IN THE COURT OF QUEEN'S BENCH OF NEW BRUNSWICK

TRIAL DIVISION

JUDICIAL DISTRICT OF FREDERICTON

BETWEEN:

HER MAJESTY THE QUEEN

- and -

ALLAN JOSEPH LEGERE

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

APPEARANCES:

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

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

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Proceedings of October 15, 1991

Dolores Brewer,
Court Reporter.

COURT CONVENES - 9:30 A.M. (Accused present in dock.)

MR. FURLOTTE: My Lord before you give a decision on the motions that were made last week I would like to bring to your attention that on the ATV news last night they again brought up the matter of one of the jurors being excluded as acting as a juror, and I suppose possible reasons why they also broadcast on TV that Lois Gaunce and Carolyn Norwood had been restricted from visiting Mr. Legere at the Federal Institution at Renous Atlantic Institute, and I suppose they left the implications that Mr. Legere had somehow been maybe involved in the jury tampering and that we're not going to be taking any more - or take all precautions to see it didn't happen again or something like that. But the key point to my objection to the news last night is that they brought the office of the Public Prosecutions into the scene stating that it was directives of the Public Prosecutions as to why Mr. Legere could not receive any visits from Lois Gaunce and Carolyn Norwood which would, again, enhance in the minds of the jury that Mr. Legere was behind or instigated some form of jury tampering in order to short-circuit his trial.

I have given a copy of the letter to Mr. Allman which was a copy of a letter to Mr. Legere from the warden at Atlantic Institute, a copy for you, advising Mr. Legere that under the -- I'll read the letter.

> "This is to inform you that at the request of the Director of Public Prosecutions for the Province of New Brunswick I am hereby cancelling your visiting privileges with the above-mentioned visitors including telephone or written contact for the duration of your current trial."

And the visitors being Lois Gaunce and Carolyn Norwood.

Now, where the jury may have only had an inclination that Mr. Legere was behind some form of jury tampering there would not be a doubt in the minds of the jury that the Office of Public Prosecutions believes Mr. Legere was behind it and are going to take all precautions from here on in to make sure that it doesn't happen again. It just adds fuel to the fire that was already started a couple of weeks ago and my position there now is that there is nothing anybody could do to remove from the minds of the jurors that Mr. Legere was probably behind some form of jury tampering.

THE COURT: Thank you very much Mr. Furlotte.

MR. FURLOTTE: And I don't know why the Director of Public Prosecutions is getting involved in this. Let them have their trial in court and not out of court.

MR. ALLMAN: I would just speak very briefly on that. The first point that occurs to me, and I don't know the answer to it but I think we can speculate, is how the news media became aware of the fact that apparently Mr. Legere's privileges of visiting with Gaunce and Norwood have been cancelled. I don't suppose it came from Atlantic Institute and I don't suppose it came from the Director.

MR. FURLOTTE: What's the jury going to suppose My Lord, that's the bottom line.

MR. ALLMAN: My inference is that it's Mr. Legere or Miss Gaunce or Miss Norwood that has given this information to the news media. No doubt that could be ascertained if you wanted to. But if that is the case it certainly seems the height of - I can't think of the word - the height of cheek, I would call it, to ask

for a mistrial if in fact I am right in my theory that they are the people who have leaked this.

MR. LEGERE: I certainly didn't.

MR. FURLOTTE: The only reason I bring this up, My Lord, is that we now have direct evidence, solid evidence, that the Crown Prosecutor is interfering with Mr. Legere getting a fair trial.

MR. ALLMAN: I'm sorry to have to keep getting up and down but there's two points here. The first is is there anything wrong with doing that? I don't think there is. I think that's a very sensible thing to do. The second thing is the fact of it being broadcast on the news. They are two logically unrelated things. I don't think if it hadn't been on the news that would have been grounds - the letter and the action would have been grounds for any kind of an argument for mistrial. The argument is the fact that he got on the news. That's the only point I'm making.

THE COURT: Yes. Well, I will take this into consideraton when I make my ruling on the other thing which I will do - had indicated I would do sometime today. If I want to consider it further I may delay it until tomorrow. It will be either this afternoon or tomorrow morning.

I was disturbed last week after we adjourned here to read in a weekly newspaper in New Brunswick the account of an interview with Mrs. Gaunce despite everything I said here last week. I realize that the reporters involved perhaps weren't privy to the discussions we had here or to even a separate meeting which the media requested with me in my chambers to

seek certain instruction or guidance, but unfortunately some newspaper publishers or editors don't seem to know what the rules are about this thing and it's really a problem how you get the message across. I'm not blaming any media who are here for that at all. It's not their fault. However, I don't think we'll see a recurrence of it with that particular newspaper.

Well now, are we ready to go ahead this morning?

MR. WALSH: Yes, we are, My Lord.

THE COURT: Now, okay, we'll have the jury in Mr. Sears, please.

(Jury in. Jury called, all present.)

THE COURT: Members of the jury, with the Blue Jays out of the world series we can thankfully, I might say, we can now concentrate on Deoxyribonucleic Acid, if you can learn to spell that as I have done. At least I presume that that's what the trial is going to be immediately concerned with. Who has a witness to call.

MR. WALSH: I do My Lord. I would like to call Doctor John Waye.

DOCTOR JOHN WAYE, called as a witness, having been duly sworn, testified as follows:

DIRECT EXAMINATION BY MR. WALSH:

Q. Would you give the court your name, please, and your present occupation?

A. John Stewart Waye. I am Assistant Professor at McMaster University in Hamilton, Ontario.

MR. WALSH: My Lord with your permission I would like to take Doctor Waye through his curriculum vitae.

THE COURT: Yes.

MR. WALSH: Doctor Waye you received a Bachelor of Science in Microbiology from the Department of Microbiology at the University of Guelph, Guelph, Ontario, is that correct?

A. Yes.

Q. You received a Masters in Science and Biology from the Biology Department of McMaster University in Hamilton, Ontario, is that correct?

A. Yes.

Q. You received a doctorate degree, a Ph.D. in Medical Biophysics from the Department of Medical Genetics at the University of Toronto in Toronto, Ontario, is that correct?

A. Yes.

Q. You are also a Postdoctoral Fellow in Medical Biophysics with the Department of Medical Genetics at the University of Toronto in Toronto, Ontario?

A. That's correct.

Q. What general field of science do you belong to, Doctor?

A. Medical Genetics.

Q. And what is Medical Genetics?

A. It's the study of genetics as it applies to diseases, in my case human diseases, disease conditions.

Q. Would that come within the field of Molecular Genetics?

A. Yes.

Q. And what would molecular genetics be?

A. In my case the study of molecules such as DNA.

Q. What is DNA and what application would it have to the field of molecular genetics?

A. DNA is the genetic material that basically is the blueprint of life. It tells - it's the code that governs all the physical and chemical properties of a human being that makes a human being. Errors in the code produce disease and that's the area that I am concerned with.

THE COURT: Can the jury hear the witness adequately? I would ask you to speak rather slowly and somewhat more slowly than you would in one of your university classes because the jury and I are dumb people. We don't sit through classes all day. Speak slowly and deliberately so we can understand.

MR. WALSH: Doctor Waye is there DNA in other things than humans?

A. Yes, in all living organisms there is a code, from bacteria to dogs to cats to trees. There is a DNA code that makes a tree a tree, a dog a dog, a human a human.

Q. Doctor, during your educational studies you received a number of scholarships and awards, is that correct?

A. Yes.

Q. What is a dissertation?

A. Dissertation is the final written work of a thesis. In graduate school you start off with a problem, a research problem that becomes the focus of your work over a number of years and at the end of that you compile your results into a dissertation which lays out the problem, summarizes your results, and comes up with a concluding statement, whether you have proved your theory correct or incorrect.

Q. And do you go before a board of reviewers with that problem?

A. Yes. You have a review committee that reviews it at several points along the way and you have an oral exam at the end where you present your thesis, your dissertation, to that board.

Q. And you did that both in obtaining your Masters Degree and in obtaining your Doctorate Degree?

A. Yes.

Q. And both of those dissertations, am I correct, relate to human DNA?

A. Yes.

Q. Could you tell us, please, what is DNA typing? Just briefly at this stage, what is DNA typing and what application it would have to molecular genetics particularly as it applies to humans?

A. DNA typing is a general word basically means the analysis of DNA. There's a number of different ways you can analyze DNA and we just use the term DNA typing and it's all inconclusive. There could be ten different ways to analyze it and DNA typing would be a general term.

Q. Could you give us a couple of examples of ways of typing?

A. You could look at variations in the sequence of the DNA. It's a code so you can actually read the code and you can indirectly look at a DNA say through a microscope. There's various ways that you can type DNA or analyze DNA.

Q. Is the term RFLP, is that a particular method of typing DNA?

A. Yes. It's one of the first and best used methods for typing DNA. The most common methods of analyzing DNA.

Q. Are there various areas of molecular genetics in which DNA typing is applied?

A. Virtually all areas of biology and medicine DNA analysis has become a cornerstone in both research and practical diagnosis of disease and virtually anything you do in biology DNA has a part in it now.

Q. Is it used in its forensic application, that is for courtroom use or for police work?

A. Yes.

Q. For medical diagnosis, is it used in that particular area?

A. Yes. It's heavily used in medical diagnostics.

Q. And in research?

A. In research, again, in virtually all areas of biology and other disciplines DNA is a cornerstone technology.

Q. Doctor, up to January of 1990 you were a molecular genetics specialist with the Molecular Genetic Section of the Central Forensic Laboratory of the Royal Canadian Mounted Police in Ottawa, is that correct?

A. Yes.

Q. Would you briefly describe your duties there at that time?

A. My duties, along with other scientists that worked there at that time, were to develop the techniques of DNA analysis for forensic individualization. So to take existing techniques from the scientific

community and adapt them to answering forensic questions, could the sample have come from this individual.

Q. Did you do anything else in -- I'll deal with that later. Perhaps at this time, you were also an adjunct professor at the Department of Microbiology and Immunology at the University of Ottawa, is that correct?

A. Yes.

Q. You were an Associate Member of the Childrens' Hospital of Eastern Ontario Research Institute in Ottawa, Ontario? That's correct?

A. Yes.

Q. You are presently an Assistant Professor with the Department of Pathology at McMaster University in Hamilton, Ontario?

A. Yes.

Q. And you were an Assistant Director of the Provincial Hemoglobinopathy DNA Diagnostic Laboratory at the Chedoke-McMaster Childrens' Hospital in Hamilton, Ontario, is that correct?

A. Yes.

Q. Could you describe -- Hemoglobinopathy, My Lord, was a word that took a while to develop how to pronounce it. Would you describe your duties and responsibilities associated with that lab?

A. It's a lab that concerns DNA diagnostics for a group of diseases that when lumped together we call hemoglobinopathy. So that just means something wrong with hemoglobin. Hemoglobin is a molecule in your blood that transports oxygen to your tissues. The

molecule that does all this work is coded for by DNA and when you have mutations of your DNA that makes the hemolobin molecule your blood either transports oxygen poorly and your anemic or it doesn't do it at all and that's incompatible with life. They're fairly common diseases. One of them is sickle-cell anemia. World-wide they're probably the most common genetic disorder, and our job in the lab is to diagnose which mutations people have and to offer a service of prenatal diagnosis. That is a predictive service when a lady comes into the hospital, she's pregnant, both her and her husband are carriers of the disease, you can give them the information as to whether their child may or may not have the disease.

Q. This involves looking at human DNA and typing human DNA, is that correct?

A. Yes. You both look at the parents' DNA and the child's DNA.

Q. You are a member of a number of professional organizations dealing with human genetics?

A. Yes.

Q. You also consult to the Ministry of the Solicitor General for the Centre of Forensic Science in Toronto, Ontario, is that correct?

A. Yes.

Q. And you were a consultant with the Royal Canadian Mounted Police Central Forensic Laboratory after you left the R.C.M.P., is that correct?

A. Yes.

Q. And those consultations would be dealing with human DNA and DNA typing?

A. Yes.

Q. I see, Doctor, from your C.V. that you have a number of scholarly activities. You are a Journal Referee for a number of journals. Could you explain what a Journal Referee is and what relation that would have to DNA or DNA typing?

A. Well, scientists publish their works in journals. There's a sort of in-house quality control. A scientific community judges the validity of the results before they're published and what you do is if you are submitting a work, a publication to a journal, the journal editor will select experts in that field and he will send your paper to them to review. Those people will act as referees. They will look over the work, make comments about whether it's valid or not, make suggestions how it could be improved. They will advise the editor whether it's publishable or whether it should be altered or whether it shouldn't be published at all. So that's how a journal referee acts in the process.

Q. And in being a Journal Referee you do about ten articles a year, is that correct? Referee about ten articles a year?

A. On that order, yes.

Q. And would those articles be related to DNA or DNA typing?

A. Yes, all of them.

Q. You teach at McMaster University, you have indicated that. Your courses - you teach Genetic Disorders, is that correct?

A. Yes.
Q. And that deals with human DNA?
A. Yes, human genetic disorders.
Q. You teach molecular diagnosis of thalassemia?
A. Yes.
Q. And does that deal with human DNA?
A. Yes.
Q. You teach a course in DNA Fingerprinting in Forensic Medicine?
A. Yes.
Q. And that deals with human DNA and DNA typing?
A. Yes.
Q. And you teach a course called "The Human Genome"?
A. Yes. Parts of that course, yes.
Q. Just for clarification when you say the human genome what are you referring to?
A. The DNA that's contained in human cells, in human bodies.
Q. I see under "Publications", "Peer Reviewed Journal Articles", and you have over thirty of those. What is a peer reviewed journal article?
A. As we were talking about journal referees, that's an article that has gone out for formal review by your peers and has been accepted for publication.
Q. And you have done that in over thirty occasions? Approximately over thirty occasions?
A. Yes, I believe so.
Q. And do those articles deal with human DNA and/or DNA typing?
A. Almost all of them I would say deal with human DNA with the exception of maybe one or two of those papers, and DNA typing certainly all of them.

Q. I understand, Doctor, you yourself and with others have developed certain techniques or methods for typing DNA for forensics that are now being used by other labs?

A. Yes.

Q. And you have published your results?

A. Yes.

Q. With respect to those techniques. Under your C.V. you have "Publications: Short Reports and Letters (Peer Review Journals)". What would that refer to?

A. Those are shorter works of science that receive less extensive peer review. Generally the editor of the journal will look it over himself or perhaps give it to one reviewer. It doesn't receive extensive review because they're fairly short works of science, things that you want to be published fast. They're usually technical notes or small findings.

Q. You have several of those. Would they be dealing with human DNA and/or DNA typing?

A. Yes.

Q. I see under "Symposium Proceedings" you have a number of Symposium Proceeding Publications. What would that refer to?

A. Those are like you often get invited or you contribute talks to international symposia gatherings of scientists to discuss their works. At the end of that usually the person who organizes the symposium will ask speakers if they could put together a book chapter or short manuscript describing what was in their talk. It's basically for the benefit of the people who didn't go to the meeting. There will be a written version of your talk.

Q. You have several of those; do they mostly deal with human DNA and/or forensic DNA typing?

A. Yes.

Q. I understand, as well, Doctor, that you have recently completed a chapter in a textbook entitled "DNA Identification", "Forensic Evidence in Criminal Cases", is that correct?

A. Yes.

Q. What generally would that chapter - what would you actually deal with in that chapter? What aspects?

A. The audience for that book is a legal audience so it's basically a scientist writing about DNA typing, the forensic application of DNA typing for a legal audience. So it's a very basic guide through DNA typing.

Q. Under "Publications: Abstracts (Peer Review Journal)", would you explain what an abstract is?

A. An abstract is a summary of a talk or a presentation that you gave at a scientific meeting. They're generally short, usually a page long, and after you go to a meeting, again, for the benefit of the people who weren't at the meeting there will be summaries of all the presentations made and those are called an abstract.

Q. And you have approximately 18 of those. Do they deal with human DNA and/or DNA typing?

A. Yes.

Q. You have participated in a number of working groups. I see the "Technical Working Group on DNA Analysis Methods", the acronym is TWGDAM, at the FBI Academy at Quantico, Virginia. Would you explain what that is? What you were doing there.

A. That was a group of scientists from Canada, all over the United States, who had similar interests. I believe back in about 1988 we were all more or less in the same boat. We were starting up DNA typing labs in various regions in North America and we wanted to do it in a cohesive manner so we decided that quarterly, every third month or so, we would meet in Washington and we would go over what each of the labs were doing and we would make suggestions to each of the labs, and we designed projects so we could share some of the workload while we were designing this system. So it was a working group all with the same goal, to develop a system that we could interact and exchange DNA information with.

Q. You also are a member of a "Working Group on Statistical Standards for DNA Analysis" at the FBI Academy at Quantico, Virginia. Would you explain what that was?

A. That's a very similar group. It also involved some outside people. Some people that weren't from forensic labs but were invited consultants from the scientific community and that was just to deal with statistical issues as they pertained to DNA typing of forensic samples.

Q. You have participated in a number of training courses and workshops. In particular, Doctor, you were an invited lecturer at the "DNA Typing Workshop" put on by the "Canadian Society for Forensic Sciences" in Toronto, is that correct?

A. Yes.

Q. You were an invited lecturer at the "DNA Typing Workshop" put on by the Wisconsin Department of Justice, Madison, Wisconsin?

A. Yes.

Q. You were an invited lecturer to the "DNA Typing Training Course" at the Royal Canadian Mounted Police, Molecular Genetic Section in Ottawa, is that correct?

A. Yes.

Q. You were an invited lecturer to the "DNA Typing Training Course", the Centre of Forensic Sciences, in Toronto?

A. Yes.

Q. And you were an invited lecturer to the "Ontario Crown Attorney Training Course" in London, Ontario?

A. Yes.

Q. Under your C.V. you have "Presentations at Meetings: Invited", what does that refer to?

A. There's generally two ways that you can make a presentation at a meeting. You can either be invited to talk on an area that you do work on or you can volunteer to give a talk at the meeting.

Q. And in these particular meetings that you attended would that deal with DNA and DNA typing - human DNA and DNA typing?

A. Yes.

Q. Under "Presentations at Meetings: Contributed (Papers)", what does that mean?

A. That's where they usually have a call for papers. That is you are on their mailing list and they will send out announcements that there will be a meeting at such and such a place on such and such a day and

they ask for interested people to submit papers for presentation and if you are working on a piece of research and it's finished, or near finished, you submit a summary of your work and they decide whether they're interested in your presenting it. So that's a contributive paper.

Q. And you contributed a paper which was accepted at the "Annual Meeting of the American Society of Human Genetics" in Philadelphia, Pennsylvania, is that correct?

A. Yes.

Q. At the "Annual Meeting of the American Society of Human Genetics" in San Diego, California?

A. Yes.

Q. At the "Annual Meeting of the International Society for Forensic Haemogenetics" at Liege, Belgium?

A. Yes.

Q. And at the "Annual Meeting of the Canadian Society for Forensic Sciences" in Toronto?

A. Yes.

Q. You have contributed posters to meetings. What does that mean?

A. Poster as opposed to giving a formal lecture to an audience. Often at these meetings there is many more papers submitted for presentation than there are slots to actually give the presentation so what they do is they have large rooms where people put their work on large boards such as this and for a number of hours on a given afternoon they will be at that poster board and anyone is free to walk up and down the aisles and discuss the work with the authors. It's a very informal way to present your work to the rest of the scientific community.

Q. You have done that at the "American Society of Human Genetics" annual meeting in Ontario?

A. Yes.

Q. At the "American Society of Human Genetics" meeting in Salt Lake City, Utah?

A. Yes.

Q. At the "Human Gene Mapping 9" in Paris, France?

A. Yes.

Q. At the "Exploring the Human Genome", Boston, Massachusetts?

A. Yes.

Q. At the "FBI DNA Typing Symposium" in Quantico, Virginia?

A. Yes.

Q. The "International Congress of Genetics" in Toronto?

A. Yes.

Q. And the "Annual Meeting of the Canadian Society of Forensic Scientists" in Canada?

A. Yes.

Q. And the "Annual Meeting of the American Society of Hematology" in Boston, Massachusetts?

A. Yes.

Q. You have just attended I understand, Doctor, you have just come back from a recent meeting?

A. Yes, in Washington last week.

Q. Would you explain to the jury what that related to?

A. That was the "International Congress of Human Genetics" and it was a joint meeting between the "International Congress of Human Genetics" and the "American Society of Human Genetics".

Q. And how many people would attend that meeting and where would they be from and from what fields?

A. There was about five thousand geneticists at that meeting and they were from all over the world in all areas of human genetics, cyto genetics, molecular genetics, forensic genetics, medical genetics. Every type of genetics that you can think of that deals with the human body.

Q. And that's for a week?

A. One week that meeting lasted, yes.

Q. And in relation to the application of genetics to forensics were the issues discussed at that particular meeting?

A. Yes, there is an entire morning devoted to that subject, yes.

Q. Have you collaborated with individuals in the forensic fields of molecular genetics or in the medical diagnostic or research fields?

A. Yes. Generally don't do research on an island. You have collaborators in different labs and different countries. They have expertise in areas that you don't and you have expertise in areas that they don't, and the easiest way to solve a problem is to pick up the telephone and form what we call collaboration. You make a formal agreement that I'll do this part of the project, you do this part of the project and we'll work towards a common goal and get it done fast.

Q. Who would you consider to be your main teacher associated with your study in molecular genetics? Who would be your mentor so to speak?

A. Doctor Hunt Willard in Stanford. I was a student of his and I continue to be a collaborator of his.

Q. And what reputation would he have in the field of human genetics?

A. Very good reputation.

Q. What kind of DNA typing were you involved in at the R.C.M.P. Lab when you were there?

A. Principally a technique that we call RFLP.

Q. Which stands for what?

A. "Restriction Fragment Length Polymorphism".

Q. Do you have experience in other techniques?

A. Yes.

Q. For example?

A. DNA sequencing which is actually determining the code of the DNA molecule down to its lowest level. PCR, another acronym.

