation or whether always is the interpretation of expected.

Q. But in his affidavit he said it is expected and it is predicted, so how did you misinterpret that to mean always?

A. Well, I would misinterpret the predicted. In fact, I would say that it is not predicted that it would always be against the individual. It is not predicted that it would always be disfavouring the individual.

Q. He didn't use the word although, did he?

A. He used the word predicted.

Q. It is predicted and it is expected, those are the words he used.

A. Well, then, perhaps I was just thinking of the word predicted, and it is not predicted, it is expected. I know this sounds like a semantic splitting of hairs but in fact these are statistical terms that have very precise meaning, and they're being used in ways that in normal colloguial English we are not using them, and so when you say predicted you mean something different from expected.

Q. Would you try to describe what the term substructuring is - means?

A. Substructuring in human populations means - or in any population, means that if you look at a finer scale that you would find that there were local sub-groups within which there were genetic differences compared to other local areas, so that for example, if you had a situation in the Alps

and you have small villages, it may well be - I don't know whether this is the case, but it may well be that there would be genetic breeding that would go on predominantly within separate groups and that that would be an example of substructuring. If you didn't pay attention to that and sampled over that wide geographic area, not realizing that in fact there were these local areas within which predominantly matings were occurring for many generations, that would turn up in your analysis when you looked at the sample that was derived over a wide geographic area and the frequency expectations would be different than if you had taken into account that there were these smaller sub-units.

Q. O.K., would you say that substructuring - so one of the uses of substructuring is to indicate and try to convey the idea that the population that you're studying in total is not a homogeneous unit?

A. That's correct.

Q. And should not be treated statistically or mathematically as a homogeneous unit?

A. If there is substructuring, that is correct.

Q. And there is substructuring within Canada?

A. I would not agree to that, not in the Caucasian population.

Q. There is substructuring between the R.C.M.P. database and the Montreal database?

A. No, there are some differences in bin frequencies in those samples, I would not say that that is consistent with there being evidence of substructuring. That in and of itself is not

sufficient evidence that there is genetic substructure.

Q. O.K., would you say the consequences of having smaller and substructuring in populations are that you can get deviations from the predictions of the Hardy-Weinberg equation, from the prediction of the product rule and so forth?

A. I would agree that if you have substructuring you can get deviations from both Hardy-Weinberg predictions and linkage equilibrium predictions. However, that has not been shown in human Caucasian populations for hundreds of loci that have been looked at.

Q. And also that you would get gene frequency and bin frequency differences geographically?

A. You could get those. The amount of differences that we see are very small in Caucasian populations.

Q. They are statistically significantly different?

A. They are statistically significantly different, but they are still small.

Q. But you were saying they have no forensic difference?

A. That's correct, because they're small.

Q. How do you statistically differentiate between forensic differences?

A. I use what I would call common sense, Mr. Furlotte.

Q. Again there is no scientific method or calculation to do that?

A. Alas, there isn't.

Q. You say that all of those consequences could be a consequence of having substructuring in a

population and that they are very necessary to be aware of that possibility in studying human populations because, as has been well documented, human populations are not one homogeneous inter-breeding genetically uniform mixture like that?

A. I would agree with that statement.

Q. O.K., and they indeed are made up of separate ethnic, geographic, socio-economic geographic units within which sometimes there is not complete random mating?

A. I would agree, yes.

THE COURT: Do you think this evidence, Mr. Furlotte, is being very beneficial to the jury?

MR. FURLOTTE: In the end, hopefully.

THE COURT: Hope springs eternal.

Q. If there are substructures and you're saying total it is not a homogeneous unit and should not be treated statistically or mathematically as a homogeneous unit, that's correct, you said?

A. That's correct.

Q. Yes, and in order to use the Hardy-Weinberg formula and the product rule they have to be statistically and mathematically a homogeneous unit?

A. Not necessarily, actually. You have to have significant enough differences that you could detect the amount of difference that would be expected if you did the calculations with slight substructuring versus major substructuring versus amounts of difference between populations and so on. The evidence in Caucasian populations is that there are very minor differences and that while we know that there are ethnic, religious, and

cultural differences between groups that tend to cause this endogamy to happen, nevertheless, as I might put it, the proof of the pudding is in the hundreds of genetic loci that have been studied worldwide that there is not very great evidence in Caucasian populations of significant substructuring.

