VOLUME X

IN THE COURT OF QUEEN'S BENCH OF NEW BRUNSWICK

TRIAL DIVISION

JUDICIAL DISTRICT OF FREDERICTON

B E T W E E N:

HER MAJESTY THE QUEEN

- and -

ALLAN JOSEPH LEGERE

Voir Dire Proceedings held before the Honourable Mr. Justice David M. Dickson at the Burton Courthouse, Burton, New Brunswick, on the **10th** and **13th** days of **May**, **A. D. 1991.**

APPEARANCES:

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

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

Bonita DesRoches
Court Stenographer

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Continuation of Cross Examination of Dr. John Bowen by Mr. Furlotte.

(Accused Present.)

COURT: Where were we, on cross examination, Mr. Furlotte?

Q. Dr. Bowen, I believe we left off yesterday showing -- going over the slides again?

A. That is correct.

Q. Maybe we could continue on today. I believe we left off with D1S7 and the next one is D4S139?

A. Yes, the next probing was locus D4S139.

Q. Is that what we have on the screen there now?

A. That's correct.

Q. Again, Dr. Bowen, it looks as if there might be some extra bands in different lanes, lane four here. Is that supposed to be spread down? Could those be extra bands in here, and here and here? (Indicates) Or again, is that --

A. It's indicative of degradation of the sample.

Q. Degradation, and would that be the same for here, here, and these little bulges that come out here? Is that indicative of degradation? (Indicates)

A. Again, in lane 109F, and as you pointed previously in 115D, that is indicative of degradation, yes.

Q. And what about up here in this lane, these marks across here? (Indicates)

A. That's not specific binding, as far as I can tell.

Q. That's specific binding? Non-specific binding?

A. Non-specific binding. It's very faint. It's enhanced in the slide; again, that makes it look more than it really is in the original.

Q. What causes non-specific binding?

A. This is sometimes slight inefficient washing of the probe on the membrane. It just give you a shadow, a smear, a background.

Q. You say insufficient washing of the probes, insufficient washing or insufficient stripping?

A. In this case, it would be washing. It gives you a shadow, a smear. It doesn't give you the appearance of a band.

Q. So basically it can just stick anywhere at all at random?

A. The probe binds specifically to the fragments that it has a complementary characteristic. It also binds throughout the membrane. The purpose of high stringency washing is to remove all that non-specific

binding so you can actually see the bands. So what you end up with is sometimes a shadowy background.

Q. So, like, all the whole complete dark bands in here, would you call that non-specific binding also, or overexposure?

A. No, that is due to degradation and there is specific binding fragments but they have been degraded to the extent that they don't migrate as a band. They migrate as a smear.

Q. So even, the complete dark band, that's indication of degradation?

A. Yes.

Q. Is there any reason why you have most -- you know, why is there degradation in some of the lanes and not the others? Like here in 1IF, the female fracture lane, there's a lot of degradation but not much degradation transferred over into the 1I lane?

A. There's not much degradation in the 1I lane. As I mentioned yesterday, degradation, there is also the cells breaking open, DNA being degraded. Now, the nature of the differential extraction is to, in the first step, a gentle license to break open the fractured cells. Now, if the cells are already broken, all the degraded DNA will be in the first fracture. Therefore, there's much less degraded DNA in the male fraction.

Q. Is there any specific reason why you wouldn't see the non-specific binding in, say, lane 19? It seems you see a lot of non-specific binding in other lanes but in the male fractions of the swabs there doesn't appear to be non-specific binding. Everything that's there seems to be a band.

A. That is correct. Basically it's a cleaner sample in that respect. You can see some shadowing in the lane there. That may be degradation or non-specific

Q. that could be, then, some degradation could have transferred over into the --

A. Oh, yes, there's always the possibility of some degrading and they will be in the male fraction. It's generally the less of the --

Q. -- so when you separate -- generally less?

A. In the male specific fraction.

Q. At times could some of that degradation be mistaken for the band?

A. Not in my experience. What you'll notice is the major band here and the major band here on the original autorads are much more intense than the degradation products. These would not be mistaken for bands because they're more circular smears and I would never call something like that a band.