Q. For what?

A. "Polymerase Chain Reaction". It's just another technique for analyzing DNA.

Q. Are all these techniques that you have described used in medicine and research as well?

A. Yes. They all come from other fields. None of these techniques were invented for forensics per se. They were borrowed from other fields and adapted to our forensic application.

Q. And you have experience in the medical and research application of these techniques?

A. Yes, that's my current employ.

Q. How many DNA typing tests using the RFLP technique would you have conducted in your forensic work?

A. Many hundreds I would say. Perhaps even thousands.

Q. How many samples would you have actually run in the RFLP test, for example blood, hair, semen? How many different samples would you have run?

A. The bulk of them would be blood samples that I have analyzed. Virtually every other body fluid or tissue I can think of at some point, but the bulk of them would be blood samples and, again, it would be probably in the thousands.

Q. Could you give the jury some explanation of what kind of samples you would be dealing with that you would have run?

A. Other than blood?

Q. Yes.

A. Hair. Skin. Feces. Urine. Mouth swabs. Saliva. Semen.

Q. Where else in Canada are DNA typing tests being performed for forensic use?

A. Principally in Montreal in that province's forensic lab, and in Toronto, the Ontario province's lab.

Q. Outside Canada where is DNA typing being forensically performed, particularly the RFLP technique?

A. It's essentially world-wide. If they're not using it for case work they're developing it for case work, but in virtually every country, both in Europe, Asia, South America, Australia, every place that has a forensic lab is either using it actively now on case work or is contemplating using it so they are developing it. That's my understanding from going to meetings where there are representatives of these labs in attendance.

Q. You have had experience dealing with scientists from other countries that are using the RFLP technique for forensics?

A. Yes.

Q. Apart from case work, and that is using it for forensics, where in Canada and other countries you have mentioned would DNA typing - where would it be conducted?

A. Certainly in every university that has research facilities DNA is being analyzed for some purpose, be it medical or some other field of biology or biochemistry. Virtually any hospital that has diagnostic labs and genetics departments which involves a large number of hospitals, both teaching hospitals or research institutes in hospitals across the country.

Q. You have testified previously, I understand you actually use DNA typing techniques in the childrens' hospital you are presently working at, is that correct?

A. Yes. There's a number of diagnostic labs that -- Like our lab, for instance, does DNA typing exclusively for disease diagnosis. We have no other techniques that we do in the lab.

Q. How many DNA typing tests would you have conducted in the clinical setting, that is for medical diagnostics?

A. A number of samples. It's on the range of three to four hundred a year and I've been there almost two years and I think for every sample submitted there's probably several that we work on in related case, so again it would be in excess of a thousand I imagine.

Q. Could you describe for the jury, please, what population genetics is and what application that would have to DNA typing using the RFLP technique?

A. Population genetics is just an expansion on analyzing DNA of a person. You can analyze a single person's DNA and draw certain facts, whether that person has sickle-cell disease or not for instance. Population genetics would ask a more global question: how many people in this country have sickle-cell disease, or what is the frequency or the incidence of sickle-cell disease say in this portion of Africa or people from this region. So that would be population genetics. You want to know the frequency of genetic events in a population as a whole, so a group of individuals.

Q. You're referring to human populations. Can you have population geneticists in other life form?

A. Well certainly. Every area of genetics, whether you are a plant geneticist or an animal geneticist, or a fruit fly geneticist, population genetics enters into your studies. You're never really studying one organism or one animal. You make your findings on one animal or a group of animals and then you expand it to a population.

Q. Are there subspecialities within human population geneticists or within population geneticists generally? Can you have a specialty or subspecialty within that field?

A. Certainly.

Q. What would the phrase 'human population genetics' as it pertains to forensic DNA polymorphisms mean or identify to you?

A. That would be a very limited area of population genetics where you're looking at a very focused question. That is if I identify a DNA pattern associated with a single individual or forensic sample then you are asking the question how often would I see that pattern in the population. So that's an application, a very restricted application, of general population genetic theory.

Q. What is the probability of seeing this particular pattern in a particular population?

A. How often would I see this pattern in Canada or in this town or in this room for instance.

Q. If I understand you correctly, this would be a question you ask after you use the RFLP technique to see if the samples match.

A. Yes.

Q. You would get into population genetics only if the samples did in fact match?

A. Correct.

Q. Do you have experience in this regard?

A. Yes.

Q. And what, if any, things did you do at the R.C.M.P. Lab in relation to that aspect?

A. Well, in order to answer those types of questions the first task that you do is you develop what we call a data base, and all the data base is is that you analyze many hundreds of people and you establish how much variability there are in those people and how often I would expect to see a certain pattern in that group of individuals. It's much like a political poll that they take where they ask people their voting

opinions, ask a number of people their opinions, and then they try to predict based on that.

Q. Have you studied and read literature associated with this particular field?

A. Yes.

Q. Have you published -- Have any of your publications dealt with these aspects, data base or determining probability figures?

A. Yes.

Q. You have, Doctor, testified with respect to DNA typing in courts in this country before?

A. Yes.

Q. You have testified in the Supreme Court of Ontario on two occasions and in the Provincial Court in Ontario and Provincial Court in Alberta, is that correct?

A. I'm not sure exactly which courts I was in.

Q. You have testified --

A. I have testified in Ontario a number of times and I testified in Alberta.

Q. You have also, I understand, consulted for the Defence, for Defence lawyers on occasion, is that correct?

A. Yes. Actually I probably get more requests from defence lawyers to advise them or explain to them DNA typing results over the phone or they come to the office.

Q. And have you ever had occasion to consult with defence lawyers outside this country, that they have come to you asking your opinion on certain aspects?

A. Yes.

Q. Where for example?

A. There was a case in California where I was actually going to testify for the Defence but I had a conflict with a case that I was subpoenaed for in Alberta as it turned out, so I had a prior obligation.

Q. Do you have any difficulty in consulting to Defence with respect to any of the issues associated with DNA typing?

A. No.

MR. WALSH: My Lord at this time I am going to ask that Doctor Waye be declared an expert in the fields of molecular genetics, DNA technology and testing procedures in general, clinical and forensic DNA typing in particular.

THE COURT: Yes.

MR. WALSH: And human population genetics as it pertains to forensic DNA polymorphisms.

MR. WALSH: Perhaps if I may, My Lord, just further clarification, if I could ask Doctor Waye a question. What is a DNA polymorphism?

A. Just a recognizable difference between individuals at the level of their DNA.

MR. WALSH: I have that motion My Lord.

THE COURT: Do you have any questions, Mr. Furlotte, you want to ask the witness in respect of his expertise, or alleged expertise at this point?

MR. FURLOTTE: I have no questions at this time My Lord.

THE COURT: Thank you very much. Well, I think the examination has established the witness's expertise in the fields you have described for the purpose of this trial. I point out to the jury, of course, that it

will be up to you people to decide whether he knows what he's talking about or whether he doesn't. Okay.

MR. WALSH: Thank you My Lord. Doctor Waye, I understand that this morning part of what your testimony is going to relate to is explaining to the jury the biology underlying DNA and to explain the procedures involved with respect to DNA typing, is that correct?

A. Yes.

Q. And for that purpose you have a number of slides you wish to show to the jury, am I correct?

A. Yes.

Q. And I believe there's ten slides. I believe there are --

A. There's a number of slides.

Q. Yes, there's a number of slides for which we also, Doctor Waye, you have provided schematic diagrams that are mounted on a foam board, is that correct?

A. Yes.

Q. And these schematic diagrams are essentially identical to the slides?

A. Yes.

MR. WALSH: My Lord at this time I would ask that if we could have the schematic diagram marked as an exhibit, one exhibit numbered 1 through 10, that would obviate the necessity of having the actual slides entered into evidence. What it will help is this way. If Mr. Furlotte was cross-examining the Doctor on a particular aspect he would have to start the slide projector up and find it, or if the jury wish to later look at something it would save them going to the slide projector. We have identical or essentially identical

schematics mounted on foam boards. So I would ask that those ten schematics be marked as one exhibit number, 1 through 10, and I have the particular order I would like to follow.

MR. FURLOTTE: I have no objections to that My Lord.

THE COURT: Let's call it then exhibit 158, 1 to 10. If there are any -- you say they are essentially the same as the slides.

MR. WALSH: I believe there's one instead of the description being on the top it's on the bottom. There's no --

THE COURT: No material --

MR. WALSH: No material discrepancies My Lord, no.

THE COURT: Fine. Now, what do you propose to do? You will have these marked but then you are going to put them up on the easels, are you?

MR. WALSH: We are going to put them on easels and try to display them as much as we can.

THE COURT: Yes. But when the slides are being shown Doctor Waye will be speaking to the slide?

MR. WALSH: To the slides. He may refer to one schematic that's shown. If he happens to be on one slide and to save trying to find it he might refer to one that's here. We can put the light on it. It works. We tried it last night.

THE COURT: Okay.

MR. WALSH: The first one marked 1 is headed "Genetic Blueprint of a Living Organism", to differentiate. The next one, My Lord, if we could designate it as a schematic of the "Human Chromosome". The next one, number 3, could be designated "Human Chromosome Showing Highly Polymorphic Areas". The next one,

number 4, is headed the "DNA Molecule". I am going to run out of room in a hurry. The next one would be the "DNA Molecule with Probe Attached". Number 6, My Lord, you could entitle it "DNA Typing, First Section". Number 7, My Lord, is entitled "Fragments of DNA Released by Hae III Restriction Enzyme Digestion".

THE COURT: And that could be shortened up to three words?

MR. WALSH: "Hae III Digestion". The next one, My Lord, is entitled the "Sieving Properties of an Electrophoretic Agarose Gel". That could be shortened to "Gel Electrophoresis". The next one, number 9, would be "DNA Typing Procedure, Second Section". The last one My Lord, number 10 is a "Forensic Case Illustration".

(Clerk marks exhibit #158-1 to 10.)

MR. WALSH: Doctor Waye I understand you are going to use the slide projector to start your testimony. Just as a beginning, a place to begin, I am going to ask you to describe through the use of the projector and then take us from there, but I would like you to describe what a cell is and what a chromosome is and explain how DNA is connected to those descriptions or those substances? Okay, and if you would, please.

A. All of those terms are going to be very important over the next little while, the term cell, chromosome, DNA. There will be a lot of technical jargon but hopefully we can cut through some of the scientific words here and bring it down to something that everyone can understand.

Q. I am going to ask you just to speak up just a bit, Doctor.

A. To begin with, there are a number of different cells that make up your body. Your body is made of a lot of different compartments and we call them cells. There are cells in your hair follicles, there are cells in your skin, cells in your blood, cells in virtually all tissues of your body. There's a human body. This is a cell. One type of cell. And all it really is is a very small microscopic compartment. Within that cell there's a subcompartment. It's called the nucleus and all it is is just a bag of information. It contains the DNA that tells that cell that it's a skin cell or a hair follicle cell. It basically has the program - has all the information to make a human being but it also has the program that tells that cell what it should be doing in the body. So the DNA is contained in each cell of your body and it's contained in this compartment called the nucleus, and the DNA is just a chemical and it's contained in these structures called chromosomes, and all they are is long strings of a chemical and it's all compacted into the nucleus, and remarkably these chromosomes that contain the DNA somehow contain all the information, this microscopic nucleus that would tell the cell what to do and basically has the whole blueprint for the human being itself all contained within that little package in each cell of your body.

Q. Does DNA vary from cell to cell? For example the cells in your hair versus the cells in your blood versus the cells in your semen, etc.?

A. Yes. There's three real features to be understood about why you want to analyze DNA forensically. One

is that there's cells throughout your body and that with the exception of a few cells that don't contain nuclei all cells will contain DNA so it doesn't really matter what type of cell you analyze there will be DNA in it. So you can analyze cells from the skin of your toe to the top of your head to everything inside of you and there will be DNA to analyze. The second feature is that the DNA in your hair follicle or in your blood or in your semen or in your saliva will be the same in all cells. So it's not going to vary depending on where you got your DNA from. That's a second feature. And a third feature is that the DNA of different individuals, with the exception of identical twins, is different. So it's the same within an organism, within a person, but it's different between unrelated individuals, or related individuals unless they're identical twins. So those are the three features of DNA for forensic tests.

Q. Okay.

A. And going on in the slide there's the molecule of the model itself but that's illustrated I think better in subsequent slides so I'll go beyond that now.

These are the chromosomes. In each of your cells the DNA is arranged in these 46 linear chromosomes they're called, and all a chromosome is is a long string of DNA. The chromosomes are numbered 1 through 22 with the largest being chromosome 1, the smallest being chromosome 22. This DNA pattern would be from a male cell, a cell from a male individual. There's a Y chromosome and an X chromosome. If this were from a female there would be two X chromosomes. You note

that in each - as you go along here, that there's two chromosome ones, two chromosome twos, two chromosomes threes. That's because you inherit half of your genetic material or half of your chromosomes from your mother and half of your chromosomes from your father. So this chromosome one would perhaps be inherited from your mother or your father and the opposite for the other chromosome one. So if this is inherited from your mother this is inherited from your father, and so on. And in the case of males you inherit your Y chromosome from your father because your mother doesn't have one, and your X chromosome from your mother. In the case of females you inherit two Xs, the X from your father and one of the two Xs from your mother. But basically this is the blueprint for a human being. All males will look like this; all females will look like this, excluding the Y chromosome - they have another X.

Q. Will other life forms, for example animals, will they have chromosomes?

A. Yes, all life forms have chromosomes. The length of the chromosomes, the number of chromosomes, that varies from humans to dogs, to cats, trees, etc., but they all have chromosomes. The shape and size and the number of chromosomes will vary from species to species.

Q. And these chromosomes are contained within each cell?

A. Yes, within the nucleus of each cell. Again, all human beings have this basic structure of their chromosomes and the bulk of the DNA in these chromosomes will be very, very similar between my chromosome one from my father and my chromosome one from my mother. Essentially the same information is contained

on those two chromosomes. Most of that code will be the same for my two chromosome ones as well as for all the chromosome ones present in this room. Most of this material codes for essential functions so the material, for example we spoke earlier the molecule that has the code for the hemoglobin molecule that transports oxygen, that's essential for life and your hemoglobin is virtually identical to my hemoglobin, so that the DNA that codes for that is on chromosome 16 and chromosome 11, there's actually two regions that code for your hemoglobin, those are going to be very, very similar between everyone in this room if you're a human being. There are, however, regions on the DNA molecule that we know are very different between individuals and those are the regions that we will be hearing about in the subsequent parts of this talk are the regions that we know are different between unrelated individuals. Some of these regions are highlighted here. The ones that are used in forensic labs are the ones that we characterize and we know with a high probability that my pattern at this particular region on chromosome one will be different from your pattern or someone else in this room. That it is very unlikely that two people would have the exact same pattern. So these are the types of regions that you focus in on for forensic investigation. You want to look at regions that you know have a high probability of being different among different individuals, and there is a number of them that have been characterized: one on chromosome one, chromosome two, chromosome four, chromosome ten, chromosome 16,

chromosome 17. These are the ones that are commonly used in forensic labs.

Q. What does the term 'highly polymorphic' mean?

A. Well, you can have regions on chromosomes that are just polymorphic. Perhaps there will be two forms of the DNA there. You can be an A form or a B form.

Q. For an example?

A. Well one form of variation would be your blood type. Your blood type is coded by DNA molecule and there's not many forms that you can be. You can be an "A" type. I'm an "A" type. I'm sure there's a lot of "A" types in this room. You can be a "B" type, you can be an "AB" type, or you can be an "O" type. There's not much variation. It's polymorphic. That is there are differences between different people but there's not many forms. Highly polymorphic is the same thing. There are differences between people but instead of it being "A", "B", "AB" and "A" - I mean a "B", an "AB" or an "O", you may be using the whole alphabet so somebody might be an "AF", a "GF", a "ZY" There may be hundreds and hundreds of different forms that people could be so it's much less likely that two people would be the same form because there's so many different possibilities.

Q. In these areas that you are looking at shown on that schematic, these are highly polymorphic areas?

A. Yes.

Q. As opposed to polymorphic areas?

A. Yes.

Q. What do the designations -- What you are depicting there, correct me if I'm wrong, Doctor, is the

particular location on the chromosome where the DNA - the section of DNA you would be looking at?

A. Yes. These are locations or the genetic term is a locus. It just means a location on a chromosome, that we have highlighted here, and each locus is given a number and these are catalog numbers or identification numbers. They are called "D" numbers and that "D" just stands for designation. The second number gives you the chromosome that it's on so it's D1. "S" means that it's only found in one spot on all the chromosomes so it's found in this spot on chromosome 1. It's single copy. That's what the "S" stands for. And 7 is the catalog number. It was the 7th piece of DNA on chromosome 1 that was given a map location. 7th piece of DNA that was discovered on that chromosome and mapped on that chromosome. So it's a catalog number.

Q. When you say mapped is this something that's kept just by one particular lab or is it kept world-wide?

A. At one point it went lab to lab. People would map a piece of DNA and keep it to themselves. Many years ago, I guess about a dozen years ago, people who were interested in mapping the human genome got together and every other year they meet throughout the world and have what they call "G-Mapping Workshops" where they get together and they organize all their information in an organized fashion like because they give them catalog numbers and they organize them on the chromosomes and they exchange information, and all that's stored in one central data base.

Q. Are these numbers recognized worldwide or are they just recognized in a particular area?

A. Worldwide. There's one numbering system otherwise you have total confusion. There's one numbering system for all these DNA - pieces of DNA.

Q. And are these areas that you have shown on this schematic are these recognized as highly polymorphic areas worldwide?

A. Yes. The ones I pointed out. There's one down here on the "Y" chromosome that's not highly polymorphic.

Q. We will be getting into the reason for that later?

A. Yes.

Q. Okay.

A. Now, rather than look at the entire chromosome 1, if you can just picture taking a microscope and looking at one tiny part of chromosome 1 if you will, this is what the DNA molecule looks like in schematic form. What it is, it's a very simple code. All the information contained in that molecule can be broken down into a very simple code of just four different letters. They're chemical letters. They describe the chemicals but it's a four base code, T, G, C, A. Those are the only four letters you will find in this entire code and that contains all the information that makes you a human being. A very simple code. The other feature is that the molecule is actually two molecules intertwined together in what they call a double helix. So it's these two ribbons and they're intertwined together and what you find is between these chemical bases - the letters are just called bases, that T always lines up with A and G always lines up with C. So there's not much to the structure

of this molecule. You have a four base code; it's aligned in two ribbons; and the ribbons align in a particular way that wherever you have a "T" on one ribbon, or one strand, it will always pair with an "A". If you have a "G" here it will always pair with a "C". So if you know the order of the bases on one strand you can deduce what's on the other strand because "T" always pairs with "A", "G" always pairs with "C". And that essentially is the structure of DNA found in all organisms and that miraculously codes for all the information that makes the living organism.

Q. When was this particular structure discovered?

A. The structure of the molecule was discovered in the early 1950's.

Q. And did the discoverer win anything for -- was he awarded anything for that discovery?

A. Yes. The discoverers of this molecule which is called the Watson and Crick double helix after the discoverers Watson and Crick, they won the Noble Prize for this discovery.

Q. Okay. You have mentioned base pairs - or you mentioned bases. Can you explain what a base pair would be?

A. Yes. Along here we have "T" pairing with "A". That would be one base pair. Now, this is a very, very small piece of DNA. I think there's - I'd have to count them up - probably 30 or 40 base pairs. That would be base pair one, base pair two, base pair three, base pair four, et cetera, down to the bottom.

30 or 40 there. And the human body there's three billion in each cell, base pairs, so you can see that this is a very, very, very small piece of DNA as compared to all the DNA that is in your cells - in each of your cells.

Q. We have all heard the term, Doctor, genes. Can you relate to that molecule what you would refer to as a gene?

A. A gene has many different definitions but probably the most widely accepted definition, a gene is a heritable unit of DNA, that is a unit of DNA. So if this had a coding function, or if it didn't have a coding function, you could look at this as it being a gene, a piece of DNA. Usually when people talk traditionally about genes they have some sort of function. It will be the gene that codes for hemoglobin, the gene that codes for eye color, the gene that codes for hair color, but you can't have pieces of DNA that have no obvious function yet be called genes.

Q. And for future purposes could you tell us what an allele is?

A. As we discussed before, you can have different variations of genes. Say for the hemoglobin molecule you could have a normal hemoglobin molecule or you could have a sickle hemoglobin molecule. Those are two different forms of hemoglobin molecule. One will produce a healthy individual, the other will produce an ill individual. But those are two forms of the hemoglobin molecule. An allele is just a form at a given locus. So in that case you could have the normal allele or the diseased allele.

THE COURT: And how do you spell it?

A. A-l-l-e-l-e.

MR. WALSH: The DNA molecule you talked about coding. Could you explain that, please, how similar or how different a DNA molecule will look from say between yourself or myself?

A. Well, for the most part the working part of the DNA molecule, the part of the molecule that these letters actually translate into a function, that is say hemoglobin or making eye cells or some function like that, those parts of the DNA molecule are very highly conserved. We all have hemoglobin, we all have eyes, we all - there's parts of our bodies that function very similarly and that's because the DNA molecules are very similar.

Q. So if you were talking about three billion base pairs in a cell a certain section of that three billion may produce the cells for eyes, a certain other section may produce the cells for hair, etc., etc.?

A. Yes, but it's not that simple. It's usually -- For a given tissue and all the things that go on in that tissue there's probably thousands of genes that interact together, I'll do this function, you do that function, and in the end all those genes will come together and they'll make a functional eye. It's not as simple as one piece of DNA making an eye and having it function properly.