Q. But between the FBI and the R.C.M.P. database what does that tell you in relation to substructuring?

A. It says that in the samples that were compared for a couple of these genetic probe sites that there were some differences in the bin freguencies, small differences but statistically significant differences.

Q. Does it tell you that there is substructuring?

A. Not in and of itself, no, I wouldn't say so. You could have a uniform change, for example, from one area to another, a very, very gradual change, that could be the result of historical processes, of migrations of people and so on, that while they could lead - when you sample the extreme ends of the range could be statistically different from one another, you would say if you sampled along a transect between those, that is a line of samples between them, that in fact they were very gradual changes, and that's what you find in Europe and has been documented many times.

Q. Doctor, I'm going to show you a transcript of the evidence you gave in May on this hearing, Volume VII, Page 70. I put the same question to you that, "between the F.B.I. and the R.C.M.P. database what does that tell you in relation to substructuring", and was your answer different

then than it is today?

A. "It tells me that that there is some substructuring present. That is, that you do find these differences in bin freguencies, and that - but that that substructuring, when you look at it in terms of its effect on any calculations that we are going to make in terms of forensic inferences, has no consequence." And I would stand by that statement.

Q. Right, but in May you said that the difference between the FBI and the R.C.M.P., that that was an indication that there was substructuring?

A. And the question there is the degree of substructuring we're talking here. Indeed, any differences you could say well, since it's some indication that they're not completely homogeneous you could call that substructuring. I'm using a sense of amount of difference in my answer today that is reflecting the fact that we have more information from more samples from more populations through North America and the amount of substructuring that we see in those is really quite minimal.

Q. For forensic purposes.

MR. LEGERE: Can I be excused, Your Honour? I'm tired of hearing that over and over and over. All the money they're wasting on these fellows here they could have had a database taken on the Miramichi, but the only thing is you'd run into the Indian caste system -

THE COURT: Let's stop here now. How much longer are you going to be, Mr. Furlotte?

MR. FURLOTTE: My Lord, I believe this doctor wants to

get away on a 4:55 flight or something and I could probably shorten it up -

MR. LEGERE: No, I want to leave now. I don't want to stay and listen to him any more. The Crown's got half a dozen of these guys coming up like elephants and telling the same story over and over but all they have to do is take a database up the Miramichi, but they'd have to take one up in Nordin, up in Douglastown, up the Chaplin Island Road, up the -

THE COURT: Sheriff, if the accused doesn't want to stay would you take him out, please?

MR. LEGERE: I don't want to stay because he's missing the factor. He's wrong in the substructure and Mr. Shields is right and that's why they're all screwing things around. Move to the Miramichi and take a database and if I'm wrong I'll eat my shirt. You have fathers making love to their own daughters and vice versa. My own son was raped at five years old and the police did nothing about it, they keep it underground. You don't see this stuff, see? That's your missing factor, substructuring, guaranteed. Go back on Chaplin Island Road, you have cousins marrying cousins, you wouldn't believe it. You never seen it before, it's like the modernized Sodom and Gomorrah of the Biblical era. You've never seen it before. Open, lock. I'll have to make a key.

THE COURT: Well, I would ask the jury to go out. We'll bring you back in a minute.

MR. ALLMAN: I respectfully suggest that we adjourn and leave the officers to deal with their problem.

THE COURT: I think we should do that, and I would ask

everyone, please, to leave the court room and we'll leave the officers here themselves.

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

(ACCUSED IN HOLDING CELL.)

THE COURT: Let me see, the - well, you were going to be a short time, did you have very much?

MR. FURLOTTE: Well, My Lord, there's no way I can finish cross-examination of this witness today and I know this witness would like to get away, his flight is out about 4:55 or something like that.

MR. WALSH: We changed the flight so we could accommodate the cross-examination. We had hoped that it would only be the one issue on Monday morning that we would have to deal with, so Dr. Carmody, you've changed your flight schedule, did you not?

A. I have a flight now that leaves at 6:10, yes.

THE COURT: Our understanding this morning from discussion with counsel was that this witness would be totally disposed of excepting for certain one remaining issue that would be dealt with in cross-examination on Monday morning, so let's get down to that point.

MR. FURLOTTE: Yes, I don't even think I'll be able to reach that point today but we can get on with as much as we can.

THE COURT: We'll keep at that for another three-quarters of an hour.

(JURY CALLED - ALL PRESENT.)

THE COURT: Now, your cross-examination will continue, Mr. Furlotte?