Q. Now, are most of the tests that you run in other cases, are they all of equal quality?

A. Some are much better quality than this, some are of less quality. It really depends on the nature of the forensic sample.

MR. WALSH: I was wondering if Dr. Bowen would just -- low voice but they're close together. If he would just speak up a little louder.

COURT: Dr. Bowen is whispering into Mr. Furlotte's ear and the rest of us are finding it hard to follow.

DR. BOWEN: Excuse me.

COURT: Yes, if you would just try to keep your voice up a little. Is this recording all right on the machine, Dr. Bowen's voice?

COURT STENOGRAPHER: It's probably difficult to get it on the machine.

COURT: If you could, perhaps, try to stay as close to the mike, not right on top of the mike necessarily, but fairly close to it.

Q. Okay, I believe the next slide has a reprobing of this probe?

A. Yes, this is the reprobing with locus D4S139.

Q. I notice in this reprobing we still have a lot of degradation in the -- well, not a lot, but --

A. In lane 1IF and 1KF?

Q. Yes?

A. Yes, the degradation products are always there.

Q. Yes, once they're there, they're not removed on washing or --

A. No.

Q. Or reprobing?

A. No. You do lose a little DNA with each subsequent stripping.

Q. So depending on the sensitivity of your probe, it may pick up some degradation in one probe and not in the other?

A. That's correct.

Q. You have to say yes.

A. Yes, I said that is correct.

Q. Item 109 here, would this be a band?

A. Yes, that is a band.

Q. And I assume the top one is a band?

A. That is correct, that is a band.

Q. What would this be? (Indicates)

A. That is a smear. It's a degradation product. It's enhanced in this slide, in the photographic process of making the slide.

Q. And 134F, would this be a band?

A. That right there is a band, yes. (Indicates)

Q. That top one?

A. Yes.

Q. And what about right underneath, would that be a band?

A. For this particular lane, that's a very poor representation but there is a band, almost level with that marker right there.

Q. Almost level with that marker?

A. The rest --

Q. This here would be degradation or a band?

A. That's all degradation. If you look at the original, that really bears no resemblance of what you see here. It's very light gray background with two dark bands.

Q. It's just almost as if it wasn't degradation, almost looks as if there could be a double band right there, just as here there could be another one here. (Indicates)

A. Not if you looked at the original. There's two very distinct bands here on the original and the rest is the background.

Q. Okay, we can go on to the next slide.

A. This is locus D17S79.

Q. I believe you said there's a lot of extra bands in these lanes because of improper stripping from the last ones?

A. Incomplete stripping, yes. The bands in the upper quadrant of this particular probing are from the previous hybridization which was pH 30, or locus D4S139.

Q. Maybe we could for a minute -- I missed something in D4S139, so we could back up. Could you back up one more time? This was the probe taken when? This one here? In 1989, or was this one taken in 1991?

A. This was taken in November 27, 1989.

Q. How many bands in lane one? Not lane one, lane 20NM?

A. There are two bands in lane 20.

Q. Two bands in lane 20?

A. NM, yes.

Q. I'll show you Exhibit VD-68, Dr. Bowen, and your sizing sheets. How many bands do you have registered?

A. I scored one band in lane 20.

Q. Why did you only score one band in lane 20?

A. It was by accident. I scored the bands visually first to confirm that it was within our match criteria for that particular allele control. When I was actually doing the computer scoring, I accidentally scored only one band.

Q. Or is it because you visually observed this to be one band and you did not score this as a band which you felt was degradation?

A. No, no. If you look at the original autorad, there's definitely two bands. There's no -- there's a good line separation.