Q. But a gene would be a particular section of the DNA molecule?

A. Yes.

Q. And are there areas of our DNA molecule that are not similar between us?

A. Yes. A small portion of our DNA molecule has a lot of variability to it. There are regions of the DNA that don't code for obvious functions. We don't know what they code for. They don't make a product like hemoglobin or proteins in your eye. They don't make proteins period. Nobody really knows what purpose they serve in the DNA molecule. What we do know about them is that they're different in different individuals. There doesn't seem to be any pressure to maintain a particular linear order of the bases. It's quite variable amongst different people.

Q. Is this the highly polymorphic areas that you talked about earlier?

A. Yes. A good proportion of the genome consists of these regions throughout all the different chromosomes that will be highly polymorphic. We have looked at only a few forensically but there are thousands of them.

Q. And these base pairs it depends on the order of the letters? Is that how it's determined whether it's a gene, what kind of gene it is, or if it's a highly polymorphic area, the order of the letters?

A. Yes. If the gene has a function the order of these letters will spell out that function much like the order of the letters in a book will spell out the message in a novel. When you are looking at these highly polymorphic regions it's much like my son sitting down at my computer, he hits the letters at random and he sits down two days in a row, he doesn't

punch the same numbers two days in a row, and you don't really get a message that means anything but it's different.

Q. From person to person?

A. And each day that he sits down at my computer sort of thing.

Q. These base pairs, is there anything you can do with the DNA molecule that you can use for DNA typing later? You were saying that "T" connects with "A", "G" connects with "C".

A. Well one of the features in virtually all methods for analyzing DNA is that you take advantage of the structure, the base pairing laws, "T" with "A", "G" with "C". What you can do, because this isn't a very stable molecule, simply by heating the molecule up or subjecting it to treatment with alkali or base raising the pH this molecule will come apart into its two ribbons. You can also bring the molecule back together following these laws. So I can break it apart by raising the temperature. If I lower the temperature back down again it will reform and this will pair here, this will pair here, this will pair here, "A" will pair here and so on down the length of the molecule. So you can take the molecule apart and you can put it back together. And using that principal you can also investigate these regions and that's shown here. You can use - and this is a word that you will hear, again, a lot - the word 'probe'. All a probe is is a piece of DNA that I know its sequence, and it will be complementary or opposite to a region of DNA that I want to study. If I want to study this

region, say it's on chromosome 1, all I need in the lab is a piece of DNA that will base pair with that region and now I have a homing device that I can add to the DNA and it will go to this region and find it. So now I have a way to sort through all those three billion base pairs and find the regions that I'm interested in looking at.

Q. Is there a universally-accepted theory regarding DNA?

A. Well in general there's a lot of different theories. Again, where we're concerned forensically there are principals of DNA that can be used in identification and that is that DNA is in all the cells of your body, it's the same in all the cells, and it's different in all individuals except identical twins. That's the premise that all the testing is based on.

Q. You have pointed out, Doctor, that you can identify sections. Apparently using these probes you can identify sections of a person's DNA, is that correct?

A. Correct.

Q. When did they start doing that? When was this procedure first developed and what was it used for?

A. Well the idea of taking molecules apart and putting them back together using that to deduce the sequence of the molecule is in excess of 30 years old. This exact technology of using probes to hone in on particular regions and study the sequence has been used medically for about 15 years.

Q. What's the purpose medically?

A. Medically, again, rather than looking at hypervariable regions, medically you want to look at a particular gene. If you are interested in, as I am, the gene for hemoglobin I will want to design probes that will go to the chromosomes, the regions that make hemoglobin, the regions on chromosome 16 and on chromosome 11. Those are the only regions I'm interested in so I develop probes that will find those regions and allow me to analyze the DNA in those regions.

Q. And for forensic work instead of looking at those areas you would look at these highly polymorphic areas?

A. Yes. You would use the exact same technology, now you would just move to a different spot on a different chromosome. Say the hypervariable region that I pointed out on chromosome 1, you would go to that spot and you would use the exact same technology, you would use a probe to that region of chromosome 1, and you would literally look at the sequence in that region.

Q. This technology that was used in medical diagnosis, what kind of diseases were identified or isolated using this technique?

A. The list is, as of last week, growing into literally the hundreds of common genetic diseases having sorted out using this type of technology. More famous examples, recent examples, would be cystic fibrosis, Huntingtons disease, muscular dystrophy. There's a lot of very common genetic diseases where the cause of those diseases is now known because they were able

to actually look at the DNA molecule to find out what is wrong with it. Say for instance in a child that has cystic fibroris you can find out what's wrong at the DNA level that causes a person to either carry cystic fibrosis or have children that have cystic fibrosis.

Q. Are these the same techniques that are used for forensic - for courtroom use?

A. Yes. Again, in the case of cystic fibrosis you are looking at a region on chromosome 7 that codes for a protein that is involved in healthy lung function and healthy cell function but you are basically just switching probes.

Q. Could you give an example of how, for example, -- You're talking about the RFLP technique is used in this fashion?

A. Yes.

Q. Could you give an example of how it's used in medical diagnosis to identify certain - differentiate between people for example?

A. Well, in the medical profession - it's not really a medical application but one commercial application is paternity tests. You can analyze people's DNA to sort out whether an alleged father is indeed the biological father of a child, and often times that does have medical implications. You would do it in the course of a medical test.

Q. Is there any other things that are used for it to differentiate between people?

A. They're all variations on the theme.

Q. I am thinking more in terms of the area of you see a lot of medical transplantation occurring today. Is there anything that's used there?

A. Yes. One way that they can use this type of technology is when they do bone marrow transplants which are quite common in diseases that involve the cells that make blood. If you have leukemia the cells that produce those blood cells they're cancerous. One way to actually cure a person of certain types of leukemia is to destroy those cells that make your blood cells and they do that by exposing the person to irradiation and chemotherapy and then replacing their bone marrow with a donor's bone marrow, a healthy donor's bone marrow. At the end of that you have to have some way of monitoring the process of whether you killed all the recipient's bone marrow and it's been replaced with the donor's or whether the recipient's bone marrow, his diseased bone marrow, has come back and the person is going to be sick again. So you have to monitor the process and one of the ways they do it is by simply after they do the transplantation they draw blood from the person each week and if the procedure worked well what you are going to find is the donor's bone marrow will take over and the person will be healthy. If you find the opposite happens then you know that you probably have to do the procedure again because this person's diseased bone marrow is coming back and they are going to continue to have leukemia. They are going to come out of remission, they're going to be sick, and they're going to die.

Q. Would you use probes to determine whose bone marrow is --

A. Yes. One of the medical and commercial uses of these exact same probes that are used forensically is used in that type of application.

Q. When did the technology begin to be used to differentiate between individuals for police or courtroom use? Was there any discovery associated with that aspect?

A. Well these types of polymorphic regions were actually discovered in the early eighties, several years before somebody came up with the idea to use them forensically, but in 1985 a lab in England first used them forensically, Doctor Alex Jeffreys. He's the founder, if you will, of the use of DNA in forensics.

Q. And what happened after his -- Did he publish his findings?

A. Oh certainly. Many publications.

Q. And what, if anything, happened after that publication of the discovery or the application of it to forensics?

A. Well, the labs in England started doing routine case work using DNA analysis and labs virtually around the world read his findings, read about their exciting work, and looked into implementing it in their own labs, and the R.C.M.P. was, you know, one of many labs that looked at his work and decided this would be a way to go and proceeded that way.

Q. Where do you fit into this historical development from Jeffreys in 1985?

A. When the R.C.M.P. decided tht they were going to develop a system for that I was one of the people that they hired from the academic community to come in and try to develop methods that they could apply this and integrate it into their own forensic testing scheme.

Q. And you did in fact stay there for that purpose?

A. Yes.

Q. We have covered it in some fashion but just before we get into the actual technique that you use I was wondering if you could just briefly explain to the jury what the RFLP technique is designed to do?

A. The RFLP technique is designed to look at differences in restriction sites. Remember it's restriction fragment length polymorphism. It's a mouthful but all it really means is that you are going to in-directly look at the code of the molecule by looking at what we call restriction sites. There are chemicals, proteins, that you can purchase that we use in science that will literally look at the code and where they see a particular sequence or a linear order of bases they'll cut the molecule at that position. So if an enzyme had as its recognition sequence "T", "G", "C", "A", everytime it saw that sequence in the molecule it would come along and cut the molecule.

Q. You are referring to a horizontal cut as opposed to a vertical cut?

A. Yes. This is splitting the molecule by denaturing it. This actually cuts the molecule like this. So you are literally sectioning the chromosome into thousands and thousands of pieces and it's cutting

at a specific spot. "T", "G", "C", "A" actually isn't a restriction site but I'm using it as a -- It's not a common restriction site that I'm aware of but I'm using it as an example here.

Q. When you cut it, when you're referring to a horizontal cut of the DNA molecule, you will cut it in several places along this three billion base pair chain, is that correct?

A. It's a four base code so you can expect that the order of T, G, C, A, will come up literally millions of times along the DNA molecule, and every time the enzyme sees that it will cut it and it's been alluded to or compared to as a molecular scissors. It cuts the molecule but it cuts it in an orderly and predictable fashion. It's not random breaking of a molecule. It's cutting it wherever it sees T, G, C, A. It will snip the molecule.

Q. And the fragments that you are left with, that's what you refer to as a restriction fragment?

A. Yes. If there's millions of sites you'll create millions of fragments and each of those is called a restriction fragment because the restriction enzyme generated that fragment. Now, in a test all we're looking at is where the sites are. You are looking at how big the fragments are. And because the order of sequences differs between different individuals, where these sites are will also differ between different individuals. So all you are looking at is variability and how big or how small the fragments are generated by these enzymes.

Q. So after you cut it you're looking at a particular section or particular fragments to see how different they are between people?

A. Yes. You will look at one particular region on the molecule, say the region identified by this probe, and you will ask the question how big is the fragment generated by a site up here and the next site which would be down here further along in the molecule. But that particular fragment length will be different in different individuals.

MR. WALSH: My Lord at this time I would suggest that probably a break would be appropriate before we continue.

THE COURT: Fine. So we will recess then for 15 minutes. I will not send out any of these sketches with the jury to the jury room because perhaps we're not sufficiently deeply into it yet to appreciate that exercise. All right.

(RECESS - 11:05 - 11:30 A.M.)

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

THE COURT: Mr. Walsh, please continue, please.

MR. WALSH: Yes, My Lord. Doctor Waye you testified earlier that the restriction fragment length polymorphism technique, the RFLP technique for DNA typing, is used at the R.C.M.P. lab, is that correct?

A. Yes.

Q. And you were at the R.C.M.P. lab when that particular technique was adapted for forensics for the use by the R.C.M.P.?

A. Yes.

Q. Would you take the jury through the various steps of that technique, please, and I understand you are going to use the slide projector for that purpose.

A. The technique is a multi step technique done over a number of days. It has a beginning and an end and it has a lot of steps in between and I'll try to go through them slowly so you can get an appreciation for how we can derive information by analyzing the DNA molecule.

Now, this schematic would be a typical forensic case where you have two samples and you are asking a question could these two samples, say they are two blood stains, could they have come from the same individual or did they come from a different individual? It's a very simple question you start out with and there's a lot of steps that you subsequently do in the lab to answer that question. But it's a simple question at the beginning, sample A and sample B. Say they are two tubes of blood that you are looking at. You take the blood, or whatever it is, and isolate cells, break open those cells, and release the chromosomal DNA into solution. That's a fairly simple procedure and involves literally mixing your cells with a detergent that breaks open the cells and releases the DNA.. Then you have this garbled mess of DNA. All the DNA is intertwined with each other. Chromosome 1 will be mixed with chromosome 16 and you have an unorganized clump of DNA after you break open these cells.

Q. Doctor, before you go any further, you say you break open the cells. You're extracting the DNA from the cells, is that right?

A. Yes.

Q. You had mentioned previously that you did the technique with respect to various substances, hair, blood, semen, a number of substances. Are the same techniques used for each substance?

A. Well, there's variations. Obviously, if you are dealing with a fluid like blood your starting material is a little different than if you are dealing with a dry stain on say a fabric, or if you are dealing with a stain on a piece of dry wall. A blood stain on a wall material or something like that. So sometimes you have to do little tricks at the beginning to get your starting material into a form that you can put into a test tube and add the chemicals to break open the cells, etc. So at the beginning there's a little bit of manipulation, whether you're scraping the wall to get the blood stain off it, whether you're swabbing the blood off the fender of a car, or just simply pouring blood from a tube. At the beginning there's some manipulations and it depends on what the officers give you or what the lab gives you to analyze. Once you get by the initial step it's essentially the same for most fluids and substances.

Q. Doctor you were describing substances located on certain kinds of material.

A. Yes.

Q. Have you had any experience in relation to unique kinds of material that you have had to extract DNA from?

A. Again, a lot of the examples I just talked about, scraping blood off a piece of dry wall, I worked on a case where they sent you a piece of a wall that they cut out from the Accused's apartment building and it had a blood stain on it and you had to scrape that off. In another case you were given a belt, a man's belt, and it had DNA on it and you have to soak the belt and remove the cells off the belt and then analyze the cells that come off the belt. So you get all sorts of different exhibits in a forensic lab. The first thing you do is you isolate the cells and, again, that depends on what they have sent you.

Q. Apart from the actual material on which the substance is located on are there various techniques used, for example just for the blood alone, or just for hair alone, or just for semen alone?

A. Yes, there's little twists or versions of the general extraction formula that you'll use. You'll extract differently a semen sample than you will a blood sample but the differences are subtle.

Q. Could you describe what the term 'differential extraction' is and how this would relate to what we are dealing with?

A. Differential extraction as it applies to forensic samples is a procedure that you use to extract DNA from sexual assault swabs. When a sexual assault occurs the swabs that they take either at autopsies or from a live victim will contain semen from the person who committed the crime and they will also contain skin cells, epithelia cells from the vagina of the victim. So you have two sources of DNA, from

the victim and from the accused, and they're different cellular sources. One is epithelia cells from the victim and one is semen or sperm cells from the accused, and in the lab you can differentially purify those two different types of cells using a very simple modification of general extraction procedures. What you do is you can lyse or break open the vaginal cells and keep the sperm cells intact, all in one test tube, and then separate out the sperm from the vaginal cells and analyze them separately. So at the end you have two DNA samples, one that's mostly from what we call the female fraction or the vaginal epithelia cells and one the male fraction, the sperm cells, so you end up with two samples that you look at there rather than a mixture of two cell sources.

Q. Continue. Now, these extraction techniques that you have been testifying to, are these something that was simply developed by the R.C.M.P. or something that's used elsewhere?

A. Well, DNA extraction procedures have been around as long as people have been analyzing DNA which is decades. The modifications that I just described for getting DNA out of peculiar substances like off a belt or off a wall or for the differential extraction, those are all things that have been tinkered with in forensic labs to suit that purpose. In research labs you don't usually see material like that. So those little adaptations came out of forensic labs but in general the procedures have been around for decades in the research and scientific community.

Q. Are these techniques used only by the R.C.M.P. forensic labs for extraction or are they used in other countries?

A. No, world-wide they would be used.

Q. Continue.

A. So at this point from both of the samples you have the DNA extracted from the cells. The way you analyze it, the first thing you have to do is you cut it with these molecular scissors or the restriction enzyme.

Q. Before we go to the cutting, I understand that - and correct me if I'm wrong, but I understand that after you extract DNA from the cell you also quantify it. Determine how much DNA and how much of it is human, is that correct?

A. Yes, that is done before cutting.

Q. Would you describe that and the reasons for that?

A. Okay. At this point you have DNA from both of the samples. One of the questions you want to ask as the investigator doing the test is how much DNA do I have. There are minimal amounts of DNA that you have to have to make the test work. So it's important at the beginning to know whether you have enough DNA to do the test. And the other question you want to ask is is it human DNA. Remember that there's DNA found in all living organisms so just the fact that you receive a blood sample it could be blood from another species, not necessarily a human's. You want to ask that separate question, how much of this DNA is human?

Q. How do you go about doing that?

A. Well, the first question, how much DNA do I have, you simply take a small portion of your DNA and you

analyze it in the lab on what we call the gel. It's just a way that you can visualize how much DNA you have. You take a small portion of it. We can stain for -- We have a stain that will stain DNA and if you shine a UV light on it it will glow and that's a visual way to say yes I have DNA and I have a certain amount of DNA. So that just tells you that you have DNA. It doesn't tell you anything about its source. It could be from another animal, it could be from a plant, but that tells you how much DNA you have.

Q. Now, what does the term 'high molecular weight' mean in reference to the amount of DNA that you are looking at?

A. Well that tells you the quality of the DNA. When you extract the DNA you can either have very large pieces of DNA or if the DNA has been degraded in some way, sheared, broken up by mechanical forces or environmental forces, you'll have very small pieces of DNA. For the test to work you need DNA that's high molecular weight or large pieces of DNA. So at the same time when you're doing a test to find out how much DNA you have the test will also tell you how big are the pieces in general. So in the beginning you know that I have enough DNA - if it's human I have enough DNA for the test to work and its quality is sufficient for the test to work as well.

Q. Are there any factors which would affect your ability as a DNA scientist to extract DNA from a cellular material? What kind of factors would affect your ability to get high molecular weight DNA?

A. Well, there's all sorts of ways you can degrade DNA and, again, those things are out of your control. You have no control over what happens to a sample at a crime scene. So there are things that will break down DNA to the point where I can't analyze it or I'm compromising my ability to analyze it.

Q. For example?

A. Direct exposure to sunlight over prolonged periods of time. If the DNA - if the stain is say washed in a strong acid or base. Things like that.

Q. What about soil?

A. Soil is - in all the environmental studies if you mix blood with soil, semen with soil, or other cellular sources with soil, soil is jam-packed with bacteria, bacteria feed on these as nutrients, so what you find is over a very short period of time in those types of environments you literally have no DNA to analyze. No human DNA.

Q. And you know all this before you even begin your test, the typing test itself?

A. Well, you know the types of environments that will hamper your ability to get out high molecular weight human DNA. There's no guarantees. If blood is deposited at a crime scene on soil and you get there in time, like it's not a week, if you get there perhaps the same day, you may be successful in doing the test. There's no real way to predict. A lot of these variables are out of your hands because you're not at the crime scene controling how the sample is deposited and how long it's there.

Q. You determine the effect the environment may have had on your sample, if I understand correctly, Doctor, by this test of determining how much DNA you have and whether it's human, is that correct?

A. Yes. Actually, all you're asking is the question is it worthwhile to do this test? Is there anything to analyze here? If there's no DNA at all, it really doesn't matter whether it's human or not, if there's no DNA I can't do the test. I can't analyze nothing. So that's something you want to answer right away.

Q. Could you give an example to the jury of a case that you would have worked on where you were trying to analyze a particular material and were unable to get high molecular weight DNA out of it for environmental reasons?

A. One case comes to mind is where the undershorts of a little boy who had been murdered - there was a blood stain on the shorts, he had been sodomized before he was murdered, there was fecal material on the shorts. I could isolate DNA from the shorts. The problem was that none of that DNA was of human origin. Probably all bacterial origin given where the shorts had come from.

Q. Where did they come from?

A. Well, next to the little boy's rectum.

Q. And what would be your explanation for not being able to take DNA out of that blood stain?

A. Well you get DNA out of it; you're just not getting human DNA out of it. What you are really isolating is the bacterial DNA that proliferated and grew on the shorts after the boy was murdered and prior to the shorts arriving at the lab. At one point there was

human DNA there, there was human blood there, but that in fact is a nutrient source for these bacteria.

Q. The bacteria actually feed on the blood?

A. Yes.

Q. Feed on the DNA breaking it down?

A. Yes.

Q. Why is it important to know in advance how much of your DNA is human before you begin your test?

A. Well, again, in that particular case I had a lot of DNA and it was in very good shape. It was high molecular weight DNA. There was sufficient DNA to analyze, but it wasn't human, so there's no point in going on to do a test to identify which human it came from if none of the DNA is human. So that's an important piece of information at the beginning of the test.

Q. In addition to finding out how long your DNA or how much high molecular weight DNA you had?

A. Yes.

Q. Who actually developed the technique for determining how much human DNA you had to have before you start your test?

A. The forensic application of that type of test -- There's been lots of different tests to identify human DNA. Forensic applications of those types of tests were developed at the R.C.M.P. lab.

Q. By whom?

A. Myself, Doctor Fourney.

Q. And has that been picked up by other forensic labs in North America?

A. Yes, some labs use that test, yes.

Q. All right, continue, please.

A. So at this point you would know that you have DNA from both of these samples and you would know that it's either all human or half human or you would know the proportion of the DNA that is from humans. If we take the example that these were tubes of blood it would be 100 percent human. The blood samples are sterile. Comes out of your vein and goes into a sterile tube. So all of this DNA you would know that I have X and Y amount of DNA and it's all human. So you have answered the question that yes the DNA is there, it's human, it's in good enough shape to analyze, and you proceed on with the test.

Q. This determining human DNA you said was developed for forensics at the R.C.M.P. Lab, did you publish your results in that regard?

A. Yes.

Q. In the scientific literature?

A. Yes.

Q. Continue, please.

A. The first step would be to use these molecular scissors, restriction enzymes, to cut the DNA in an orderly fashion to analyze the DNA. You go from having very long pieces all knotted up to shorter pieces after they have been cut with the restriction enzyme.

Q. These restriction enzymes were they developed simply for forensic use or have they been around for a while?

A. They have been in use since the early seventies.

Q. And the development of these restriction enzymes did the developer of these - did he win any award for that particular development?