Q. O.K., Dr. Carmody, I may have - I believe I did

make a mistake when I told you that I had posed a question to you about questioning between the difference in the FBI and R.C.M.P. database, what does that tell you in relation to substructure, and your answer tells me that there is substructuring present. Those were questions posed to you by Mr. Walsh at the previous hearing. Would you agree with that?

A. I don't recall who they were posed by.

Q. That's from under the direct testimony.

A. I see.

Q. And under direct testimony by Mr. Walsh, and that's also when you said that one of the uses of substructuring is to indicate and try and convey the idea that the population that you are studying is not a homogeneous unit and should not be treated statistically or mathematically as a homogeneous unit?

A. Right.

Q. So you gave that on direct evidence to Mr. Walsh when you testified?

A. Yes.

Q. And at that time you did not believe that there was any statistically significant substructuring within Canada?

A. That's right, and I would still hold to that opinion.

Q. You would still hold to the opinion that there is no statistical significant -

A. - substructuring in Canada despite the fact that some - two of the six probe sites in the Montreal database have shown that statistical difference.

Q. But you agree there is a statistical significant

difference between Montreal -

A. For two of those probe sites of the six, yes. If one wanted to - and one could do a calculation, in fact, where you amalgamate all information from those six probe sites, you could do a test and you could show that in fact when you put all of those probe sites together and compared them in Montreal to all six probe sites melded together from the rest of the R.C.M.P. database you wouldn't find a statistical difference. It so happens that two of the six do show that when you tease them out and look at them individually, so that's why I'm saying that when you look at two sites like that and you do find some differences you have to keep that in perspective. That's only one-third of the VNTR loci that you've looked at that show some difference like that. It doesn't necessarily reflect that there is significant genetic sub-structuring necessarily. It would suggest that and it would suggest that perhaps we should look at further places, which we're continuing to do and I know the R.C.M.P. is continuing to do, and we want to look at more samples taken from throughout North America and indeed from throughout Canada. I think that the conclusions, though, that we're going to reach, are not going to in any way change the conclusions that we draw from using the present database. They'll be more refined and they will be more reliable but - and will have narrower confidence intervals on them, but I would still hold the opinion that these numbers are quite robust.

Q. But the basic test to find out whether - and it

is a basic test to calculate whether there is any statistical significant difference between Montreal and the R.C.M.P. database?

A. For two of the sites you do find differences, yes.

Q. Right, and that test is not in dispute amongst scientists?

A. No, there's quite universal agreement on using that test. It's quite a reliable test, it tests what we think it is measuring, and I don't think there's any controversy about that.

Q. So if Mr. Shields or any other expert witness says that the statistical significant difference in bin frequencies between two populations proves that there is substructuring you would disagree with that?

A. I'd have to know the amount of difference, how many sites were looked at, I think just that information alone in isolation wouldn't convince me that there was absolutely important substructuring that I would have to take into account in any of these type of calculations.

Q. But it could convince other scientists?

A. Perhaps; I'm not even sure of that. I -

Q. Comparing the difference in bin frequencies between different geographical areas, do you feel that that's important?

A. We can always, and I think it's important to always have new information. There are places that haven't been distinctly sampled. From the samples we already have and from the studies that have been done not only in Canada but throughout North America by different state agencies and the FBI and so on and different paternity clinics in

different states in the United States, it is useful to get more information but I would say that we could make a prediction that we're not going to be surprised. The only places I think that there is still some hope of being surprised, if I could express it that way, because as a scientist I'm always excited about finding things that are unpredictable, unpredicted, would be in fact in the Quebec samples taken from Abitibi and Chicoutimi. I think that there there is the greatest potential for there being some difference that would be still reflected and could be seen by taking reasonable sized samples and by using this approach with these VNTR loci, and it's hard to convey my interest in this but I'm very excited about getting my hands on those and actually analyzing them.

THE COURT: Surely, Mr. Furlotte, you could go on to another subject now, because this one has been beaten to death for two hours.

MR. FURLOTTE: I would rather stay on this subject for a while longer, My Lord.

THE COURT: Well, what are you trying to do, drag this out, the trial out, for days and days, or what is the object?

MR. FURLOTTE: My Lord, I want to get this trial over and done with more than anybody.

THE COURT: You're not showing very much sign of that but if you say so. Well, I can't very well cut into your cross-examination. I can, but I'm not going to at this point cut into your examination, but I do point out to you that we're just beating the same thing over and over again, this substructure

business, and we've gone over question after question. There have been five hundred questions directed at this witness on the matter of sub-structure, and he's going through the same answers now time and again answering the same questions, and this is of no benefit to the accused, to the Crown, to the jury, to counsel, to me, to the witness or anybody else. Well, you're competent counsel, or meant to be, and I put some reliance on your ability to be somewhat discreet in the type of question you ask. Go ahead. I might say, I think the understanding here is that this witness would not be concluded today and that he would be recalled to the stand on Monday after defence counsel had an opportunity to consult its expert over the weekend on one aspect of the case and that this witness would be further cross-examined at that time but that all other aspects of the cross-examination would probably be concluded today. Now, you've said here a few minutes ago, I'm not sure whether this was after the jury went out or - no, the jury were here at the time, that you questioned your ability to complete even the other aspects today. Well, you'll never do it if you're just going to repeat and repeat and repeat on this matter.

MR. FURLOTTE: My Lord, I could keep this witness on the stand for a week if I wanted to -

THE COURT: I know you could, but I'm not going to permit that.

MR. FURLOTTE: I would like to get it over and done with as quick as possible. I would like to hit on the points where this witness may or may not be

contradicting his testimony from the previous hearing, and I think I have every opportunity and right to do so.

THE COURT: You kept him on the stand at the voir dire for three days, or I don't know what the time, I haven't checked the thing, but if one checks the transcript, you did, and if you're going through every single answer he gave there and saying why did you say this, well, we've seen no divergence, really, between anything he's said now and what he said then in anything that you've brought up to date. There may be minor - this is what I call nitpicking. Now, this is a prime example of nitpicking, I suppose.

MR. FURLOTTE: My Lord, you can call it nitpicking because you heard all the arguments before, and it may be that you don't like to hear them over again, but these jury has not heard these arguments before.

THE COURT: We're not talking about arguments, we're talking about evidence. We're not talking about arguments. The time to argue is when the addresses are made to the jury, and if there are points then you want to make in your address to the jury you make these points but - well, I don't know what more I can say at this time. I just ask you to hurry along as quickly as you can and cover the territory you should be covering. All right.

Q. Doctor, the difference between your opinion and maybe Dr. Shields's opinion that this type of bin frequency differences does not or does prove substructure, your opinion has not been put to the scientific community for peer review, has it?

A. No, it has not.

Q. And if you ever intend to put your opinion to the scientific community for peer review it's very well that the scientific community would accept Dr. Shields's opinion rather than your own?

A. I'm not in a position to say that. I feel that I could defend what I would say in a publication and that it would be accepted by the scientific community and accepted for peer review.

Q. And it's possible that they won't accept your opinion?

A. That is possible.

Q. If you were given a grant to prove linkage disequilibrium in the Canadian Caucasian database or in the Canadian population, how would you do it? What would be necessary?

A. In fact I've given this question considerable thought and I have the potential of getting some samples that would allow me to do this, and they would derive from samples where you had information on what the genotypes were of children and what their parents' genotypes were. Now, it's quite clear that one can predict what children's genotypes will be from the parental genotypes, but what you don't know when you sample the genotype of an individual is what parts of the genotype came from its mother and what parts specifically came from its father, and in order to rigorously measure linkage disequilibrium you need to know which combinations of things came together from one parent and which combinations came from the other parent. When they are both present in the child you cannot distinguish which of these

two at this locus came from the mother and father, which of these two at the other locus came from the mother and the father. If you had the information from the mothers and fathers it would be possible to measure another term which is called gametic phase disequilibrium, which is just a fancier way of describing linkage disequilibrium, but you'd be able to tell when the two components that came into making that child, the sperm and the egg, what exact genetic composition were present in those gametes, that's where we get gametic phase, so we would be able to see if there were any correlations there if we had enough sets like this, if we had enough sets of parents and child to be able to ascertain whether there were any abnormal statistical differences in the components in those gametes that made that child, and I have a potential collaborator who says he can provide me with a large number of those types of trios where you have both parents and the single child, and the potential is to be able to analyze those for gametic phase disequilibrium or this linkage disequilibrium.

Q. When do you hope to have this study completed?

A. That data is a while in coming and there's a certain irony about that data in that it's being provided by a person who runs a paternity clinic in the United States in the State of Texas where you are trying to ascertain who the real father is, and he would have the sub-set coming from samples where it was ascertained that this was the father, and you know the mother and you know the child. You can go back to those samples and

whatever to be able to ascertain that. I would think to do that kind of a study is likely - wouldn't be completed for, I would guess, a minimum of a year from now, something like that, presuming we got the samples within a couple of months. To extract the DNA, run the blots, do the statistical analysis on it, I could say we could have it done in a year if everything worked very smoothly.