A. The Noble Prize.

Q. Continue.

A. This slide shows how a restriction enzyme would work. For forensics at the R.C.M.P. and labs throughout North America one particular type of restriction enzyme is used and it's a restriction enzyme that everytime it sees G - G - C - C it cleaves the molecule after the second G or the first C. So this shows - and what I have done is I have taken the two strands of the DNA molecule, remember A is always opposite T as we see here, G always opposite C, and here I have highlighted two areas where you see G-G, C-C and G-G, C-C. Now this restriction enzyme will go along the molecule and where it finds this it will cut here and cut here, and what you see now is what we call the restriction fragment. The enzyme has cut the molecule and you have a piece of DNA that has a defined length. You can count up the number of bases in that DNA and that's like saying I'm five foot eleven. This is - I don't know how many - 25 bases long. It is defined length for this restriction fragment.

Q. On the bottom of that schematic it says "Fragments of DNA Released by Hae III Restriction Enzyme Digestion". What is Hae III?

A. Hae III is the particular restriction enzyme that has this as its recognition sequence. There are several hundred of these enzymes and they don't always --

Hae III is the one that recognizes G-G, C-C. There's others that recognize other codes, say G, A-A, G-T-C, every time it sees that code it will cut it. They all have their own codes.

Q. Was there any study done by you or your lab at the time you were with the R.C.M.P. as to why you would use Hae III? Why you would select that of all the restriction enzymes?

A. Yes. There's quite a number of enzymes looked at when we were developing this system. It was one of the first questions that as a working group in North America, the TWGDAM working group that you talked about earlier, that we had to wrestle with is which enzyme would we choose to analyze for forensic purposes and Hae III was one of the enzymes that was a candidate early on and turned out to be our choice in the end.

Q. Are there any other labs that use this particular enzyme?

A. In North America, excluding a couple of private labs, most law enforcement agencies have gone along with the decision to use Hae III.

Q. Did you publish your reasons for adopting or using Hae III in the scientific literature?

A. Yes.

Q. Are restriction enzymes used other than for forensic use in medical research, etc.?

A. Forensic use would be one of the smaller uses. They're used throughout medicine, throughout biology. They have been in use for more than 20 years now and, again, forensics is probably one of the smaller uses globally for these enzymes.

Now, if I could back up. At this point you have added the enzyme, it's cleaved everywhere it sees G-G, C-C. Now remember there's three billion base pairs and there's going to be a G-G, C-C combination about every four or five hundred base pairs, sometimes even closer than that, so there's literally going to be hundreds of thousands or millions of fragments generated by cleaving the molecule with this enzyme. So what you have done is it's a gross over-simplification here. There would literally be hundreds of thousands of fragments all of which have been cleaved at G-G, C-C. So it's not a random process. It's an orderly cutting.

Now, we have to go into dimensions. It's a little bit complex but I'll give it a try. A way of sorting out length differences between different people. As I said, where G-G, C-C will occur throughout your three billion base pairs will be different for everyone in this room because their DNA is different unless we have identical twins here, and you have to have a way to sort through all these hundreds of thousands of fragments and order them. Put them in some sort of arrangement rather than this ball of different size fragments. The way that's done is using a technique called 'agarose gel electrophoresis'. Simply stated what you do is you take all this sample and the test material is actually a jello-like material, agarose gel, but it has the consistency of jello once it's solidified, and you have a flat sheet of this. It's much like a pad of paper. It's about maybe a quarter of an inch thick

and it's dimensions would be maybe 10 centimeters by 20 centimeters. A flat sheet of this flimsy jello-like material. And at one end - this is in two dimensions here, at one end you will have slots or troughs carved in where you can put your sample. Here we have shown the two samples we're comparing, sample A and sample B. Here would be their starting point, their wells, that's the term used for these, these depressions, and you would also have what we call marker fragments, and they have their own well and these fragments differ from DNA from the samples in that what they are is a collection of fragments of known size. So we know the size of this fragment, the size of this fragment, this fragment, this fragment, etc. There's a number of those, and that's sort of like a ruler or the yard lines on a football field. They give you a reference point at the end of the test. After you load all these samples at the beginning you turn on an electrical current and you let the current pass through the gel for it's usually about 12 hours. What happens there is that the largest fragments they don't travel very far from the gel. They have a harder time moving through the gel. But the small fragments they migrate very fast through the gel and when you stop the test the fragments that are the smallest, say this fragment here, will be the furthest away from the starting point; mid-size fragments will be midway through the gel; and very large fragments will be at the top. Remember you have hundreds of thousands of fragments here so what you are going to have is more or less a smear of different

fragment lengths. So if you could dissect that smear it would be smaller fragments here, larger fragments here. And what you have done is you have taken all of these hundreds of thousands of fragments and you have literally ordered them from largest to smallest, from the top to the bottom. So now you have a library. You have literally arranged these as a library from largest to smallest.

Q. This gel electrophoresis is this something that was simply developed by a forensic lab for this use or just developed by the R.C.M.P. or is it something that's used throughout science?

A. Again, it's something that's been in place for analyzing both proteins and DNA for decades and it's, again, another technology that was just taken from the scientific community and adapted for forensic analysis.

Q. I realize, Doctor, that this is only for teaching purposes but perhaps so we can orientate ourselves to that, when you say that you load DNA into one end of a gel is the DNA from each sample put in separate lanes in the gel, across the gel?

A. Yes. If I wanted to analyze three samples I would have to have three separate partitions where I load the samples in. So there's no mixing of the two samples together in a lane. It's much like a track race. Every one starts off in their own pen and when the gun sounds you stay in your lane until the end of the race.

Q. What kinds of things would you in a normal forensic case, what would you be loading into a gel? That

there shows two lanes. I take it that you can use more than two. Three lanes in that there.

A. Depending on how you structure the gel. You can have 10, 20, 30 different lanes in a gel depending on how many samples you want to analyze. There is a practical limitation. You can't have thousands of lanes or you would need gels the width of this room. But generally they're on the order of - they can be perhaps a foot or so wide and the wells are small, you could have 30 or 40 maximum lanes. But generally it's around 20.

Q. All right, for a forensic case that you would be working on what would normally generally go into a gel? What would you load into the gel in separate lanes?

A. Well you would obviously have the samples that you're comparing and here we have two samples, sample A and sample B from the particular case. You would have to have some sort of fragments of known size, and in forensic cases you not only have them on one side of the samples you're analyzing but you have them flanking the samples that you analyze.

Q. Those are called molecular weight markers?

A. Yes, marker fragments.

Q. Now, when you say two samples do you need known samples and unknown -- Do you need known samples loaded in there along with your unknown?

A. Well this would be the minimum for doing it - for doing the test, that you would need the samples that you are comparing and you would need marker fragments on both sides. What's normally incorporated into the

test as well is you analyze DNA from cells of a defined nature and different labs will use different cells, but what it amounts to is that on every test you incorporate the analysis of DNA from a person or cell line from that particular lab. So you have a sample of human DNA that you analyze with every test and it's the same human DNA that you analyze with each test.

Q. And is that for a male and a female both?

A. Yes. In the R.C.M.P. system it is, yes.

Q. Just so if I can understand and you correct me if I'm wrong, Doctor, in a normal forensic case you would load into one well, for example, DNA extracted from a substance taken at a crime scene, correct?

A. Yes.

Q. A standard - a known standard from either a victim or a suspect, is that correct?

A. Yes, something to compare it to.

Q. Something to compare it to. You would put in these molecular weight markers which you say are something like the yard markers on a football field, reference points. You would load those in wells - separate wells?

A. Separate wells again, yes.

Q. Separate lanes. And you would also put in male and female known DNA as a control?

A. Yes. Those controls are important because you have analyzed them before and you know what the result is going to be. I know what my DNA patterns are because I've analyzed my DNA patterns. So if I incorporate my DNA in a test I know what the end result should be

and if I don't get that result something went wrong with the test. So these are important controls because you know what the end result will be.

Q. What kind of precautions would be taken to ensure that you didn't mix the lanes up? What I'm saying is say, for example, you extracted DNA from sample A and from sample B and you put DNA into a lane that you thought was sample B when in fact it was sample A. What kind of controls would you use to ensure that you have the correct DNA in each lane?

A. There's a lot of different things but that's just good scientific practice that you lay out an experiment and you conduct it as you laid it out. What it amounts to is good notetaking and following your notes. At the beginning of doing a test, if it were this particular test where you're comparing A to B, you will outline the strategy that I will be analyzing sample A in lane 3, sample B in lane 4, my markers will be in lanes 1 and 5 and my controls will be in lanes 7 and 8 for instance, and all that will be written down and you take your time loading them and at the end of the procedure after you have separated out all the molecules again, you can use a stain called ethidium bromide. All it is is a dye but it stains DNA, and if you take this gel after you have conducted the test you immerse it in this dye, it will bind to the DNA and when you shine ultraviolet light on it the DNA will glow. So you go back to your notes and you know which lanes you said had markers in them and when you look at the gel and the glowing pattern you should see markers in there. You know which

lanes you said had male and female DNA; you look at the gel, you can see male and female DNA. There's a number of visual controls where you can actually look and say yes this is the way I laid out the experiment yes this is the way it was loaded.

Q. Do you use any dye when you are loading the DNA?

A. There's a color dye. What we're loading at the beginning here is a fluid and we add a dye so we can see the fluid so it's not clear. It just makes the fluid blue. And at the end of the procedure the dye will be at the bottom of the gel. That just tells you that during the procedure the electricity didn't get turned off after you left the room and that in fact the current was going all night long because the dye did migrate to the bottom. Just another visual control that tells you things worked the way I planned them.

Q. Do you have an illustration of the electrophoretic process, I believe you used the term a cartoon of that?

A. Conceptually, this is a gross over-simplification of how electrophoresis actually works. What we have here is a DNA fragment, another DNA fragment, and yet another DNA fragment. They all differ and they differ in their base composition but they also - their main difference here is that this fragment is larger than this fragment which is in turn larger than this fragment. If this is the top of the gel what you find is that this fragment has a harder time proceeding through the gel than the midsize fragment, and the smallest fragment can zip through the gel

to the bottom. At the end of the procedure when you turn off the power or the current what you find is the smaller fragments will have proceeded through the gel faster and for a longer distance than the large fragments, and there will be gradient fragment sizes in between.

Q. So this schematic or cartoon, I think one time you used that phrase, not here but earlier, this cartoon, this is a description of one lane, what you would see in one part of one lane?

A. Yes.

Q. In a gel.

A. It's basically to get through the concept that if all the fragments start as a mixture at the top the smallest fragments will have the easiest time passing through the gel and will therefore proceed furthest in the gel.

Q. What is the negative and the positive, above and below? What does that refer to?

A. That just gives you the polarity of the system.

Q. Would you explain that, please?

A. You hook up electrodes at each end of the gel and this would be the negative electrode and the positive at this end and you will run a current in that direction. The DNA will migrate this direction. Which takes us back, again, to the process where you have taken all these fragments and you have separated them from largest to smallest in an orderly fashion. That's all this is meant to do. Again, what you have is all these fragments separated from largest to smallest but they're separated in a jello-like flat sheet of jello. Now, if you go like this with this flat sheet

of jello it will break. That is flimsy. It's not a very manageable substance so it certainly isn't something that you would want to work on for weeks or a month. So at this stage you have to have some way of taking these fragments that you have carefully separated from largest to smallest and making a permanent record of them, somehow getting them out of the gel and on to something a little more stable than a sheet of jello-like material, and this is done using a technique called Southern blotting. The man who invented this his last name was Southern. It was back in 1975 and, again, it wasn't invented for forensics. It's been adapted for forensics but it's a technique that's used throughout biology. All it really entails is this is your flat sheet of agarose gel. What you do is you take a nylon membrane so it's just like a piece of paper but it's made out of nylon and it's very durable. You can bend it, crinkle it and pull on it, it's not going to break. And you lay it on top of in contact with the surface of the gel, and the simplest way to do this is to just put paper towels or some sort of absorbent material on the other side of the membrane and what happens is fluid gets forced through the gel and on to the surface of the membrane and acts like a sponge. It draws the DNA out of the gel and on to the surface of the membrane. So now you have all these fragments that you separated and now you've got them transferred on to a durable sheet of nylon. Now we can work with that forever.

Q. Do you do anything in actually transferring the DNA from the agarose gel, the DNA that's been set out in its lanes now, distributed in its lanes, in transferring it to the nylon membrane do you do anything with the DNA other than transfer?

A. It's a step I always forget. The step going -- Right here what we have is double-stranded DNA. This DNA has been cut up but it's still in its double helix. There's two strands together. What you do either before you do this transfer or actually during the transfer is you should subject the gel to an alkali solution and that pulls the strands apart. They still remain where they were separated on the gel except now they're single strands. The strands are just pulled apart.

Q. Just so we can refresh our memory on that, Doctor, we have the DNA molecule exhibit P-158-4 over here. What are you doing? You have described, I think, that process before.

A. If this were one restriction fragment separated on that gel the DNA at the end of the electrophoresis, or the separation, would be in this type of form, the upper half of the molecule. It's a double ribbon. All we do then is we soak the gel in alkali, a basic solution, and it assumes this form. Fragments don't move through the gel. All they do now is the ribbon comes apart. So now you have exposed all these bases here and we can work with those.

Q. That's as you described this morning previously?

A. Yes. Takes 15 minutes to do. You soak the gel, the strands come apart, they're still where they were before, and then you transfer them to the nylon

membrane in this state, single strand.

Q. On your schematic it says "Denature to produce single stranded DNA fragments". Is that what you are referring to?

A. Yes.

Q. Is that something that -- Denaturization of the DNA molecule, is that something that was only developed by the forensic labs or is that used elsewhere?

A. It's used elsewhere and it's been in practice as a method for analyzing DNA since the early sixties.

So at this stage we still don't have anything we can see. We have a nylon membrane that has your two samples that you're interested in, has their DNA separated from largest to smallest fragments in a single-stranded form. You still can't see anything on the membrane. There's nothing that I can look at and say this sample came from this person or it didn't. It's nothing visual to that process.

The next step is to go into the DNA molecule that you have on this membrane and look at particular regions of particular fragments from different chromosomes. You will look at one of these hypervariable regions. I showed you the chromosomes earlier. We have all the DNA separated on to the membrane and now the task is I want to look at one spot, in this case the hypervariable region on chromosome one, and I want to ask how big are the fragments on this region in these samples. Are they large? Are they small? Are they in between? I want to ask that question: how large are the fragments

generated from this particular region? We don't care about the rest of the DNA in the cells, we just want to know this one spot on chromosome 1 for your first test. And that's done using a DNA probe. And if this section of DNA indeed corresponded to that region on chromosome 1 in the lab I would have access to pieces of DNA that have the complementary sequence to that spot on chromosome 1. Now I have something called a probe, or literally a homing device for that spot on chromosome 1. So I can sort through all those hundreds of thousands of fragments and I have a mechanism now that I can go on to that membrane and find sizes of fragments that correspond to that one region on chromosome one. And the way I can tell where the probe goes on that membrane is that in the lab we attach to the probe molecule radioactive molecules, so we make the probe radioactive, and chemicals that are radioactive you can follow with a Geiger counter, you can follow with x-ray film, but you have a way to follow them. Now you have a character that you can follow on the membrane. So this is the procedure here. It's called hybridization, again, a technical term, but this is the membrane and this would be just a tray. You usually use Tupperware trays in the lab and you literally take your probe that corresponds to chromosome 1, it's made radioactive, you have it in a solution and you dump the solution on top of the membrane. Now this radioactive piece of DNA will go on to the surface of the membrane and it will find fragments that correspond to that region on chromosome 1, and that's shown here

in dark lines. So if these were sample A and sample B what the probe has done now is found two sizes of fragments in sample A from chromosome 1, and the way this works is that this would be the length of fragment that you inherited from one of your parents and this would be the length of fragment on chromosome 1 that you inherited from the other parent. So if you inherited this size fragment from your mother this would be the size of fragment you inherited from your father, or vice versa.

In this sample there are two different size fragments that the probe bound to. Now, again, what we have here is something that you can't see. The radioactivity is there. I can detect it with a Geiger counter and it will beep where there's radioactivity but you still can't see it. You know it's there but you can't see it. So to get a visual impression of where the radioactivity has gone and how big the fragments are in these samples you simply take a piece of x-ray film, standard x-ray film, and lay it against your membrane and leave it there for a certain amount of time and then develop the film, and what happens is the radioactivity comes through, it reacts with the film and when you develop the film, as shown here there will be visible dark, we call them bands, but dark lines or bands where the radioactivity was and it corresponds to where the radioactivity is on the membrane. You're at the end of the test now. You have a visual impression of what the DNA looks like at that particular region on chromosome 1 for these two samples. Now, all you're comparing here

is how far the fragments have migrated from the origin or how large the fragments are. What we find from sample A is that I have two fragments, one of them is smaller than the largest fragment in sample B and one of them is larger than the smallest fragment in sample B. What you can note from here is that the fragments are not the same size. What that tells you is that sample A and sample B could not have come from the same individual. They're different. The patterns are different. And anyone with eyes can tell you that those patterns are different. They're similar in that there's two bands but most people in this room will have two bands. It's the position of the bands relative to the top and the bottom that are the identifying characteristics and in this particular case you make the conclusion that sample A and sample B could not have come from the same individual.

Q. Now, you go back to this hybridization where you apply a probe to the membrane for the purpose of honing in on the particular section that you want to look at, and you've given the example on chromosome 1, you've referred to the area that's marked D1S7.

A. Yes.

Q. You would have a probe that corresponds to D1S7 and put that in that solution and hybridize it to the membrane, is that correct?

A. Yes.

Q. Would you just look at the one section or would you want to look at other sections?

A. Well, in this particular example you really wouldn't have to look at any other sections. You have already

drawn your conclusions that these samples didn't come from the same individual so it would be pointless to go on analyzing other regions of DNA. You have already made your conclusion and it's an absolute conclusion. If, however, sample B and sample A have two bands and they're at the same position now your conclusion's different. The samples match - it's called a match, and the conclusion you draw from that is that these samples could have come from the same individual. There will be other individuals who can have that pattern but a large proportion of the population won't. It's called an inclusion. You can't exclude the fact that it came from this person so you include it. It could have come from that person. It's not absolute like the other situation. These samples did not come from the same individual. If they do match it means they could have come from the same individual.

Q. So what would you do in that case if they in fact had matched when you applied your first probe? What would you do?

A. I would start the procedure over again, and you don't have to start it right from the beginning. What you can do here is take the membrane and remove this radioactivity from the membrane. You still have the DNA from sample A and sample B separated on the membrane but what you have done is you have removed the probe and you can go back to this step with your probe from say chromosome 2 and start the procedure again.

Q. And that would be D2S44?

A. Yes. And if at the end of that test they still match well you would go on to get a third probing, say D4S139, and you continue those tests as long as you kept getting matches.

Q. What would you do - 10, 12, 20, 30, 40, 50? What is the normal place to stop in actually repeating your probings if you were getting matches each time?

A. Most labs in the world doing this type of testing will stop at 4 or 5. Some labs even 3, 3 probings, but 4 or 5 is the norm.

Q. Is there anything that restricts -- Say, for example, you do have a match on the first probe. What, if anything, could restrict the amount of probes that you could actually apply to the membrane?

A. Well if you started off with a small amount of material, say a very small splatter of blood at a crime scene, you're not going to get much DNA to analyze so the patterns themselves are going to be more difficult to detect, and each time you strip off the radioactivity the next test becomes somewhat more difficult to do. So if this first test is difficult to do by the time you hit the 5th test it may be impossible to do. Sometimes you have so little DNA that you may only get one test to work or two tests to work and then it becomes very difficult to get them to work.

Q. So each time you strip a probe off the membrane you may remove a little bit more of the DNA?

A. Yes, it's not a perfect procedure where you just remove the radioactivity. You remove a little bit

of the target with it as well. It's a -- You're literally boiling the membrane. It's a fairly aggressive procedure to get the radioactivity off the membrane and with it comes a little bit of your target DNA.

Q. Are some of the probes that you use more sensitive than others? What I am saying is say for example would one probe be able to detect a smaller amount of DNA than another probe?

A. Yeah. There are subtle differences between the probes. Some of the probes can detect smaller amounts of DNA than others. The level of detection or the variability in detection levels isn't all that extreme. For example, D4S139, that's a very sensitive probe and often times samples that don't have enough material to be analyzed in say D2S44 this one is very sensitive. You can get it to work. But the differences aren't that great. Three fold sensitivity differences.

Q. But each time you apply one of these probes you're looking at a different highly polymorphic area of the DNA chain, is that correct?

A. Yes, different tests. You're going to a different spot on a different chromosome.

Q. Which, shown on that particular - I don't know what the exhibit number - this one here, P --

A. 158(3).

Q. On that you have a number of highly polymorphic areas shown which correspond to the probes, I take it, that would be used, is that correct?

A. Yes. I have shown 1 - 2 - 3 - 4 - 5 - 6 highly polymorphic probes.

Q. Would you just name them and what chromosome they're on.

A. D1S7 on chromosome 1; D2S44 - chromosome 2; D4S139 - chromosome 4; D10S28 - chromosome 10; D16S85 - chromosome 16; and D17S79 - chromosome 17.

Q. Okay. Are those probes that are actually -- Are you just using those for demonstration or are those probes for areas of the DNA that are actually used by the R.C.M.P.?

A. Yes. These actually correspond to loci or regions on the chromosomes that are analyzed as part of the forensic test.

Q. And you testified earlier, correct me if I'm wrong, that these areas are known worldwide as being highly polymorphic? They are mapped so to speak.

A. They are mapped and it's one of the features that went into their original discovery in publication, the fact that they are highly polymorphic. Again, these regions weren't isolated and characterized for the forensic community. They were isolated as part of other research projects.

Q. Was there any study or any effort that went into the selection of the probes that the R.C.M.P. used, why those particular areas?

A. Well, like choosing a restriction enzyme, one of our first tasks was to sort out which regions on which chromosomes we would incorporate into the tests and there were a lot of different variables that we looked at to select a handful of probes for use in forensics.