Q. O.K., but so far in your studies or in any of the forensic field in the databases equilibrium has never been proven?

A. Well, there's the problem of you never prove equilibrium, you disprove disequilibrium. I know this gets into semantic splitting of hairs, but you can show the absence of disequilibrium and you then conclude that if you do that in a powerful enough way that the alternative explanation that there is no disequilibrium means that there is equilibrium, so you don't prove equilibrium, so to speak, you disprove disequilibrium, and the studies that I've done, the studies that I've seen other people like Dr. Weir in North Carolina do on the FBI database, are of varying degrees of power to be able to exclude amounts of disequilibrium that are very large. At the present time with the data sets we have and with the technology that we have you're not able to exclude small amounts of disequilibrium. On the other hand, I know of a computer simulation study where people have deliberately generated a computer database not derived from real people but would have the same properties that a database that was derived from

real people would where they deliberately put in varying degrees of disequilibrium and then did statistical tests to see if they could detect it as a way of ascertaining the power of the test, and this is Dr. Brookfield at the University of Nottingham in England, and I've seen a manuscript of his that has been submitted for publication where he attempted to measure the amounts of disequilibrium that could be detected in samples of, let's say, a thousand with this technology, and was able to conclude that there had to be only - that you could detect levels of disequilibrium that were above, let's say, 5%. That is, that the levels of disequilibrium that are undetectable by current technology and tests are likely to be so small that they're not going to lead to very great differences in our calculations, so one can take an approach where you deliberately fabricate a computer database that has the properties that you think you would like to be able to find and then see if you can find it, and it avoids the problem of having to go out and collect blood samples in an unknown population where you can't control all the variables, but yet you can do very significant studies where you can show the amounts of disequilibrium that still could be present that would remain undetected by present technology and present database sizes, and you can put some limits on how great that amount of linkage disequilibrium could be. The amounts are, in fact, quite low. I don't remember the actual numbers, in fact I do not have a copy of the manuscript, I saw it in passing from a

visiting scientist, I've written to Dr. Brookfield and he's about to send me a copy of it, but that the levels of disequilibrium that would be present that we could not detect are - again I have to use these qualitative terms, unfortunately - relatively minor.

Q. O.K., if you were doing your studies in a population to find out if there was linkage disequilibrium, what might be the first indication that you would come across for you to suspect that there may be linkage disequilibrium?

A. Well, the first one that I would expect was that you would see in one of the tests that I ran, this non-parametric median test between loci, that in fact you had certain genotypes occurring; that is, the genotypes at one locus with a particular genotype at another locus, that you would find them occurring more frequently than you would expect just at random; that is, by looking at the frequency of this and the frequency of that singly and multiplying those together, which is what your random expectation would be. If the numbers that appeared in your sample showed that these two genotypes occurred with a higher frequency than you would predict by knowing the individual frequencies, that would be the first indication that there was some disequilibrium there.

Q. Would another first indication be that the first thing to do and the simplest thing to test would be to test bin frequencies, and if the bin frequency was the same in two places and there was no evidence of heterogeneity that way or

population substructuring that way?

A. By comparing bin frequencies at one locus you can establish whether there is any deviation from randomness within a locus, which we term the Hardy-Weinberg equilibrium, but that would not tell you by studying that single locus in a number of populations whether in fact there was linkage disequilibrium between loci, so the bin frequencies alone, they could tell you that potentially whether there was some substructuring but it wouldn't necessarily allow you to conclude from that that there would be necessary linkage disequilibrium present. You'd have to do a separate kind of study.

Q. If there was no difference in the bin frequencies which would show a slight degree of substructuring you'd be less apt to find linkage disequilibrium, would that be safe to say?

A. Yes, that's right, although you'd be less likely to find it but you could still nevertheless find it.

Q. So therefore if you do find a difference in bin frequencies you're more apt to find linkage disequilibrium?

A. If those differences were of a great enough order that they would suggest some substructuring, then, yes, when you looked across different loci you perhaps - you would have, in fact, a greater likelihood of finding some linkage disequilibrium.