Q. And were your results published with respect to the selection of most of your probes?

A. Yes.

Q. Apart from the highly polymorphic probes which you pointed out I note that there are two probes there that you haven't pointed to yet. One is on chromosome 7, D7Z2. What is that?

A. That's what we call a monomorphic probe. So rather than being polymorphic, that is different between different individuals, this is a fairly boring region of DNA that's the same in all individuals, males and females alike as we all have chromosome sevens. So this is a region of DNA that if I analyze it for everyone in this room I can predict to you what the result will be right now because everyone has the same pattern at that region. We analyze this region for a number of reasons, the first being that we know the result that we should get at that region. So if the test works properly we know exactly what the result should be. If you get that result you have confidence that the test worked properly for these other regions where you don't know what the result is going to be. So you have to build in controls where you know what the result will be.

Q. So, for example, Doctor, say you went through the five probes, the five highly polymorphic probes on chromosome 1, 2, 4, 10, 16 and 17, when would you apply this monomorphic probe on chromosome 7, D7Z2?

A. Generally at the end of all that procedure. It really doesn't provide any other information other than what we're dealing with is human and you already knew that right at the beginning of the test. The

information it does provide is that, yes, the test worked and the test worked fine.

Q. How would this show on the schematic? Say, for example, you had applied the monomorphic probe to this particular schematic that's on the screen now and you have sample A and sample B. Where would you expect to find the bands between sample A and sample B?

A. Both of them would give a single band pattern so there would only be one band and it would be at the same position, and I would be able to tell you what size that band should be because we know its size.

Q. And I see there's another probe shown on the diagram there, DYZ1.

A. Yes.

Q. That's on the "Y" chromosome. What is that?

A. This, again, is another monomorphic probe. It's the same in all individuals but it's found on the "Y" chromosome so only males will have it. So when I use this probe and I analyze female DNA I see nothing because females don't have a "Y" chromosome. When I analyze male DNA I see a predicted pattern. I'll get one fragment and I know its size. So that gives me information that none of these other probes can tell me. All these other probes I know I'll get two bands but I can't tell whether they're male or female with any of these polymorphic probes as with the monomorphic probe on chromosome 7. It doesn't give me any idea about gender. When I analyze this probe I can answer the question did the sample come from a male or did it come from a female.

Q. You mentioned before that in this test you also put a known male and a known female control DNA in the test, is that correct?

A. Yes.

Q. So if you applied the sex typing probe, the DYZ1, you would get a predetermined result from the male and female control DNA?

A. Yes. Again, these controls, a male and female known control run with every test, is important because, for example, if all your unknown samples were from females and you didn't have male and female controls you would get no results. You wouldn't get a pattern and that could be interpreted two ways: you either forgot to add a probe or they're all from females. Now if you incorporate a male and a female control the male will be positive, the female will be negative, so you know that the experiment worked. If there was male DNA on that experiment I'll be able to detect it because you detected it in your control. So those controls are critical to interpreting sex typing results.

Q. Same as the monomorphic probe is only for the purpose of determining if your test is run correctly?

A. Yes.

Q. But your bands would be in a predetermined position.

A. It gives you confidence that yes this type of system does work because I know the size of this fragment and if at the end of the test I didn't get that size of fragment or I didn't get that fragment itself something is wrong.

Q. Have you ever developed a probe yourself, Doctor?

A. Yes, many.

Q. Any probes that are now being used in forensics or for forensic purposes?

A. The monomorphic probe came out of my research when I was a student.

Q. And is that being used by other forensic labs as well?

A. Yes.

Q. And did you develop any other probes that are being used in forensics?

A. I have many other monomorphic and polymorphic probes. None that have been adopted worldwide forensically. I have some wildlife probes. Probes that will identify species of wildlife, moose, deer, etc.

Q. That you have developed yourself?

A. Yes.

Q. And this D7Z2, the monomorphic probe, this has been picked up by other forensic labs?

A. Yes.

Q. And you have already explained the catalog, the numbers and the letters there, what they stand for, or did you? I just want to make sure you did.

A. The "D" is just the designation. The next number tells you which chromosome it's on. "S" stands for single copy; "Z" means that it's in more than one copy. It's in one spot on the genome but it's repeated over and over and over again so it's very easy to detect. And, again, the 1 is the order that it was discovered on that chromosome.

Q. When you are selecting these probes to be used in forensics did you have to give any consideration as to the kind of enzyme you were using? You have indicated that you selected Hae III as the restriction enzyme. Did that have any bearing on the kind of probes that you had to select?

A. Yes. The choice of the enzyme and the choice of the probes it was a joint decision. If you pick probes just based on how much variability they detect, if they didn't work with Hae III then they couldn't be part of the choice, or if they didn't work with a single restriction enzyme. So you have to pick the enzyme to be compatible with the loci you are analyzing. So the two decisions had to be made at the same time. So you analyzed a number of enzymes and many, many more loci than there and then you came up with a number - a limited number of loci that Hae III works with and that you can detect considerable variation amongst the general population.

Q. You have used the term - what's interjected into your testimony is the term 'loci'. What are you referring to when you use that term?

A. It just means a region on the chromosome so D1S7 would be a locus, loci is just plural, so these are two loci, D1S7 is a locus. Just means a region on a chromosome.

Q. So when you use that term locus or loci it would be the same as saying site or sites, is that correct?

A. Yes.

Q. All right, Doctor, each time you applied a probe would you get a separate x-ray so to speak?

A. Yeah, these x-rays are called, again another long word, autoradiographs, or autoradiograms. That's shortened to autorads. It's much easier. Or x-ray. But basically it's an x-ray film with these dark images on them and each time you do the test you will get a different x-ray film or a different autorad at the end. It's the result of the test.

Q. Now, on this particular schematic and, again, I realize you are only using it for teaching purposes, but the bands where you see sample A and sample B, they look very dark and very precise in terms of their length and width. Would you expect that when you are actually looking at a case autorad, when you are actually looking at a real life autorad and looking at DNA samples?

A. Well the darkness and the shape of the bands is dependent on a lot of different factors. In general what you find is the larger the band is the darker it will be and it will be more thicker than say a band that's smaller. But its shape and its darkness really doesn't matter at all. It's where the band lies with respect to the top and the bottom of the gel. How big the fragment is. It really doesn't matter how easily it was detected. What really matters is where it's positioned.

Q. It doesn't matter how light the band is or how dark it is it's its location on that membrane?

A. Yes, correct. You can have patterns that visually you will look at and say those don't look the same to me because the two bands here are very dark compared to two matching bands that are very faint. That's

still a match because they're in the same position, although visually you'll look at them and say those patterns don't look identical. One is darker than the other. But if they're in the same position that's the critical variable.

Q. So, for example, Doctor, if you had a substance at a crime scene that had very little DNA in it and you compared that to a known standard, say a blood sample from a victim that had a lot of DNA, you would expect the blood sample from the victim where there's a lot of DNA to have a dark band whereas the sample taken from the crime scene that had little DNA would have a light band, is that correct?

A. Yeah. The more DNA that you analyze the more target you have for the probe to bind, the more radioactivity comes off the membrane and the darker the image on the membrane. So if I analyze 10 units of DNA in lane "A" and one unit of DNA in lane "B" the darkness of the bands will be roughly 10 to 1 because I had 10 times more DNA to analyze in one lane than the other. The patterns will look different even if they're from the same individual because I have analyzed more DNA in one lane than the other but the bands will still be in the same spot so it's still a match.

Q. When you have an autorad like you have generated here in this schematic say, for example, using D1S7, you would generate an autorad and then you would go back and strip the probe from that membrane and do the process again in terms of getting an x-ray and you would come out with another autorad, is that correct?

A. Yes, and then I proceed on to the next test doing the stripping procedure in between, removing the last probe and then proceeding with the next probe.

Q. Can these autorads, apart from the person who is actually running the test, say for example you ran this test here that you show on this schematic, could another DNA scientist come in and look at your work to determine whether or not it was correctly run and could they look at the autorad and make the same decisions or different decisions than you made?

A. Another scientist could look at it. Anyone with eyes could look at it. It's very visual. It lasts forever again. It's a permanent record of the patterns.

Q. Are laboratory records kept of each step in the process?

A. Yes.

Q. What kinds of records would you keep?

A. Well, again, records certainly when a sample is logged in, who you got the sample from, what you did to the sample after you received it, how much DNA there was, how much of that was human. Pictures are taken of gels to determine that the enzyme in fact did cut the DNA; that the DNA did run properly on the gel when you analyzed it. And then you have, of course, pictures of the autorads at the end. You can make copies of the autorads. You can photocopy them and send them to other people.

MR. WALSH: Perhaps, My Lord, at this time, it's 25 to 1, it would be an appropriate time for a break.

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THE COURT: Yes, I think so. So if the jury would retire, please. Put this all out of your mind until you come back at 2 o'clock.

(Jury excused.)

Just before we adjourn, I have no objection, and I'm sure counsel would have no objection to the media taking pictures of these copies of slides, or these schematic drawings. It's just a question of when. It could be arranged by the media with the clerk and either during the noon recess, if everybody is represented, or during the recess midway through the afternoon, let the clerk know now when you would prefer to do it and when everybody is out of the courtroom. There's just one restriction I would apply. I don't know what the technique the media would want to follow here would be but any pictures taken are to be only of the drawings on the easels and so on and not of any other portion of the courtroom or any of the desks or anything like that.

Do counsel see any objection to this?

MR. ALLMAN: I have no problem.

THE COURT: Well, you check with the media, Mr. Pugh, if you would and see when they want to do that. It would be when everyone else is out of the courtroom of course. So we'll adjourn now.

(NOON RECESS - 12:40 - 2:00 P.M.)

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

THE COURT: I was just thinking, as far as the jury are concerned Mr. Brideau may be having a little difficulty seeing past the people when the slides are being on, and if you do have trouble -- Are you having trouble there Mr. Brideau where you -- You're not. I was going to say the back row could slide down this way one and you could go back to Ms. Crawford's place if you like. Well, if you have trouble shout out and we'll change it then.

Now, you were going on, Mr. Walsh, with your examination.

MR. WALSH: Yes, My Lord.

DIRECT EXAMINATION CONTINUED BY MR. WALSH:

Q. Doctor Waye before we go any further would you tell us, please, what a protocol is?

A. Protocol is actually like a cookbook. It's a recipe book that tells you how to do a procedure. It's a written set of instructions for conducting a scientific test.

Q. Okay, you have a low voice, I'm just going to ask you to speak up a little louder, please. Are there protocols - were there protocols in existence at the R.C.M.P. and did you have anything to do in terms of drafting any of the protocols?

A. Yes. When I was there and before we began case work the protocols or the techniques that we were using were written down and one of the first drafts I was the co-author of the protocol for doing this type of test.

Q. Have the protocols changed from the first one?

A. Yes. Scientific tests change over time. You find improvements to the tests and you change and update the program as needed as time goes on. So it's been updated several times.

Q. Does your audience dictate how extensive your protocol is?

A. The end use of the protocol dictates how many instructions you put in it. The initial protocols were condensed versions of the final protocols and that's mainly because at the beginning the only people working there were people who had done these types of tests for years so the protocols really didn't have to fill in all of the steps. Later on when the protocols are used more as training manuals or in a capacity of people who are learning the test they follow this protocol manual a little more than somebody who is very familiar with the test. You have to add in the steps and fill in some of the gaps to make the protocol a little more self-explanatory.

Q. I take it that you are referring to people who would come to the lab after it's set up. The protocols would need to be more extensive so that you could teach as well.

A. Yes. Many people who had worked in other disciplines in a forensic lab were being trained to do DNA work and still are being trained to do DNA work, so these protocols have to meet their needs as well.

Q. This morning you were referring to a forensic case and were referring to the different things that normally you would expect to find in a forensic case

gel when you're running a particular test. There is a schematic to your right there. I can't see the number from here. It's at the bottom.

A. It's number 10.

Q. Could you describe what that schematic demonstrates?

A. This is a typical schematic of an x-ray film from a forensic case. It has all the ingredients of a contrived forensic case. On the outside there are these size markers and, again, these are fragments that we know their size. For instance this might be one thousand base pairs, the number of bases in the fragment, 2000, 3000, 4000, etc., etc., getting larger as you go up. I don't know the exact size here in this contrived example but we would know the sizes of all these marker fragments. Then you would have the case specific material. Lane "A" you would have the sample that you analyzed from the victim. Lane "B" a blood stain, a piece of evidence from the crime scene. Lane "C" a standard that you obtained from a suspect. We will call him suspect number 1. And lane "D" another sample from a second suspect, suspect number 2. This is the final result of looking at one locus, say D1S7. This is the patterns that you get for chromosome 1. This would be the end result of the first test. And the types of things that you can see looking at this schematic is that the two-banded pattern that was obtained for the evidence in lane "B" is clearly distinct from the two-banded pattern from the victim, so you can conclude that the blood stain at this crime scene didn't come from the victim.

You can also conclude that this two-banded pattern from the blood stain or the evidence at the crime scene is different from this two-banded pattern in suspect number two. Suspect number two is not the person that this blood came from. This blood could not have come from suspect number two. What you find when you compare the blood from the crime scene to the blood - the known blood sample from suspect number one is that the bands in fact have migrated the same distance from the top and are a visual match. This means that the sample from the crime scene could have come from suspect number one.

Q. And because you have that conclusion that they could have come - the evidence could have come from suspect number one you would then go to another probe, for example you would look at chromosome two and do it again?

A. Correct. This whole pattern would be removed from the membrane and we would go on with the hybridization or adding the probe to chromosome number two and develop yet another pattern, and if indeed this sample "B" did come from suspect number one with the second probing you would have a different pattern, perhaps the band would be here or say here, in the same pattern would be here and here. If, however, this was just a fortuitous match, because remember it doesn't mean that it did come from it, it could have come from it, there could be other people as well, if this was just a chance match it's very likely that on the second probe you would have a situation where you would have a mismatch like comparing "C" to "D" here, they don't match, and that negates the first result.

He was included with the first probe. You say it could have come from him. As soon as you do the second test and it didn't match all of a sudden all bets are off. It did not come from him. So then you stop testing again. But as long as you keep getting matches you continue doing tests.

Q. And you said that normally they try to do four or five probes?

A. Yes.

Q. That particular schematic is, again, just for identification purposes, the male and female control is not shown on that, is that correct?

A. No, there's no controls. This is all case specific evidence, the victim, the suspects and the evidence from the crime scene. Normally you would also include in there a known male and a known female, samples that you run all the time in the lab and you know what their pattern will be. For instance on this probe you may have a band there and a band there but you know because you have analyzed those samples hundreds of times you know exactly what the pattern should be if the test worked for both that male and the female sample.

Q. So in an actual case work if you had a male and female control you would have two other lanes in that particular schematic?

A. Correct. And they'd have a pattern that identifies them as the controls. Patterns that you would recognize.

Q. And in this particular schematic again being used just for teaching purposes you have molecular weight markers on each end where it says "M" on both ends of the schematic. Would you have occasion in running an actual case to put the markers in the center or somewhere else in addition to the ends?

A. Yes. Generally when you have a lot of lanes, like here we have four case specific lanes and that's not a large number of lanes so it wouldn't be unusual to have four lanes from the case flanked with one set of markers, but if I had a case where there was say ten questioned samples what I would want to do is I would like to have some more marker lanes in here. You don't want the markers to be too far apart so you would perhaps have another marker lane in the middle as another reference point.

Q. The marker lanes actually help you line up how far down the bands have gone on the gel?

A. Yes. Well eventually you want to ask the question how big is this fragment and how big is this fragment? How many base pairs are they? And the way you do that is you compare that to the reference lanes that you know their size. For instance if I know this is four thousand base pairs and this is five thousand base pairs well just sitting here my eyes will tell me that this is somewhere in between so it's maybe four thousand five hundred base pairs. There's computers that can do a better job of determining that number but you can just look that it's in between the four and the five so it's somewhere between four thousand and five thousand. That's how this ruler or marker is used, as a scale.

Q. Just to refresh our memory, Doctor, when you talk about base pairs, when you say four thousand base pairs you are referring to the number of these combinations, is that correct?

A. Yes.

Q. So T and A would be one base pair, G and C would be another one.

A. Yes.

Q. And when you are talking four thousand base pairs you would have four thousand of these combinations down the section you're looking at?

A. Yes.

Q. One other thing that perhaps we can clarify. You spoke this morning, you testified that the higher molecular weight or the longer the fragment lengths are at the top of the gel and as you go down the gel the smaller the fragments become.

A. Yes.

Q. This schematic here shows the length as being the same length. How is it depicted on an actual autorad and what would you actually normally expect to see there?

A. Well on an actual autorad you would see this sort of - the band has a dimension this way. That isn't the length of the DNA fragment. That really is defined by the dimensions of the slot where you load the sample in. It has nothing to do with this fragment being larger than this fragment. This dimension going this way is determined by the length of the slot where you load the sample in at the beginning.

It has nothing to do with the fragment size. Fragment size is determined, again, by how far it migrates from the origin slot. So this is very close to the origin so it's a larger fragment. This is far away, it's a smaller fragment.

Q. I am going to get into the question of how you actually interpret. You have went over some parts of it but I am going to ask you how you interpret an autorad once you have one completed, but before we do that perhaps if you could just summarize, briefly, what we have gone through to this point.

A. The entire procedure?

Q. Yes, just briefly if you would. We could use the schematics that are there. Just so we can have a reference point when we go on later.

A. Again, you are always asking simple questions: could sample "A" and sample "B" have come from the same individual. So you begin by isolating the DNA, breaking open the cells, purifying the DNA, cutting it with the enzyme, using electrophoresis to arrange the fragments from largest to smallest in a linear fashion, transferring that information on to the stable nylon membrane after you denature them and make them single-stranded, and then for each of the loci that you are interested in in a successive manner, one after the other, you use a radioactive probe or homing device that will bind to the fragments that correspond to that region on the chromosome, and in general people will have either one or two bands in each lane. If you have one band in each lane it means that both your mother and your father had the

same size fragment. If you have different bands it means that your mother and your father differed in the size of their fragments. But the formal expectation for each person is that you will have one or two bands. In this particular case -- And then you overlay it with an x-ray film and you create this visual image at the end so your x-ray film will have dark marks on it. In this particular case the patterns are different, both these people have two band patterns but they're in different positions. This is higher up than this band, this is higher up than this band. These samples could not have come from the same individual. And anyone with eyes could look at these types of results and draw their own conclusions from it.

Then we're back to the schematic again, this being typical inclusion, these samples could have been from the same individual because the bands are in the same relative position from top to bottom, and similarly these two samples could not have come from the same individual nor did these two samples come from the same individual.

Q. And because you have an inclusion between lane "B" and lane "C" you would then go to another probing at another chromosome location?

A. Yes.

Q. You would put another probe on. Strip that one off and put another probe, is that correct?

A. Yes. You could make inclusions at this point. At this point you could go to your data base, the hundreds of people that you have analyzed, and say how often

have I seen this type of pattern. And the numbers that you might arrive at is that not everyone has that type of pattern but maybe one in a hundred people have that type of pattern. Now if that's the type of significance that you would like you could stop at that point or you could go on to another probe and ask the same question, how many people would have this matching pattern.

Q. If the second probe matches and then the third probe, and the fourth, and the fifth, however many you wished to do or how many the technology allows you to do.

A. Yes. And with each probing the discriminating factor becomes that much greater. Instead of it being one in a hundred might have this pattern how many people would have both of these patterns. Well, if it was one in a hundred people have this pattern and one in fifty have the next pattern the chances of somebody having both matching patterns would be one in a hundred times one in fifty which is one in fifty thousand. And you can see why you would want to do more and more tests because it finetunes the discriminating power of the test.

Q. The theory being that the more probings that match the higher the probability that it came from that particular person?

A. Correct.

Q. Before we leave that I understand, Doctor, that you have a model here that you can just refresh their memory with respect to the DNA molecule, is that correct?

A. Yes, something three dimensional.

MR. WALSH: My Lord I have shown this to Mr. Furlotte. This model is a teaching aid that's used. They don't want to have it entered as an exhibit. We have a photograph of the model and Mr. Furlotte agrees to enter the photograph as an exhibit and we could use this just to - before we leave this particular area if that would be all right.

THE COURT: Yes.

MR. WALSH: I would move to have the photograph entered as an exhibit.

THE COURT: P-159.

(Clerk marks photograph of model exhibit P-159.)

WITNESS: This is the double helix model that I have been talking about all morning and what you can see - you don't have to even be able to read the letters, is that there's a number of different colors, four to be exact, T's being green, C's being yellow, G's being blue, A's being red, four bases, and A is always lined up opposite T, G always lined up opposite the C, and the two strands are wound around each other in this spiraling double helix. To give you some idea of dimension, this is 12 base pairs, there's about three billion in each cell, so if this were to actual scale the amount of DNA or the length of DNA, the chromosomes stacked head to head, the length of DNA in a single cell if this were to scale would be about a hundred thousand miles or around the world four times. So this is a gross exaggeration of the actual size of the DNA molecule. And all this is in every cell of your body that has a nucleus.

Q. You talked this morning about digestion, cutting it up with the enzyme. You called them molecular scissors. Could you demonstrate using that model what actually is taking place when you digest it, cut it up in fragment lengths?

A. Yes. Here it goes - you can see the base sequence. It goes A, G, G, C, C, A. In the middle of there we have a core unit, G, G, C, C. That's the recognition say or the code that our restriction enzyme or molecular scissors recognizes. When it sees that it will pull these apart and we cut - cut these ribbons. You basically pull the top off the model. So now we have two pieces of DNA and that's essentially how it works. And the other step in the procedure, unwinding the strands, we would be pulling them all apart this way, so you're pulling these two ribbons apart and you end up with two ribbons.