Q. And basically you agree that if you found some differences in gene frequencies and bin frequencies in the two places then you would say, hey, maybe we would pursue this further and maybe

there will be some disequilibrium, maybe there will be some deviations from Hardy-Weinberg equilibrium?

A. Well, that's about the Hardy-Weinberg, certainly, we would want to test that if we found some bin frequency differences. We would be interested in testing for Hardy-Weinberg equilibrium even if there weren't, however, and we've done that on the databases to corroborate that in fact when we say that there's Hardy-Weinberg equilibrium basically what we're saying is that within that probe site the frequency of occurrence of the different bands is not showing any correlation with each other and that they are appearing in frequencies that you would predict jointly from the individual frequencies.

Q. And if you were going to compile a population database for the Newcastle area in New Brunswick how much of a difference would have to be shown so that you would not be able to use the R.C.M.P. database in calculating your frequencies?

A. That's a difficult question to answer simply. If the question was whether we wanted to calculate the forensic probabilities here that would be used in a court room I would say that there would have to be quite great differences, and I know you're going to ask me to quantify this - greater differences in that instance than if we were doing some quite much more esoteric study that had to do with the linkage to a particular disease gene or whatever where we were looking at specific pedigrees and specific sub-groups within the Newcastle area. Just the presence of differences

in bin frequencies overall at a locus I would say would be insufficient to cause me to say that we had to therefore get a complete new database from that area. As I said earlier, what happens in general when you have slight differences in one area to the next is when you run through these calculations one is a little bit higher and another one is a little bit lower, another one is a little bit lower, another one is a little bit higher, and the net product of multiplying those together is that you get an answer that tends to be balanced out and you draw the same conclusion, that whether you run it on a database from Vancouver, a database from the Canadian Forces in Kingston, the Montreal database, the database from Florida, you find that in fact the particular genotype that you're running through, and every genotype that's been run through, is a rare genotype, and by rare I resort to my notion, my common sense notion, that if one is one in a million I would call that rare.

Q. How much of a variation would you need?

A. As I say, it's very difficult to quantify because if I gave a percentage I'm not sure what I'm conveying by that percentage. You see, we're talking about differences in let's say 25 different bins. Now, do we add up the differences across those bins, is that what you want me to give you, or do I give some number that is some composite of those, the average difference in bin frequencies that there would have to be? I'm not sure -

Q. I'm leaving that up to you, Doctor.

A. Right, and what I'm saying is that the question is imprecise enough that the answer has to be imprecise, and the imprecision of the answer reflects the fact that there is no single one way. People have calculated things that we call genetic distance. There are at least a half a dozen different ways of measuring genetic distance between populations.

Q. What kind of a confidence level would you use?

A. I would use this confidence level that I've used and applied here which is coming strictly from sample sizes, and I would say that you could use the sample sizes to see what the differences were. If, for example, one measure that I could imagine being used in a forensic situation like this would be to sample the thousand people from the two areas, generate the databases, look at the frequencies of those genotypes for those thousand individuals in their own databases, and then do the calculations of each of the thousand on the other database. If the differences were not greater in the total calculations of greater than two or three per cent, even ten per cent, I would say that I would not be worried about the differences in those two databases, so I'm trying to convey in my answer is that there is not a simple glib statement that I can make and say, well, there would have to be such-and-such percentage difference. It's not that simple.

Q. Would you support any proposal to do further studies on a local scale just to make sure whether or not there is local enough variation?

A. Yes, I would. I would like to see that actually

done. I have made that recommendation informally to the R.C.M.P.

Q. And basically in being a scientist you want to see the evidence?

A. That's correct.

Q. And you don't just like going by what people's feelings are?

A. That's correct.

Q. And in the scientific community it's just the feelings that there is not sufficient substructure within the Caucasian population?

A. No, I would say that there is evidence. The evidence is not perfect, the evidence is not completely definitive, but I would say that there is very strong persuasive evidence that leads me to have great confidence in the fact that we're not making grave mistakes in our calculations.

Q. Doctor, are you sure that the forensic community is not using the numbers to support the theory rather than using a valid scientific theory in order to obtain the numbers? In other words, are you sure you're not putting the cart before the horse?

A. I don't see as we are, personally, and I'm not sure I fully understand what the two alternatives are. I have these images of carts and horses in my mind and it gets confused with my notions of the R.C.M.P. and their mounted horses and so forth so I don't have a simple answer to that.

THE COURT: Well, I think we've all got carts and horses in our minds at this point, so we're going to adjourn now until 9:30 on Monday morning.

MR. FURLOTTE: Maybe I have - I have one last question to

ask in relation to this and then it would be fine.

THE COURT: All right.

Q. Well, I would say, Doctor, that as a lay person that I would look at it ignorantly and I would probably say that, well, it is the numbers that are influencing your decision rather than the principles which you use to justify the numbers. What would your answer be to that?

A. What was the question?

THE COURT: The question hasn't come yet.

Q. That I would look at it ignorantly and I would probably say well, it is the numbers that are influencing your decision rather than the principles and first principles on which you use to justify the numbers.

A. Well, that's what you've said but I don't understand the question. I didn't hear a question in that.

Q. How would you look at it?

A. How would I look at it?

Q. Yes.

A. I would say that we have a theory, we have a well established theory that has been rigorously tested, that we are applying it in a legitimate, bona fide scientifically acceptable way and generating numbers that we can feel quite confident in, that would be my assessment of what we do.

Q. But you're not coming at it from an abstract way and using prior principles in order to obtain the numbers?

A. I'm using prior principles of population genetics; namely, I'm using Hardy-Weinberg law, I'm using

linkage disequilibrium for the product rule, I'm using contingency table Chi square tests to test if there are bin frequency differences between two populations. I'm looking at confidence intervals on the estimates that we get, I'm using the whole repertoire of scientific statistical paraphernalia that we have at our disposal. The repertoire is still to be invented, I suppose, but we're using what we have, and as I see it we're developing this from first principles, taking in mind the account that when we generate samples we're always looking for surprises. We haven't found them yet.

THE COURT: One more question.

Q. Basically when I asked that question that it is the numbers that are influencing your decision rather than the principles upon which you use to justify the numbers would you say that that is partly true but that is because you think it is always the case and one has to make some decision based on empirical evidence and using the empirical elements to inform your decision rather than coming upon it in some abstract way from prior principles?

A. I think the way science operates, and it's not unique to my vision of science, is that you have certain principles that you're testing against the world, and you're testing against some empirical facts that you're generating and that we often have to modify the theory to take into account aspects of reality that we hadn't theretofore considered, and so there always is a dialogue going on between the theory and the empirical data and the experimental results. That is the

exciting thing about science and that's why we do things and that's why we need more information and that's why we generate more data to be able to look at it, because that's the fascinating part, that there never is an ultimate answer in science.

THE COURT: Now, we will send the jury home until tomorrow. You're stood aside for a continuation on Monday morning.

DR. CARMODY: Thank you, My Lord.

THE COURT: Just for the record I want to say one thing before the jury retires, and that is the accused is now out of the court room. He's not out of the court room, I want to make clear, because he requested to go out of the court room. He has been put out of the court room by an order I've made under Section 650 of the Criminal Code because of his continuing discourse after he made the request.

This again is a fairly long weekend. The indications are as far as I can see that this witness will be concluded with in, we hope, fairly short order on Monday morning. When he is completed I believe that will constitute, as I'm led to believe, the end of the Crown's case, at which point the defence will be asked if they intend to call witnesses. Mr. Furlotte has indicated, although be's not bound by it, that he will be calling at least one expert witness. I believe the plan is that his evidence would be concluded on Monday, and where we go from there I don't know, but after the other - if there are other defence witnesses they would proceed immediately after that, of course, and then when

they're concluded and all the evidence is in, then we would - I would think we would probably have a day in between to give counsel an opportunity to prepare their addresses to you, a day or two, and then the judge's charge would be delivered to you and then you'd be retiring to consider your verdict. Now, whether that comes next week or the week after I can't say at this point, and I wouldn't know or we won't know until next week, but I for my part realize the trial is drawing on now. I'm sure we're all getting tired to a point and I'm not going to prolong it any more than is necessary, but I remind you again, please don't discuss this case with anyone and don't accept what you may read in the papers or hear on television or radio.

MR. WALSH: My Lord, if I could, the jury will be retiring to the jury room to go home. If I could impose on you to, when the jury retire to the jury room, just ask them to remain for a minute. I have a matter to discuss that may or may not require them being informed of something, and if they could just stay for a minute after they're disbanded.

THE COURT; All right, would you wait there, then, and if it's necessary, if there's any change in anything, we'll call you back. If you get word through the constable that you're not required again you'll know there's no change.