Q. You're denaturing it in that fashion?

A. If you're denaturing. So they're opposite actions: one cutting this way, the other pulling apart that way.

Q. Do you have anything else you wish to add on that?

A. No, I think that's fine.

Q. Doctor, I would like to get into the area of how you actually interpret an autorad. When you generate an autorad that has a banding pattern what is the accepted method for interpreting the autorad or determining whether bands match or don't match?

A. Well, the first thing you do, and this is done universally whether it's for forensics or for medical diagnostics or for research, is that you look at the

patterns with your eyes and make a decision, do these match as does lanes B and C, are they completely different like C and D, or is there too little information. Like if this were very faint and I could hardly see these bands are we in a situation where we really don't want to go out on a limb and call it either way and just call the result inconclusive. So you're going to have three conclusions: it matches, which would be an inclusion; it doesn't match, that's an exclusion; and it's inconclusive, I don't have enough information to make a call either way.

Q. Okay. I can understand from that schematic you have an inclusion and an exclusion. What would be an inconclusive? When would you arrive at an inconclusive decision?

A. Well if I had very little DNA say in lane C such that the bands are very, very faint or perhaps on borderline of detection with the human eye which is the most sensitive instrument for looking at these things, if I can't reproducibly convince myself and others that there's actually bands there you would be in a position where, you know, as a good scientist you would call that inconclusive.

Q. And is there any other reasons why you would call something inconclusive?

A. Well, if the sample's degraded. The way samples degrade are the largest fragments become smallest first and then the smaller fragments progressively degrade so sometimes you get in a situation where if you have a very large band here it may be degraded yet this fragment down here is not degraded. So what you end up with is a pattern like this and a very

faint band up here or an absent band up here. In those situations, depending on the situation and what you're comparing it to, you may be in a position where you call that inconclusive.

Q. When you call something inconclusive are you excluding that particular person or including that person or just making no decision on that particular probing?

A. You're making no decision and you're excluding these test results. You're taking these test results out of the analysis. You're not saying this came from him or it didn't come from him. You're just saying I can't tell. The test did not work.

Q. Could you have a situation that, for example, we look at lane "C" being the suspect in that lane, could you have the situation that where, for example, you used the probe D1S7 and you come up with that pattern but the bands in lane "C" are too faint to see. You can't see them. So you would call that inconclusive according to what you have told me, is that correct?

A. Yes. I have nothing to compare it to.

Q. Okay. Now, in the hypothetical, Doctor, if I went and say took another probe, say D4S139 on chromosome 4, stripped that off and applied that probe, could it be possible that a more sensitive probe would pick up a banding pattern?

A. Certainly. You may run into the situation where I can - with probe 1 I can see this but I don't get any result for this lane so I call it inconclusive. If I go to a more sensitive probe, one that has say two fold sensitivity, I may now be able to detect a pattern that either matches or doesn't match and then I'd call it inconclusive or I'd call it an inclusion

or an exclusion depending on what the pattern was.

Q. Is a visual match an accepted way of looking at an autorad, with your eyes only?

A. I would say probably 99.9% of all the autorads looked on in the world are only looked at with eyes, with no other mechanism.

Q. And for forensic purposes is there anything else that's used to back up a visual match?

A. In forensics early on in the development of the procedure it was anticipated that a visual match would be viewed as a little bit subjective, and a visual match is hampered by -- Eventually we have to put sizes to these fragments and, as I said, visually I can tell that it's somewhere between four thousand and say five thousand. But I need to be more precise than that. That leaves a lot of leeway, a thousand base pairs to be exact. So what was developed early on were computers that would look down the marker lanes on one side, look down the marker lanes on another side, look at all these bands, and they would be able to precisely tell you a point estimate for this size, say it's four thousand six hundred and twenty, and I can't do that with my eyes but the computer can. So that type of technology was developed specifically for forensics.

Q. What, if any, use is made of the monomorphic marker that you mentioned this morning, or the sex typing probe to help you interpret the autorad?

A. Well, again, the monomorphic marker if we ran say the D7Z1 monomorphic marker, this one here, on these sample lanes what we find is a single band, it would

be here, would be in the same spot for sample "B", the same spot for sample "C" and the same spot for sample "D", and it would be at a predicted location. It would be 2,731 base pairs because that's how big it is, and it would be in the same spot across visually, and the computer would be able to tell you it's in that size range.

Q. And these types of conclusions that you mention that you can arrive at by looking at an autorad, either it's an inclusion as shown on lanes "B" and "C" there, or an exclusion as shown on lanes "A" and "B", an inconclusive where, for example, you might not have enough DNA to see the bands. Are those standardized calls that are made throughout forensics or throughout science in general or are they just something that was developed by the R.C.M.P.?

A. That's standard scientific method. I can't think of a test that doesn't have those three types of verdicts or whatever at the end, plus, minus, plus - or both, a test is positive, negative or inconclusive. All tests have those three endings or three possible endings.

Q. What does the term 'false positive' mean to you?

A. A false positive would mean if I conducted - to my mind if I conducted this test and I obtained identical patterns when in fact if the test had been run properly the patterns may look like this. So you're attaining matching patterns from samples that shouldn't have matching patterns. That's a false positive.

Q. What are the risks of that happening if the test is correctly done?

A. If these tests are correctly done and interpreted properly I would think there's no risk of that happening.

Q. What does a false negative mean?

A. False negative is precisely the opposite. If you have patterns that if the test is done properly should give a non-match and in fact the test generates a match that's a false -- I just described the other one again. If you have patterns that should be a match, if the test is done properly, and the test results actually show that they're not a match that's a false negative. You're excluding somebody that should give a match if the test was done properly.

Q. And what are the risks of that if the tests are done properly, excluding someone who should in fact be matched?

A. Again, like false positives if the test is done properly and interpreted properly the risk of those things happening I think is nil.

Q. We touched on it a bit this morning with respect to substances that are subjected to certain environmental conditions. You mentioned soil and bacteria, a number of -- heat, sunlight, you mentioned sunlight. Can you tell us what, if any, work was done either by the R.C.M.P. or anyone in the R.C.M.P. you were collaborating with in terms of subjecting various substances to environmental insults?

A. When these types of forensic tests are first designed it's common practice to manipulate the test and try out different things that you suspect may come into play in a forensic case. For example you may take a blood stain and deposit it on denim because you often get blue jeans coming in in a criminal case with blood on them, and see if the dyes or the fabric itself can influence how the test operates when you extract DNA from denim. You may also mix DNA with say household cleaners. Somebody trying to simulate, perhaps somebody trying to clean up a blood stain, and what's the influence of say cleaning a blood stain with javex or putting it through your washing machine. How does that affect the DNA? If you want to simulate environmental factors you leave blood stains outside for a length of time, you bury them, subject them to all sorts of different conditions that a body or piece of evidence might be subjected to in the natural environment.

Q. What conclusions have you arrived at from your own environmental studies and any ones that you have seen as to how it affects the DNA?

A. Well, they're fairly uninteresting results. There's certainly a lot of environmental factors that will destroy DNA, break it down, impair my ability to analyze it. That's probably the biggest finding in those studies, that there are things that will destroy the DNA molecule and render the test useless. I can't analyze something that's been degraded. So you have a lot of environmental influences that will do that.

Q. You're referring to not being able to actually run the RFLP test at all because you can't extract it or get enough human or high quality DNA?

A. Yeah, correct. The test material is destroyed.

Q. Assume for a moment in a hypothetical that semen was found laying on top of a body and that semen was subjected to heat, the heat, smoke and soot of a house fire, what effect, if any, would you expect on the DNA composition of that semen?

A. Again, it would be very, very difficult - it would be impossible for me to sit here and without knowing all the parameters, which we would never know in something like that, you would have to know temperature, duration, humidity, how long afterwards the fire, all these variables that you really - you can't control, you can't simulate, so you can't really comment on. What you can say is that that's certainly an environment where the DNA could be destroyed or the DNA could partially be destroyed. What we do know of these studies is that we haven't found anything that's going to take this pattern and turn it into this pattern and do this over five probes. We haven't found anything that's going to take this pattern, the matching pattern, and turn it into this pattern over five probes. We're not going to find anything that's going to take a two-banded pattern for five probes and turn it into a one-banded pattern for five probes, or vice versa. These patterns don't shuffle around depending on whether you leave them in the cold, the hot, the soot, the water, on a body or under the ground.

Q. The determining factor being whether you can extract enough human high quality or high molecular weight DNA from that substance?

A. Yes. This is why we do the test every time because even with very seemingly fresh stains you may be able to guess that there might be enough blood there to do a test, sometimes there may be nothing and you're fooled again. You do the test every time because the only rule of thumb is that there's no rule of thumb. There's all sorts of things that do degrade DNA and since you have no control over those factors you can guess but you have to do the test really and observe it.

Q. That is the test right after you extract it. The test to determine how much DNA --

A. Yes. You have to ask that question every time: is there DNA; how much is there; what quality it is; is it human.

Q. And if you had a substance subjected to some environmental insult, for example like a house fire, and you do extract high molecular weight DNA and it's human DNA, what, if any, bearing would where it's been have on the actual test results?

A. None.

Q. Population genetics, Doctor Waye, you touched on it when we were going through your C.V. this morning. From what you have testified to to date, once you start making calls of inclusion that's where population genetics comes into effect, is that correct?

A. Yes.

Q. You want to determine what the significance of the particular match is, is that right?

A. Yes. It's not enough that you show that the evidence matches the person. If, for example, 90% of the population is going to have that same pattern it's not a very probing analysis. You have a 100 people in this room that have that pattern. So what you have to do is you actually have to go out in the population and make a survey, a poll if you will, and say how many people in the population have this pattern. What significance can I put on this being a match. Is it very common or is it very rare, or is it something in the middle.

Q. So what is it that you first must compile before you can get into determining that question?

A. A data base of individuals, an actual poll. You have to do these tests on a large number of people and define how often this pattern occurs in the population, this pattern, all the different combinations occur in the population.

Q. Did you have anything to do with the data base - or the compiling of a data base for the R.C.M.P.?

A. Yes, that was part of my responsibilities when I was there.

Q. Could you tell the jury what data bases were compiled and why?

A. The first data base that we compiled was the Caucasian data base. These were blood donors from a military base in Kingston, from Ottawa and from Vancouver.

Q. Military base in Kingston, you are referring to Canadian Forces Base Kingston, Ontario?

A. Yes. There were several hundred individuals, I think all together upwards to 8 or 900 individuals, from the Military Base. That would represent people from all over Canada and that was the largest portion of the data base were from the Military Base. They weren't all born in Kingston; they were from all over Canada.

Q. And why a -- First of all, what is the Caucasian? What are you referring to when you use --

A. In general terms white. You're a Caucasian; I'm a Caucasian. Most of the people in this room are Caucasians. And in Canada in general 90% of the population would fall into Caucasian.

Q. The person sitting between the two police officers over against the wall with the white shirt what, in your opinion, is he?

A. He's a Caucasian.

Q. Why the Caucasian data base for Canada? I think it's obvious but you were saying a certain number of Caucasians in Canada, does that have a bearing on it?

A. Well, you're asking the question this matches this, this pattern, so these two samples could have come from the same individual. The question you're really asking is how many other people in the general population could it have come from. So, for example, Canada has about .1% - .2% Hispanics. Making a Mexican data base would be kind of meaningless. You really want to target a population of people who

could have left that sample and since we're in Canada 90% of the people falling into a Caucasian racial grouping, that would be the most obvious choice.

Q. How does the size of the R.C.M.P. data base, meaning the number of donors, compare to other data bases being used by other forensic laboratories in the world?

A. It's a large data base comparatively to other data bases.

Q. Pardon? I'm sorry.

A. It's large relative to other data bases that are in use. That's not to say it's better than other data bases but it's large.

Q. And what, if any, opinion do you have with respect to the R.C.M.P. Caucasian data base being applied to Caucasians in New Brunswick?

A. As with Caucasians throughout North America I think it would be applicable to New Brunswick.

Q. In terms of the size did you have to take into consideration the size of your population? For example do you know what the population of Canada is?

A. Just under 26 million. In that area.

Q. And in terms of New Brunswick the size of the total population? That includes all races.

A. 700,000.

Q. And in New Brunswick the percentage of Caucasians? Could you remember the percentage of Caucasians in Canada and the percentage of Caucasians in New Brunswick?

A. It's higher in New Brunswick than it is in Canada. Racial minorities such as Blacks, East Indians, and Orientals is higher across Canada than it is in New Brunswick due largely to metropolitan areas like Toronto and Montreal and Vancouver.

Q. And the rough percentage of Caucasians in Canada?

A. In Canada around 90%.

Q. And New Brunswick would even be higher than that?

A. Higher, yes.

Q. With the Caucasian data base what do you do with it to actually determine how common or how rare the pattern is you're looking at on each autorad? The match pattern.

A. It's a fairly simply process. There's a number of ways you can do it. The way it's done in a forensic test is you first analyze hundreds of people, we'll say a thousand people just for convenience sake, so you're not looking at a thousand events, you're really looking at two thousand events because if we're using D1S7 as our example we're looking at two fragments for each individual because they each have two chromosome ones. So if you are looking at a thousand people you're looking at two thousand fragments. What you basically do is you analyze all these people and if this were the fragment I'm interested in I ask how many times in those two thousand events did I see a fragment of that or similar size, and it may be on the order of two hundred times, so one in ten individuals - or one in ten fragments was of that size. So that gives a frequency to that size of fragment in the population.

Q. Correct me if I'm wrong, so what you have to do is take each one of the people in your data base and do an RFLP typing technique procedure for each one and generate an autorad for each of the probes that you want to look at in your case work?

A. Yes. You have to do this entire procedure, isolating the DNA from the blood, running the gels, generating the membranes and going through all the probes for all those thousand people and then going to the computer and having the computer determine the size for all two thousand of those fragments across five probes, so now you've gone two thousand times five so you are at ten thousand fragments that you've surveyed the size for, and you generate these large data banks or data bases.

Q. And that's so that you can determine the frequency you would find one single band in a particular location on the autorad?

A. Correct. And then you would do it for the second band in the pattern, and then there's simple genetic formula that you can take the frequency of this band, the frequency of this band, and doing one mathematical statement two times the frequency of this band and the frequency of this band you determine the frequency of individuals that have both of these fragments. That's the key information that you want. How many individuals -- You don't really care if somebody has a fragment here and a fragment there because your evidence didn't have a fragment up there. You want to know how many people have both of these and that's a simple mathematical formula.

Q. Since we may be getting into the terminology later with other witnesses or in fact with you I am going to ask you the determining the frequency of a single band, how often you would expect to find a particular one band in a particular location in your data base, is that term called binning?

A. Yes.

Q. And the calculation of once you find the frequency of one band and the frequency of another band you multiply them together?

A. In a pattern like this if the frequency is "P" here and the frequency is "Q" there, the formula for determining how often "P" and "Q" are found together in an individual is 2PQ, and that formula is called the Hardy-Weinberg formula. It was published over 80 years ago and it's been in use. It's sort of a cornerstone of genetics.

Q. So using both the binning and the Hardy-Weinberg formula you can determine on one probing - you can determine the frequency that you would expect to find, for example in this case schematic, the frequency of finding those patterns together?

A. Yes. Again, that's one way. The other way you can do it is you can just look at all the patterns that you generated from those thousand people and ask directly how many of them had these two bands. What you find is that the formula and your eyes adding them up will give you pretty much the same answer.

Q. Now, you talked about previously about the frequency of one probe times the frequency of another probe. Depending on the number of probes the frequency

increases, the probability of a match decreases, correct?

A. Correct. If you have matches across multiple probes the likelihood of finding somebody else fortuitously matches across multiple probes decreases and decreases as you go.

Q. So for example, Doctor, and correct me if I'm wrong, if this, for example, was the results you obtained from using D1S7 probe and you determined a particular frequency for that by individual band frequencies and then using Hardy-Weinberg formula determining the two bands together?

A. Yes.

Q. And if you did another probing, say D2S44 and you stripped this off and you came up with another set of matching bands, so you would do the same calculation to determine the frequency for that probe, and then if you can continue you would do it for each of the highly polymorphic probes you use, is that correct?

A. Correct.

Q. And then what would you do to get a total frequency for the number of probes that you were able to use? Say for example you come up with a three probe match or a four probe match or a five probe match.

A. You would multiply those frequencies, each one. Multiply the frequency of one by the frequency of two, by the frequency of three, and that's how you expand from individual frequencies of one in 50 to one in a hundred and finally when you multiply all those together you're just adding one or two zeros each time and the numbers become progressively

smaller. The denominator becomes bigger but the likelihood becomes smaller.

Q. What mathematical formula is that?

A. It's called the "Product Rule". It's an algebraic term but it has nothing -- It's not a forensic term.

Q. How extensive is the use of the Product Rule or the theory underlining the Product Rule in science generally?

A. Well, it's fundamental probabilities. It has nothing to do with forensics as its origin. It's just fundamental probabilities. What we are looking at is independent events. The pattern that you have on chromosome 1 is unlinked to the pattern that you have on chromosome 2. Those are fundamental laws of inheritance. So an event on chromosome 1 is not linked to an event on chromosome 2 so the probability of an event on chromosome 1 is not linked to the probability of an event on chromosome 2. So you can multiply those probabilities.

Q. So just as an example, say for example the one probe, you determine the frequency for one probe to be one in ten and you go to a second probe and you have another match and you determine the frequency to be one in ten, and if you go to the third the same, one in ten, and the fourth one in ten. What would be the total frequency you will see in that particular pattern in the Caucasian data base, for example --

A. Well it's one in ten times one in ten, times one in ten, times one in ten, times one in ten. You've got five zeros there so it's one in ten thousand.

THE COURT: One in --

A. Ten thousand.

Q. This method of calculation using binning to determine individual band frequency, Hardy-Weinberg equation to determine the frequency of the probes, two bands together, and using the Product Rule, is that something only developed by the R.C.M.P. or is it used elsewhere?

A. It's used in both forensic labs and genetic labs worldwide. There's nothing novel about this type of logic or this type of mathematical approach.

Q. Are there any, to your knowledge, population geneticists who are working with the, for example, the R.C.M.P. Caucasian data base doing things with it, assessing it, things of that nature?

A. Since the data bases were first generated which is several years now, they were in place before I left the R.C.M.P. which was two years ago, the data has been distributed to scientists virtually around the world and many people have reviewed it in many different ways. In addition there are outside consultants that the R.C.M.P. have acquired their services, people that do statistics for a living, to analyze the data. So they act as consultants and they provide their expertise in helping us analyze the statistics.

Q. When you were at the R.C.M.P. Lab what things, if anything, did you do to show the world, so to speak, what kind of system you had, what kind of a system you were implementing and what kind of a system that you were going to actually use in Canada?

A. Well, the first thing you do when you have the data in place and you finish analyzing it is publish it, and along with publishing it -- Publishing takes a little bit of time. You submit the papers and by the time they actually reach the scientific journal stand it's usually about a year. So that's not a fast way to spread information around to other scientists so what you generally do is you make use of telephones, fax machines, and symposia. You present your results at meetings for other scientists to review, you send your results to other people, you talk about your results with other scientists.

Q. And did in fact you do this when you were at the R.C.M.P. lab?

A. Yes, and they continue to do it. Their work's routinely presented at scientific meetings of geneticists and forensic scientists.

Q. Is this a normal way in which scientific information is distributed with respect to any field?

A. It's essentially what drives science. People enjoy presenting their work and it's the only way that we can critique other people's work and come to some sort of scientific truth is for scientists to get together and review other people's work and add to other people's work and put it all together, try to make a story.

Q. With respect to the case specific evidence here in the case of The Queen Versus Allan Legere, did you have any function - did you play any function in this particular matter?

A. I had no function in actually conducting the tests or handling the exhibits. I did, as other people in the lab, I did have the occasion to look at the final products of the tests. Look at the autorads and review the autorads.

Q. And is this something that -- You've indicated before, is this something that's normally done? Other people looking at an autorad generated by someone else?

A. Yes. It's something that - you know - as I said before, virtually anyone with eyes can do and when somebody is doing a case in the lab it's pretty hard to keep other people from looking at it. People are curious and you like to see other people's results and go over them, but it's a nice way to check your conclusions too if somebody looks at your results and they, of course, come to the same conclusions.

Q. Did you have occasion to review -- you had occasion to review the results in this particular case?

A. Yes.

Q. And you're prepared to testify to those results?

A. Yes.

Q. And did you have occasion to review the method of probability calculation and the numbers generated associated with this case?

A. Yes.

Q. And are you prepared to testify with respect to those results?

A. Yes.

MR. WALSH: My Lord at this time I have finished my direct examination of Doctor Waye on this aspect. I am going to ask that he, after cross-examination by my learned friend, I am going to ask that he be stood aside and to be recalled after Doctor Bowen testifies. That's for the case specific evidence obviously.

THE COURT: The further examination would be confined to the case specific evidence.

MR. WALSH: Yes, the results generated in this particular case.

THE COURT: As will be testified to by Doctor Bowen.

MR. WALSH: By Doctor Bowen.

THE COURT: Do you want to reserve cross-examination until this witness's direct examination is all through, Mr. Furlotte, or do you want to do this portion of it now?

MR. FURLOTTE: No, I'll do this portion of it now.

THE COURT: You are going to be a little while I gather.

MR. FURLOTTE: I expect I'll be a while with this witness so it's a good time for a break.

THE COURT: I think we'll have a break now then and come back in 15 minutes. You shouldn't, of course, Doctor, discuss the matter with anyone until all your testimony is finished, as you know.

(RECESS - 3:00 - 3:25 P.M.)