(JURY WITHDRAWS)

MR. WALSH: My Lord, I just wanted some direction, particularly from Mr. Furlotte, as to what's going

to happen on Monday. My understanding was that he was going to complete the cross-examination of Dr. Carmody subject to that one issue of background band sharing which was going to be addressed on Monday, and I'd like to have some indication of what is going to happen on Monday now in conjunction with what's happened here today. We obviously haven't finished his cross-examination. I haven't even discussed this with Dr. Carmody. I can tell you that one of the inclinations I have is that we continue with the cross-examination. Now, he has a flight going home, he probably - I don't even know if he agrees, I haven't had a chance to talk to him about the travel arrangements, I know he has appointments at Carleton, but one of the inclinations I would have is to continue with the cross-examination tomorrow until we reach the point that was to be addressed on Monday morning. That would assure Dr. Carmody that on Monday when he arrives he's going to be getting out again, and it would assure us as to what's going to happen on Monday because one of the fears I have is that we'll end up going over the whole thing all over again come Monday. That may not even be a practical alternative, but I would like to have some indication from Mr. Furlotte as to what's going to happen on Monday in terms of how much more he's got to cover.

THE COURT: Can you enlighten us, Mr. Furlotte, as to - let me just say, my understanding and the understanding we had this morning was that the cross-examination of Dr. Carmody on all aspects

excepting one aspect of it with respect to which Mr. Furlotte wanted to consult with Dr. Shields would be completed today comfortably and that Dr. Carmody would then come back on Monday morning and perhaps within a half-hour or at most an hour he would be finished. Dr. Shields would be called by the defence, would come on for the rest of the day and would be finished before Monday was out. Is there any change from that, Mr. Furlotte?

MR. FURLOTTE: Well, yes, there is, My Lord. As I explained this morning, that because of the new development when Dr. Fourney took the stand yesterday that I was under the impression that there was going to be no opposition to the common band sharing in the Newcastle area, background band sharing in the Newcastle area, but as a result of testimony yesterday, which surprised me, that is in issue now and as I explained to Crown counsel and yourself that because of that new development, then I feel that I have to do more cross-examining of Dr. Carmody than I had originally intended, because now that there's a new position being taken by the Crown, then I feel that there's other areas that I have to get into to support the common background band sharing, and for that reason it has taken longer than I expected to cross-examine this witness today, and therefore that's why I fell short of my expectation.

THE COURT: Well, can you give us an indication of what your timing would be?

MR. FURLOTTE: I've been wrong every other time, My Lord, and I guess - I would expect I'd be all morning

with Dr. Carmody on Monday. I sure wouldn't say that I'd be any less.

MR. WALSH: May I suggest if I had a minute to discuss with Dr. Carmody, I realize he's on the stand, but just travel arrangements only. I'm going to suggest that if Dr. Carmody can make it - now, if he can't, then obviously we would have to move over till Monday, but one of the suggestions I'm going to make is Dr. Carmody can accommodate us, I'm going to suggest we continue with the cross-examination tomorrow and then finish up that one particular aspect on Monday morning. That may not be a viable alternative but I'm just saying that because - we had set aside this week for Crown witnesses and I know Dr. Carmody didn't even think he'd be here till Friday. He never envisioned that he'd be here at least till Friday.

THE COURT: This would make sense. Now, I was led to believe that some of the jury felt they have obligations?

CONSTABLE: One of the jurors is heading for New Hampshire to a function or something down there.

DR. CARMODY: Would it be proper for me to inject my own -

THE COURT: Yes, I think so. This is a voir dire, of course, and nothing is being reported.

DR. CARMODY: I have some important appointments that I would prefer to be back in Ottawa tonight for, and since in any case I have to be here on Monday whether I'm on the stand for the whole morning on Monday or half an hour, it seems the same travel time to me, so I'd rather go back tonight.

THE COURT: I think we'll adjourn now and we'll start out on Monday. There's one thing I want to point out, and I suppose I can do it as well here as anything. One of the considerations for Dr. Shields was of course that his attendance is financed, as I understand, out of public funds, and there was some suggestion, well, if he had to stay over a second day because of delays that that might be difficult to arrange, and I said to counsel this morning that if there was anything I could do to facilitate any reasonable request in that regard I would certainly put my weight behind it, but I want to make clear that I'm not going to support anything of that nature and I retract what I said insofar as supporting any request that he go over into Tuesday in the present circumstances. I just make that clear. Now we'll recess until Monday morning at 9:30.

(ADJOURNED TO OCTOBER 28, 1991.)