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

CROSS-EXAMINATION BY MR. FURLOTTE:

Q. Doctor Waye how did you first become involved with the forensic laboratory in Ottawa, the R.C.M.P.?

A. If I can recall, I got a phone call from a friend of a friend from a colleague of mine that I studied with in Toronto. He first approached the R.C.M.P. I guess this would be shortly after Doctor Alex Jeffreys brought up his initial application of DNA typing to forensics, maybe 1986 or '87. The wheels got rolling in an administrative way at the R.C.M.P. to looking into DNA typing and sometime after that they started--

Q. And who was that in particular? Would that be Doctor Fourney you're talking about?

A. The person who contacted the R.C.M.P.?

Q. No. You said you were contacted by a friend of a friend.

A. The person at the R.C.M.P. that I first talked to is Gary Shutler, and the scientist who first went to them and said this might be something you should look at is Doctor Cornaluk, and he's at University of Ottawa and at Childrens Hospital in Ottawa.

Q. And you were first hired by the R.C.M.P. then when?

A. I started there in March of 1988.

Q. And that was basically what? To set up a forensic lab for testing DNA, RFLP's?

A. Yes, that's the bulk of my responsibilities were developing and implementing the tests.

Q. And how long did it take you to set up the lab?

A. Well, a lot of the work had been done before I got there. As I said, Gary Shutler was with the R.C.M.P. at that time, still is with the R.C.M.P. He equipped the lab. Went to labs at Ottawa, saw what would be needed equipment-wise and facility-wise and set up the lab and actually started doing some testing before I went there, so it's not fair to say that I set up

the lab. The lab was really set up and operating somewhat by the time I arrived there. When I arrived there I started evaluating different probes, evaluating different enzymes and evaluating different equipment.

Q. And I assume you would have consulted maybe a lot with other laboratories that had already been set up, something like the FBI?

A. Well, we were all at pretty much the same level of implementation at that time and I wasn't there very long before the technical working group on DNA analysis methods was formed in Washington and that involved our lab, the R.C.M.P.'s lab, people in Toronto, various people from State labs. We all got together with the common interests of trying to put together some protocols to do this type of work.

Q. But you were a member of that working group for a while?

A. All the time I was at the R.C.M.P. I'm still in contact with a lot of those people.

Q. The acronymn is called what? - TWGDAM?

A. TWGDAM.

Q. Were there certain standards to be set up in the lab for quality control or standards for the interpretation of autorads by this working group?

A. That's part of the process, yes.

Q. And the R.C.M.P. Lab in Ottawa, while you were working there was that lab following the quality control standards that were set out by your working group?

A. You have to put these things in a context of time.

Q. While you were working there.

A. I worked there both before the TWGDAM was ever conceived so therefore there were no guidelines; I worked there when TWGDAM was operational and we were forming guidelines; and I worked there after guidelines and drafts of guidelines had been submitted. You're going to have to put us into an era that I can deal with.

Q. Okay, how about 1989? Was TWGDAM formed at that time?

A. TWGDAM was formed by 1989, yes.

Q. And was the R.C.M.P. lab in Ottawa following the standards or guidelines that were set by TWGDAM for quality control?

A. I'm not even aware that there were guidelines at that time. There may have been.

Q. Were there any proficiency tests conducted at the R.C.M.P. lab in Ottawa during 1989?

A. There may have been.

Q. You don't know?

A. That's not my job.

Q. Whose job --

A. I was a researcher.

Q. You were what?

A. I was a researcher.

Q. You did case work yourself though?

A. Yes.

Q. In 1989?

A. Yes.

Q. Did anybody do quality control checks on your work?

A. In the context of somebody testing my work?

Q. In other people assessing your work as blind assessments to see that you were doing good quality work.

A. A blind proficiency test? What are you asking? A blind proficiency test?

Q. Blind proficiency tests and open proficiency tests.

A. No.

Q. Nobody has ever done that to you?

A. Not formally, no.

Q. Had you performed any proficiency tests on John Bowen?

A. No.

Q. Do you know if anybody performed proficiency tests on John Bowen?

A. Yes, I believe tests were conducted.

Q. By who?

A. Again, it wasn't my job. There's a lot of administrative capacities in various jobs that go into a department like that. That wasn't one of my jobs and I can't recall whose job that was. I wasn't involved in formally training people, proficiency testing them. All those things came after I left the R.C.M.P.

Q. And you left the R.C.M.P. in January of 1990?

A. That's correct.

Q. And I believe at least some of the testing or half of the testing in say this case before the court, Mr. Legere, was done in 1989?

A. Some of the testing was done then, yes.

Q. So as far as you know in 1989 there were no proficiency standards or quality control guidelines being followed by the R.C.M.P. lab in Ottawa in 1989?

A. No, that's not what I said. That's what you just said.

Q. But what did you say or what do you want to say?

A. I said that wasn't my job. It wasn't my responsibility and I can't comment on how or how many times it was done or if it was done. It wasn't my job.

Q. Do you know whose responsibility it would have been?

A. No.

Q. Doctor Waye it appears from your education and your knowledge about testing - running tests on DNA and the typing, and your experience seems to be considerate - considerable, would you agree with that?

A. Yes.

Q. So how would you rate in the scientific community? Average scientist as far as eminence within the community?

A. I'm not sure that that's something that you ask the individual. I think you ask other people.

Q. I notice amongst some of - a lot of your experiences, you have conducted quite a few - or you have acted as a lecturer at quite a few different organizations across North America?

A. Part of my job has always been somewhat of a teacher.

Q. And somewhat in relation to the forensic application of DNA testing and profiles?

A. Yes.

Q. And I believe, as was mentioned, you recently completed a chapter in forensic DNA analysis for identification, and that was for legal purposes I understood. For a legal audience.

A. It's for a legal -- It's not a primary scientific publication. It's a publication edited and put together by lawyers and certainly the audience is

going to be more a legal audience than a scientific audience. It's a basic book on general forensic evidence. DNA is only one part of it and I'm one of the contributors to the book.

Q. So it was more in line for people who are going to be bringing this type of evidence to court rather than to argue it within the scientific community?

A. I would have to read the beginning part of the book. I haven't seen the book itself. I'm sure it's laid out at the beginning of the book what the purpose of the book and what the audience they would like to direct the book to is. I assume it's for lawyers that of course are involved in DNA cases. It wouldn't be directed towards real estate lawyers for example. It would be directed towards criminal lawyers who are doing DNA cases. I suspect.

Q. The reliability of this type of evidence that's being brought before the court, and both in the testing procedures and the profiling of a person's DNA and also the calculation of say probabilities, is that in great dispute in the scientific community?

A. Not to my knowledge, no.

Q. Not to your knowledge. So basically are you saying that the scientific community that you belong to and this expertise that you belong to, and population genetics included, readily accept that this type of evidence or procedure is reliable in identifying or --

A. Scientists by nature are argumentative people and don't readily accept anything at face value. There's been an evolution where various things have been raised in the literature. I think as a scientific

body the controversy has died down considerable.

Q. The controversy has died down considerably?

A. Yes.

Q. Does that mean maybe that the proponents, or at one time proponents in the forensic field, are now agreeing with defence lawyers or is it vice versa?

A. The proponents have backed off and they're now dissenters, is that what you're asking?

Q. Yes.

A. Hardly the case.

Q. You're saying the dispute has died down considerably here.

A. Hardly the case.

Q. Hardly the case. The opponents to the reliability of this type of evidence haven't laid down and played dead have they?

A. The pulse is getting weak.

Q. Have you been following any of this in the past two years?

A. I have been following it up until last week. I was in D.C. last week with five thousand geneticists. It's a good way to survey the world.

Q. Do you know whether or not the National Academy of Science is looking into whether or not forensic experts can come to court and reliably state what the areas of probability are of making matches or non-matches?

A. I don't know exactly the context of their report. They are looking at DNA - DNA typing. It's my understanding that they're much more concerned about civil rights' violations and things of that sort, but I assume population genetics, as is say how a

restriction enzyme works, those are all things that are going to be covered in their report.

Q. Is their report out yet, do you know?

A. It's due out any time. It may be out. People have asked me for it so it must be imminent.

Q. Should be out any time then.

A. And they have been saying that since summer.

Q. Aside from the National Academy of Science being concerned with civil rights for whatever reason, are they not also concerned that it would be improper to use the Product Rule to multiply across loci to be able to come to your high numbers?

A. The National Academy of Science --

Q. Yes.

A. -- concerned about those laws? I don't think so, no.

Q. You don't think so. If there were great disputes within the scientific community and the scientific community I mean scientists in your field but the fields that these properties belong to, both in the testing procedures themselves and the calculation of probabilities, who would be the spokesperson for the scientific community? Would that be the National Academy of Science or some other body?

A. It would certainly be different groups that if there were controversial aspects would look at it. I know the society that I'm a member of, the American Society of Human Genetics, has over the years looked at various aspects of DNA typing for forensics and they continue to look at various areas, just as they do look at things like population screening for cystic fibrosis. There's all sorts of genetic issues that

these societies delve into and they look at it. It's part of their responsibility as a society.

Q. Just to further understand, I kind of got the impression from your testimony that the reliability of this type of evidence is no longer a controversial - or a great controversial issue within your scientific community?

A. That is my opinion, yes.

Q. That's your opinion. Was it ever a great controversial issue?

A. It's a matter of how you define great. There's certainly been a couple of people who have written many articles basically attacking every part of the procedure from when you receive the blood stain to when you look at the autorad. There are always detractors. I can't think of anything in science that hasn't had a detractor. There are people that still argue that the AIDS virus is harmless.

Q. You say a couple of people.

A. There's a - the most vocal people who are scientists, that is, there's a few of them. A couple. Four or five maybe.

Q. Do you know whether or not there was ever more opponents to this procedure than there were proponents at one time?

A. The number, in my opinion, the number of opponents to DNA typing has always been small and continues to be small, and as a society we don't vote on these things but I can tell you last Thursday morning there were somewhere over a thousand geneticists assembled in a room for an entire morning in Washington discussed

nothing but population issues and forensic DNA typing. At the end of that if there were a lot of opponents they didn't know how to use microphones or they were timid and they didn't want to express their negative views. Perhaps they wanted to save them for court. I didn't hear a lot of dissention in the crowds and there were a lot of geneticists.

Q. You didn't hear a lot of dissention.

A. I didn't hear any.

Q. Any.

A. Of course they may just be shy.

Q. Would that be a proper forum?

A. That's the forum that scientists generally work in. You would give a talk; there's microphones positioned all around the room; and there is generally almost as much time left for discussion as there is time for presentation. During that time people ask technical questions about how you would do this test, how you would apply it to this situation. There was no vocal dissention that this is invalid, this is invalid.

Q. That's the testing procedures. What about the calculations as far as population genetics is concerned?

A. The entire -- There was an hour talk given by Doctor Ken Kidd, he was the keynote speaker, about population genetics and there was no dissention at the end of that talk about the application of this to forensic science. None whatsoever.

Q. So do you take that to mean that everybody agreed with it?

A. I'm sure some people might think that it's equally possible that everyone disagreed but they felt they didn't want to speak up. It was my impression that there was very little dissenters in that room.

Q. I understand you took part in forming the R.C.M.P. data base?

A. Portions of it, yes.

Q. Portions of it. And how much of it would you have run yourself, tests, to profile different DNA samples?

A. About two-thirds of it.

Q. About two-thirds of it. How many times did you run the tests?

A. On the data base?

Q. Yes.

A. Personally, once.

Q. Just once. Once for each sample?

A. Yes.

Q. And I understand there's some kind of binning system that you use?

A. Correct.

Q. And would you explain that, please?

A. Binning is a procedure that was developed jointly with the FBI and other labs. It provides an arbitrary way that we can classify the sizes of bands. Using this type of procedure, if this were an example, if this is four thousand base pairs and this is five thousand base pairs the computer may tell you that this is four thousand six hundred base pairs. The problem with this technology - it's not a problem, it was recognized right from the beginning, is that I can analyze my - if this was my DNA sample here I can analyze my DNA

ten times and the computer will give me ten different numbers for this band. The technology doesn't have the type of precision to tell you exactly to the base pair how large that is. The number that you get will always be close to four thousand six hundred or whatever number I just mentioned, but it won't be bang on. It's incapable of getting base pair resolution. It's much like trying to measure somebody's height with a yard stick to a thousandth of an inch. You can't do it. You've got the wrong tool. And this is the wrong tool for measuring the number of base pairs, but it will tell you approximately the number of base pairs. With that situation in mind, when you start counting up in the population how often I see a band of that size you have to take into account that I can't even get that size two times in a row on my own DNA. So I have to look at how many people had bands of that size plus bands in approximately that size. So what we do is we divide the length of the gel up into a number of sectors or bins and if a band falls within a size bracket it will be counted in that size interval and that way you include not only all the bands that fell at that size, you include all the ones that are close to it. And that's simply the binning method.

Q. Okay. Now, you mentioned that you - you said if you run your DNA ten times you might get ten different measurements but they'd be awful close.

A. I think they'd be close.

Q. What do you call close?

A. Again, it's probably something different than you would perhaps. It's not within one base pair or two base pairs which a lot of people would say would be close. It's within a couple of percent of the size.

Q. What do you call a couple of percent?

A. Well, if I ran a sample and I ran it again and it was say 2% smaller that's quite acceptable. That's the norm. But I wouldn't be able to get it right on to the base pair and it would be somewhat smaller or somewhat larger or it may in fact turn out to be the exact same size. If it did turn out to be the exact same size it would be meaningless because it's more likely that it wouldn't. It'd just be luck.

Q. So you're saying it might be out by 2%?

A. Yes, that's not an unusual variance, no. Not with this type of technology.

Q. Okay. If you were out by 2% would it be that maybe the next time you would fall into a different bin when they put you into their data base?

A. Oh you very well could.

Q. Very well could. So at 2% maybe one time you'd be going into one bin and another time you'd be fitting into a different bin 2% out?

A. Yes. The bin has a precise boundary. It runs on the base pair. You could perhaps go from zero to a thousand base pairs being one bin and from a thousand to two thousand being the next bin. Well obviously you have to fall in one or the other. You can't sit on the fence; you can't be part of a base pair. So if you are on one side one time and you're a little bit lower the next time you can fall into the other bin, which is precisely why we analyze hundreds of

people and not five or six people because that would drastically affect the frequencies in each bin. That's why you analyze hundreds and thousands of people, not a handful.

Q. Okay. So say they run your DNA profile and they put you into the data base and you're slotted into all the different bins.

A. Correct.

Q. Right. So you're there for identification. Now, the next time they run your DNA profile you could very well fit into different bins?

A. Yes, and my data would be one out of thousand points, and one out of two thousand points would not affect the outcome.

Q. So if the R.C.M.P. wanted to search -- put your profile in their data base, then they found some evidence at the scene of the crime and they wanted to search their data base to see if your profile was in there, they may very well come up that gee, we don't have Doctor Waye in our data base. How come? I know I put him there. Would that be possible?

A. Nope. You've misused the system.

Q. Why not?

A. You don't understand the system correctly. That's not the way the system would be used.

Q. Well maybe the system can be used other than that but that's one way the system can be used, could it not?

A. Not to my knowledge.

Q. Not to your knowledge. So it's possible, Doctor Waye, then that if they took your DNA sample ten different times and put you into their data base the ten

different times, the eleventh time they might come out and be able to say that gee, we still can't find Doctor Waye, if they run your profile through the data base as to fitting in the different bins?

A. Again, and perhaps you misunderstood me, that's not how the system is used. You don't take an unknown sample and query the data base to see that type of information, how often did that person fall in it. It's not used that way.

Q. Could it be used that way or is it you can't use it that way because you can't get the same measurements all the time?

A. No. You're misusing - you're misusing the binning principle. The binning principle, all it's designed to do is to define arbitrary alleles. Now you're using it as a method of matching things up. So we're not misusing something, you're misunderstanding something. That's essentially what I'm trying to get at here.

Q. No, I'm not necessarily misunderstanding something. Maybe I'm just trying --

A. Trust me, you have.

Q. -- to look at it from a different light.

A. Trust me, you have, because I do understand it. I had something to do with arranging this and you have misunderstood it or you've misexpressed yourself. The system is not used that way. It's used to define alleles or to give characters to these bands that we can slot them into categories, one through thirty-one or one through twenty-seven. You have to organize this data and be able to say is that a one or a two,

is that a five or a six. It's not used for purpose of matching these two up and the computer says that's a five and that's a six exclusion. It's not used that way at all, ever.

Q. Now, you mentioned that if you run your DNA profile maybe one time you could be out by 2% the second time you run it in one of your bands. The computer might measure it and be out by the 2%.

A. Sure. I can run my DNA in adjacent lanes and the computer will say that they're 2% apart. That's a formal expectation of this type of system.

Q. What's an acceptable level for the computer for your test to be out?

A. An acceptable level?

Q. Yes.

A. Again, a primary discriminating force is your eye. Your eye will tell you what's acceptable. This obviously is unacceptable from that. You don't really have to know anything about sizes to do that. Those are bang on and, you know, if the computer happened to tell me that those were 5% out my eyes and my mind would tell me well 5% must be acceptable. So those are the things that you derive empirically by looking at things that are identical and then you ask the computer how far out can these be, and by definition if they look identical it doesn't really matter how far they're out that's an acceptable range. And 2% is well within those empirically defined numbers.

Q. Okay. But as I understand your system, in your marker lanes you run your gel, you have your marker lanes which are of known base pair lengths, am I right?

A. That's correct.

Q. And when you measure say these bands from samples out here you kind of measure them off from the known lengths of the markers? Compare them with the markers.

A. Correct. If you can equate the computer with a set of eyes the computer will simultaneously look at the markers that flank it so it will look at this marker, this marker, this marker and this marker simultaneously and then estimate where this falls in between both this and this. That's the computer's job.

Q. So say at one time these are known lengths, these are unknown lengths, so in order to calculate the approximate length of these base pairs or the approximate number of these base pairs your computer will put a value on them?

A. Yes.

Q. Now, it may be in the next gel you run the same DNA analysis and you say well your computer might this time, even taking into consideration the known base pairs of your markers, it may have put another known value in here and may be 2% out.

A. That's a given, yes.

Q. That's a given. It's possible.

A. That's expected.

Q. Would it be possible for a computer to give the known value to these maybe that would be 50% out?

A. No.

Q. So how far out would you be before you could say well, there's either something wrong with the system or I'm not running the same sample twice?

A. If I had to say a rule of thumb, somewhere less than 5 or 6%.

Q. Somewhere less than 5 or 6.

A. You're asking for an all-encompassing number.

Q. Okay. I believe your R.C.M.P. system does have something which is called a match window.

A. Yes, they currently have what is called a match window.

Q. Could you explain to the court what a match window is?

A. A match window is a tolerance that when you've made a visual call, such as this, and the computer sizes them, from empirical observations of running both the same DNA's over and over again and looking at bands that are invariant or monomorphic bands between people, we have a good idea of when things appear identical how far the sizes can actually be out from the computer, and that forms a tolerance level. You have an idea that, you know, things are 15% out. I don't even have to look at the autorad. I have a good idea that those will not be a visual match because I've looked at thousands of them and any time they are a visual match they're within a certain level, and the match criteria they use at the R.C.M.P. is 5.2% plus or minus 2.6%.

Q. And how did you determine your match window?

A. That particular number was derived by looking at the monomorphic marker across in excess of a thousand individuals.

Q. And your monomorphic marker is a fragment of known base pairs?

A. Correct.

Q. So you know exactly how far it should be travelling in the gel?

A. You know that -- You have a formal expectation of the size that it should generate. It should be 2,731 base pairs.

Q. So your 5.2% window would be your maximum degree of measurement imprecision or matching degree of error? Which would you call it?

A. I wouldn't use the word 'error'. Error implies that a mistake was made. I told you at the beginning this test is incapable of measuring to the base pair so the fact that you don't measure to the base pair you would be in error using the word 'error'. Imprecision is probably -- It's an intrinsic property of the test that you will not get the right answer.

Q. Now, do you know what the FBI's match window is?

A. Plus or minus 2½%.

Q. Plus or minus 2½%. And yours is plus or minus 5.2%?

A. 2.6. No, 2.6. Plus or minus 2.6.

Q. 2.6.

A. These are match windows that all came into effect after I left my employment with the R.C.M.P. so perhaps you're asking the wrong person a lot of these questions.

Q. Could you explain why different laboratories would have different size match windows?

A. Well, there's subtle differences in the tests. Some of the differences are in the length of the gel that you use; some of them are in the percentage of the gel that you use; some of the differences are as fundamental as the enzyme that you use for the test. So you're measuring different things so your measurement imprecision is going to be a little bit different. You're comparing apples to -- Well, you're comparing different types of apples. I wouldn't like to say apples to oranges but you're comparing different types of apples. You're not making a direct comparison of the same thing.

Q. And that's because your protocols maybe are not quite the same. You don't follow the same procedures.

A. Well conceptually the protocols are all the same. There isn't a lab that deviates from the type of thing that I was showing the court this morning. There are subtle differences. Different suppliers have this. As I said, different dimensions of the gel, different setups. You might load your standards on one side, a lab might load them on the other side. These are subtle differences.

Q. Now, you mentioned that you also have defence lawyers consulting you for information.

A. All the time.

Q. All the time. And you have no problem lending them your opinions of your expertise?

A. If they want help and the time factor is reasonable, usually it's over the telephone, I'll help them out, sure.

Q. You have helped out defence lawyers from the United States also?

A. Yes.

Q. Did you ever help anybody out in relation to the FBI using ethidium bromide in their system?

A. Help out the FBI or help out anyone in relation --

Q. No, help out a defence lawyer or an expert that was going to be called by a defence lawyer.

A. Yes.

Q. Did you ever consult with them in relation to the FBI using ethidium bromide?

A. Yes.

Q. And what was your opinion at that time of the FBI using ethidium bromide?

A. I had no opinion of the FBI using ethidium bromide. I had an opinion on the effects of ethidium bromide incorporated into the gels which I'll explain. There's two ways that you can stain a gel, both before you do the test, before you run the gel you can immerse the gel in a dye, or you can immerse the gel in a dye after you run the test, and what we found through research was that staining the gel after you run the test gave you the most accurate results, and we found that the patterns that we got were less reproducible when you did it the other way. So we've never done it the first way, staining the gel before you run it. The FBI is the opposite, they stain at the beginning. So in our system I knew that it led to less reproducible results. The FBI's system is somewhat different so for me to commment on how this dye and staining at the beginning affected their

results I'd have to do those experiments. We did the experiments with respect to our system. But by inference, that's why I got a lot of phone calls from defence lawyers. They were people from the States. The FBI had done cases. They had a difference between Canada and the United States and the trend in this business is any differences grab them and lets work with them, and it's strategy.

Q. The ethidium bromide would what? - act as kind of a contaminant to the DNA fragments?

A. I wouldn't use the word 'contaminant'. Contaminant implies that it doesn't belong there, it slipped in unbeknowst to you. That's not the situation here. You added it. You know it's there, you know how much of it's there, and you know exactly what it's doing. So it's not a contaminant, it's an additive or an agent that when incorporated at the end has absolutely no effect on how the DNA migrates because it wasn't there while it migrated. It can't affect it once it's stopped. But in our system - or in the R.C.M.P.'s system, or at least the system that was in place when I did the study in I guess mid '89, it did have an effect. That's about as far as I can go with that.

Q. What kind of an effect would it have in your system?

A. It altered the mobility of the bands. It's something called band shifting. Instead of two samples from the same individual migrating in a reproducible manner like this you would have what we call a band shift. This might migrate a little bit slower and this one a little bit slower. The patterns would

look almost the same but the bands are shifted a little bit hence the phrase 'band shifting'.

Q. So that's one of the reasons also why maybe you had environmental insult studies to see whether or not environmental insults would cause band shifting?

A. I don't --

Q. Similar to ethidium bromide.

A. I don't think we were looking specifically for band shifting per se. We were looking to see if common environmental factors would alter the pattern such that you create false inclusions or false exclusions.

Q. I believe you have been declared an expert in human population genetics as it pertains to forensic DNA polymorphism?

A. Yes.

Q. In that category. And would that also make you an expert in human population genetics in relation to something other than forensic DNA polymorphism?

A. Well, the courts themselves haven't ruled on that. I work in that capacity on a daily basis at the hospital. Gene frequencies are something that are an integral part of my job at the hospital. The disease frequencies - frequencies of the diseases I work with vary from population to population. I have to know an awful lot about how they vary for me to use the techniques at hand in an optimal manner. So it's a daily part of my job and that has nothing to do with forensics.

Q. But there is population geneticists, a specific field in science?

A. Yes, there are people that do nothing but study frequency variation in different populations. It's part of my job, it's not all of my job.

Q. It's part of your job but it's not the only thing you do.

A. No, it certainly isn't.

Q. You mentioned something about to obtain different blood types from either forensic specimens or for medical purposes do you obtain that the same as you do DNA or is there another process to type blood?

A. If you want to figure out whether I'm a type A or a type B, things like that?

Q. Yeah, if you are going to figure out if you're a type A or a type B or --

A. Yes, that's looking at genetic variation that happens to be on chromosome 9. All these things are encoded by DNA. What you're looking at there is the product of the DNA, so you are indirectly looking at variation of the DNA by looking at proteins associated with your red blood cells. There's a number of different ways that you can determine a person's blood type. They're usually based on antibodies against the various types. They have very little to do with this type of testing. People don't derive blood groupings using this type of testing mainly because the blood grouping systems were in existence long before anyone ever started doing DNA analysis and they're much cheaper and faster and easier to perform.

Q. Much easier to perform. There's not as many variable forms in blood typing as there is in setting up for your - measuring your RFLP's in a poly --

A. Well it's a simple test. You don't have to -- Like if you go to give blood they will determine your blood type while you wait. I can't determine your DNA type while you wait.

Q. No, so it's a very simple test.

A. Simple and fast and it's cheap.

Q. And accurate?

A. Yes, it's an accurate test.

Q. Basically there's no measurements involved in typing blood as there is in binning RFLP's?

A. Well, you are definitely an A or a B or an AB or an O. You're not half of one and --

Q. So you are always going to fit into the same bin. They can't fit --

A. If the test is done right, yes.

Q. It's not like when you are setting up your data base and slotting people's DNA profiles in different bins?

A. And, again, you're coming back to misuse of the system. Maybe it's something fundamental in my presentation but --

Q. Well maybe I would like to discuss the system from another slant.

A. Okay. What I can tell you, and I think we have gone through this --

Q. I just want you to explain for the jury how typing a person's DNA profile differs from typing a person's blood?

A. Fundamentally there is no difference. If I analyze my DNA over and over and over again I will get the same pattern over and over and over again just as I will continue to be an A type blood donor over and

over and over again as long as I give blood. I will continue to get those patterns and I will continue to get those patterns within those prescribed tolerance regions that we discussed a little while ago. Both systems have fidelity that way. Both systems are accurate that way. Now if you misuse the binning system, if you want to do this slide me from one bin to the other and misuse the system as you are, then certainly you have set up criteria that are improper and yes, systems do differ then. On the same hand, you may mistype or misinterpret ABO typing, I have no idea.

Q. But it has nothing to do with measurement of base pairs?

A. ABO typing, no, but it measures other things. If you do an ABO type, depending on the method you're using for ABO typing, there's tolerances in how strong a positive is, how strong a negative is, all these things are done. A lot of them are automated but, again, a person misusing the system would get wrong results, just as you've misused this.

Q. But in the blood grouping you're either positive, maybe --

A. I think we'd all like the world to be plus or minus --

Q. You're an O or an A. You're not halfway in between or you're not going to fall into an O one time and fall into an A the next time.

A. Well when the test is done properly you are going to be a discrete type, and when this test is done properly and you don't misuse the bins for another purpose as you are, I will be a discrete type.

Fundamentally there's no difference. The tests differ dramatically in what they're actually measuring but if you take it down to first level what they are doing is measuring - one's measuring a locus on one that doesn't code for a protein, the other is measuring variability on chromosome 9 which does code for a blood group variability.

Q. When you are doing blood typing you said there's not that many forms - or not much variation. How much variation is there in blood typing?

A. Well, to be honest, I've never done a blood typing. I don't give blood either, I don't like to give blood. So it's not really an area of expertise. I do know that there's a limited number of types and if my schooling is correct you can be an A, you can be a B, you can be an AB, or you can be an O.

Q. And in comparison to the highly polymorphic areas you could have how many different variables?

A. Well, some of the loci thousands.

Q. Some will go as high as five thousand?

A. Some of them several thousand, yes.

Q. Several thousand.

A. And actually, depending on how you analyze them, you can actually get into the millions depending on what you're measuring as your variability.

Q. But in the highly polymorphic areas for your binning process you will use approximately how many bins?

A. In the R.C.M.P. system, 27. So there would be all the various -- Depending on how the alleles are spread out. There's a potential that you could have a person be at bin 1-2, bin 1-1, a 1-3, a 1-4, a 1-5, through 27 and then you start 2-3, 2-4. It's much

like a lottery game. There's a lot of different combinations.

Q. But just trying again to compare your DNA profiling with your blood typing there's many, many more variables in DNA profiling, at least 27 bins that the R.C.M.P. have set up.

A. Yes.

Q. Which has been set up arbitrarily.

A. Yes.

Q. But you could set up thousands, as you say, if you want. Rather than 27 bins you could have a thousand.

A. You could make the bins smaller, create more bins and create more categories that a person could be.

Q. So you could narrow the person down to say closer identification with an unknown substance?

A. Then we would have something to argue about because then we would be getting closer and closer to a base pair resolution which I have repeatedly said is not capable of obtaining. So you would be in effect saying I'm going to measure somebody's height with a yard stick to the thousandths of an inch. It's impossible to do. You could say you're going to do it but you are not going to be able to reproducibly do it so why say you are going to do it. It's a lot easier to use a wider window and say I'm going to use a yard stick and I'm going to try and get it within two inches. Then you've used the right tool.

Q. So the purpose of the R.C.M.P. system is to set up a system where you can possible identify unknown substances with known substances?

A. You set up a system where you can ask the question did the sample come from this individual. If it didn't that's a fairly clear-cut analysis.

Q. So it's set up more to include or to make matches --

A. All of these tests are set up to exclude.

Q. Pardon?

A. All of these tests are set up to exclude.

Q. To exclude.

A. It's the definitive test. If somebody doesn't match they don't match.

Q. Okay, but if you were to refine your system to be more accurate then you would get more exclusions? Could you possible get more exclusions if you refined your system to be more accurate in measurement?

A. It wouldn't be more accurate. As I said before, if you brought those bins down closer to base pair resolution you may be thinking that you're getting a more accurate measurement there but you're dealing with a system that can't do it so what you're doing is you're creating a scenario where you're almost guaranteed to be falsely excluding all the time.

Q. Because your system's just not capable of handling it?

A. No, because the system is not designed to do that.

Q. Could you design a system to do that?

A. To actually measure something to the base pair?

Q. Yes. Or closer than what it actually does.

A. It could be done. What you do is you basically take that piece of DNA and purify it and you determine its sequence from beginning to end. You count up the bases. A lab would probably process one or two

cases a year doing that type of approach, and you gain no more information. You certainly couldn't construct a data base with it.

Q. Now, DNA profiling I believe you have also stated that aside from forensic purposes that it's used in paternity tests.

A. Yes.

Q. And, again, in using the system for paternity tests you don't have to be concerned with measurement imprecision?

A. Again, it's not an occupation that I do. It's much like blood groupings. I have never had -- I've had lots of requests to do paternity tests - I don't do them. I never have done them. I know that the labs that do do them they know what their measurement imprecision is and they do use computers to match the bands. In a paternity test all you're trying to establish is that the alleged father did pass - if he is the father that he would have passed one of the bands to the child. If the child contains a band that the father doesn't have he's not the father. So you answer the question could this guy have been the actual biological father or not. You have to measure those bands to do that.

Q. But basically you're only comparing the DNA from two known people?

A. Yeah, mother, father and child. Three people.

Q. But if you're just trying to find out who the father is then you would just run the DNA from the child and the father?

A. No, that's not the way a paternity -- It's always done as a triplet.

Q. It's always done in triplet.

A. Mother, father, child. You have to be able to sort out which bands are coming from mother and which bands are coming from father. The child was born of the mother so generally the mother's identity is not in dispute. She can usually tell you that she was the mother of the child and nobody disputes that sort of thing, in general. The father is the one that's in dispute so you figure out which band came from the mother and by exclusion the other band came from the father.

Q. But you are not worried about what are the probabilities that it come from somebody else? You're not involved with population genetics?

A. You certainly are. If all the males --

Q. With paternity testing?

A. You certainly are.

Q. Aren't you only involved in exclusions in paternity testing?

A. And then it comes to court and they want to know how likely it is he's the father and, of course, that comes with the number. If, for example, all the males have the same pattern the data is meaningless then. We know the males don't all have the same pattern so you have to say how many males could fortuitously have the same pattern as this fellow that we allege is the father.

Q. Again, for the bone marrow transplants you already have two known DNA profiles to compare that with?

A. Yes, you have the donor and a recipient.

Q. And that's just to check, again, two samples to see if one has been --

A. Which one's there.

Q. Which one's there. Which is not very technically demanding.

A. I've done a few of those, they can be. They have their moments. There's not an awful lot of statistics that goes with it. None as a matter of fact. But technically it's like any other test.

Q. I believe you mentioned that in each cell there would be what? - about 3 billion pairs of base pairs in a single molecule?

A. Not in a single molecule. In all the chromosomes combined.

Q. In all the chromosomes.

A. Combined. 46 molecules.

Q. And if you were able to stretch -- They're all curled up and if you were able to stretch them out in a single strand it would be something like about a six foot length?

A. You may be right. It's trivia. It's a number of feet, the actual length of the molecule.

Q. And you mentioned your molecule scissors, your restriction enzyme which cuts your base pairs, ones the R.C.M.P. uses, the H III?

A. Hae III. H-a-e III.

Q. And I believe - did I understand you to say that it will cut between G-G and C-C every four or five hundred base pairs?

A. Well, wherever there's a site and on average that's how often the sites occur.

Q. On an average it's every four or five.

A. It will cut wherever there's a site. If there's two sites ten base pairs apart there will be a ten base pair fragment. If there's two sites ten thousand base pairs apart there will be a ten thousand base pair fragment. But on average we know.

Q. On the average it's four or five hundred.

A. That's done by looking at long stretches of DNA where we know the sequence and we can actually measure the mean fragment size generated, or the average fragment size generated by that enzyme.

Q. Now, you mentioned when checking for comparisons or identity or whatever you want to call it that most labs use four or five probes and some of them use three.

A. Yes.

Q. Is there any particular reason why some use three, some use four and some use five?

A. A lot of it is driven by economics. The more tests you do the more it costs. A lot of these differences aren't in globally funded labs. They're labs that have to seek a price per case. The differences arise in labs that are private labs and they do this for profit. Obviously if they do ten tests instead of five tests it's going to cost twice as much to do the testing and they're going to have to charge twice as much and they're probably going to be about half as competitive as the lab doing five. So dropping one probe or knocking it down to three might give you a

price-wise competitive advantage over your next competitor.

Q. Do you know whether or not some scientists are criticizing the forensic labs and stating that they should for identification purposes, especially in forensics, they should be using maybe even ten probes rather than three, four or five to be sure of identity?

A. Again, there -- Well, I'm glad you added the last part. It wouldn't surprise me if somebody said it to be sure of identity. I don't think you're ever sure of identity in these tests. Even if I said the odds are one in a million there's a one in a million chance that someone else has it. It's a rare pattern, that's what I say. If somebody actually wants to design a test that you say I'm sure of identity I'm not sure -- Like you'd have to analyze chromosomes from one end to the other. So if that's what they're after then they're probably well within fact to say that they want more probes done. That's certainly not what we're after when we design these tests.

Q. How can you tell whether a DNA sample that you run through your test is degraded? What indication would you have that a sample is degraded?

A. Well, when I initially look at the DNA, this is before I ever cut it with the enzyme, I'll put it on one of these gels and I'll run it for a certain period of time at the end of which if the DNA is not degraded what I have is after I stain it with the dye I can visualize very large pieces of DNA up here.

A blob of DNA. They'll be all different sizes but all of them are big. That's undegraded DNA. If the DNA is somewhat degraded what you find is large high molecular weight DNA up at the top of the gel and a smearing or a trailing of DNA coming down this way. That just means that some of the fragments have been cut down randomly into smaller pieces. Now if the DNA is totally degraded what you find is a ball of fragments down at the bottom. I can't analyze that. There's no method that you can analyze totally degraded DNA and that's what you see there. So you really see all variations when you do that type of test. You either see very good DNA, DNA that's somewhat degraded, or DNA that's totally degraded, and you know that from the beginning before you ever develop one of the autorads or restrict the DNA with an enzyme.

Q. And what interpretation would you give to a sample that was degraded or partially degraded?

A. What interpretation would I give to that?

Q. Yes.

A. At that point? You just gave me the interpretation, that it's partially degraded. That's an observation not an interpretation.

Q. Would you be able to use that sample?

A. Again, it's degrees of degradation. Partial degradation could be 99% degraded in which the partial part is 1% or it could be the other way or it could be everything in between. Half the molecules are degraded a little bit, half of them are high molecular weight. Obviously if you're dealing with a situation

where you have a little bit of trailing up at the top and the degradation is minimal these tests are all going to work. If the mean size of the fragments are down here the probes that detect smaller fragments will work, probes that detect very large fragments may not work. We have both in the system. So you may get some of your tests to work, some of the others may not work, and things down at the bottom - well you're out of luck with all your tests. We don't have anything that measures very teeny, tiny pieces of DNA that are totally degraded. Not at this point.

Q. Now, in the field, again, of population genetics you are looking for a probability of - I believe you said the question you're really asking is how many other people could this have come from, and you were able to obtain an estimate or a rough estimate, whatever, from your population data base.

A. Yes.

Q. Correct? In the final answer that you come to, be whatever figure it is, that is in relation to what kind of people in the Caucasians? If you have a Caucasian data base and you can say well there's a possibility that this came from say one in a hundred thousand or whatever figure you're going to come up with in Caucasians.

A. Yeah. If you use the Caucasian data base to generate that number it will apply to the Caucasian data base. That's not to say other populations won't give the same number or similar number. That data is available from countries all around the world now and what we do know is there's no population where everyone's

DNA looks the same or that everyone's DNA is more similar than Caucasians are.

Q. And did I hear you say that any data base in North America would be applicable to New Brunswick?

A. No. I said that the Caucasian data base we're using could be used to generate numbers from any Caucasian population in North America. Vice versa you could - I think you could take any Caucasian data base from North America and apply it to a case in New Brunswick and the numbers that you generate aren't going to be appreciably different. You're not going to take a rare pattern and make it common. That's the bottom line.

Q. These figures generated by the R.C.M.P. Caucasian data base, these are restricted to -- Like say Mr. Legere's case here, you're going to say there was only one chance in so many that this could have come from somebody else, or just how did you put the question. How many other people could have this - could this have come from.

A. Well I didn't do the case so I'm not going to be putting those numbers to anyone. I don't even remember what the numbers were. What I'm here to do is convey that given a match at X number of probes, be it four or five, whether something is common or rare in this population or any other population on earth. I think we're talking generals, general trends here, not case specific evidence. I didn't do this case.

Q. And basically from a suspect you're going to say that well there's only one chance in so many that this

could have come from somebody other than the suspect, is that right?

A. With reference to the population group that we're talking about.

Q. With reference to the population group.

A. Obviously that number will change if you switch to another reference group.

Q. What are the restrictions or qualifications of that number?

A. Of that number? You're talking unrelated individuals,

Q. Unrelated individuals. So that means it could have been somebody else with much greater probability if it was somebody related to the suspect.

A. Well, it's called the family scenario and it comes up in virtually every case that you do. You will say odds of one in a million in the general population where in fact if it was his brother who did it chances are on a five probe match there's a one in a thousand - actually one in a thousand and twenty-four chance that his brother may have done it. In those kinds of cases generally the brother is alive and has blood piercing through his veins and you can bleed his brother and see if it matches.

Q. Or a half brother or a cousin?

A. Well you can screen all the relatives, if that's the test that we're going to first eliminate all living relatives. Again, there's usually an issue of access and things. Did his great-grandmother commit this rape? Probably not. There's a little bit of common sense goes into it. Obviously if somebody's got a hundred brothers and they were all at the same party

they may all be suspects and you do have to eliminate all of them.

Q. So whether your figures come out one in a hundred thousand, one in a hundred million or one in five billion, in relation to relatives like a brother it always remains one in a thousand so to speak? Does it not.

A. It's always going to be much more common with a brother.

Q. Right.

A. Which, you know, if we're -- To my mind as a scientist, scientists are in the business of seeking truth, if it is his brother let's bleed him and find out.

Q. Let's what?

A. Let's bleed him and find out.

Q. Bleed him and find out.

A. That's seeking truth I think.

Q. Or you take samples from all of the suspect's relatives?

A. Well once you go beyond immediate sibs those numbers very quickly approach the population numbers.

Q. Right.

THE COURT: I wonder if we could stop here for a moment, either a short recess or -- Are you going to be very much longer?

MR. FURLOTTE: I expect I'll be quite a while. I expect I'll be all morning tomorrow morning with this witness. It's a good time to break.

THE COURT: We will recess now until 9:30 tomorrow morning. So I'll ask the jury to go out. Please don't discuss the matter with anyone as I told you before. Don't listen to the news or read the newspapers or any of that stuff. We will see you in the morning at 9:30.

(Jury excused.)

MR. WALSH: My Lord before the Accused is taken out there is a matter that Mr. Furlotte and I discussed at lunchtime.

THE COURT: Excuse me just a minute. The Accused made a request for a brief recess here. Could you hold on?

MR. LEGERE: I can wait for this here. Yes.

MR. WALSH: What it is, My Lord, is when Doctor Bowen testifies we have a number of matters - a number of things that we have prepared for the purpose of demonstratively explaining the testimony and aiding the jury as a memory aid. I went over them with Mr. Furlotte. The first items Mr. Furlotte has no objection to. When Doctor Bowen testifies and we introduce the actual autorads we also propose to put to the jury lane loading identification so that they can have a reference that when they're looking at the autorad they'll know what is in each lane. It's very difficult to look at an autorad and retain by memory what is in each lane and what exhibit number it refers to. I'll leave a copy with Your Lordship and you may want to refer to it this evening, and another one for the second gel to ensure yourself that there is no problem with that. The other additional item that Mr. Furlotte takes exception to is when --

THE COURT: You say that he takes exception to. Do you take exception to this one?

MR. FURLOTTE: Not to those booklets.

MR. WALSH: I thought maybe you wished to review those yourself.

THE COURT: Yes, I would like to look at them, yes.

MR. WALSH: The other thing is that when Doctor Bowen testifies he will have a summary chart that's mounted on a board similar to this in which he summarizes his findings, and it's identical to this particular schematic here if you wish to take it and look at it My Lord. Mr. Furlotte takes exception to that particular chart. Perhaps if I may suggest, since the hour is late, you may wish to look at these matters --

THE COURT: Well let me look at that and we will discuss that in the morning.

MR. WALSH: And then we could discuss it perhaps after he finishes with Doctor Waye tomorrow.

THE COURT: Yes. But is this for use with this -- not with this witness at this stage?

MR. WALSH; No, it will be used by Doctor Bowen as he reveals his results. He will have that on a chart. And I would like to be able to use that and I wish to make argument as to why I should be able to use it perhaps when Doctor Waye's cross-examination is completed tomorrow.

THE COURT: The summary chart itself, the equivalent of this, you will be offering that as an exhibit.

MR. WALSH: Exactly, and something that can be referenced by the other experts as they testify.

THE COURT: Well, we will discuss that tomorrow.

(ADJOURNED 4:45 P.M. TO OCTOBER 16, 1991.)