Q. This one here?

A. Yes. It stays between the two bands. On the subsequent reprobing, I did score both bands.

Q. Yes, on the next reprobing, and we'll get to that. Now, I think you reprobed it and we have it a little clearer. You can go to the next slide. So here it looks a little more clear that there might be two separate bands?

A. Yes, you can see the two bands.

Q. So it's a matter of sometimes how long you leave it exposed as to whether or not you can tell it's one band or two, is that right?

A. If bands are close together, often with very long exposure they'll pull less, but that's not the case here. It's just I accidently didn't score that particular band. It is definitely visible in the original autorad.

Q. Or again, if it's not exposed long enough you get something, maybe, like this?

A. I don't understand the analogy.

Q. Well, it just seems to me that the longer that it's exposed, the darker and more broader the bands will get.

A. Yes.

Q. So if it's exposed for a short period of time, you're not going to have much of a mark on your autorad?

A. That is totally dependant on the amount of DNA in that particular lane, how large --

Q. How long you have to have it exposed for?

A. Exactly.

Q. Right, but if you had an equal amount of DNA in every lane, then the same length exposure you would have basically the same intensity in all bands?

A. That is correct.

Q. But since some lanes have more and less DNA in them, then in order to get a clear picture, each one should be exposed at a different length of time? It would be beneficial?

A. One can score these bands quite readily, visually and by the computer. It makes a little more

measurement in precision if one has larger bands like that. The computer has to find the exact center of that density. That is part of our measurement in precision process, the way the computer scores those bands. It's actually much easier for the computer to find the center of that band as opposed to one of these ones.

Q. Okay, we can go on to our next probe again. How many bands would be in here, Doctor? Any way of telling at this type of an exposure?

A. How many am I calling?

Q. How many might fall into here?

A. I call that a single band, I believe. Let me check the -- yes, that is, in my opinion, a single band.

Q. I see in lane 135?

A. That is correct.

Q. How many bands in that lane?

A. That is a band there (indicates) and that is a band there (indicates).

Q. Why would you call this a band, such a nice, big, round, fluffy ball, rather than a straight line across at the top?

A. The straight line across the top isn't really -- doesn't really appear like that in the original autorad. It looks more like a bit of fingernail.

Q. It pretty well compares as to what is on the screen?

A. It has a curvature that doesn't match the rest of the band pattern. It has a curvature.

Q. I'll ask you once again, Doctor, if you didn't observe these bands over here and you were just observing this, would you call that a band?

A. No, I would not.

Q. So the only reason you're calling it a band is because you see one over here in lane 3 that might match up, is that right?

A. No, it is not true. It is not a band because it does not meet the same sort of criteria that these two bands have. It has a curvature to it and it's much fainter.

Q. No, I'm talking about this one here. (Indicates)

A. That one?

Q. This bottom one here, yes?

A. That is a band.

Q. Yes, I realize you've interpreted this autorad as a band. I'll ask you again, if you didn't have the benefit of observing the bands over in this part past this marker lane and all you were doing was observing the bands in between these two marker lanes. Would you normally call that a band?

A. Yes, I would.

Q. I understand lane 135 is the male fraction of the vaginal swab from Linda Daughney?

A. No, this is a male fraction of a body swab.

Q. Body swab? I'm sorry, male fraction of a body swab from Linda Daughney?

A. That is correct.

Q. And lane 140, lane 5 is the known DNA sample from Linda Daughney?

A. Lane 5, item -- exhibit 140A is the known blood sample reportedly from Linda Daughney.

Q. If you were to call this a band in the middle, which you don't call it a band, but it would line up with one of the bands of Linda Daughney, would it not?

A. That smear is close to lining up with the --

Q. If it was a band, it would be a match with the bottom band of Linda Daughney which is found on that slide. The top one you're calling a band also matches the top band of Linda Daughney.

A. That's not a band.

Q. The top one is a band, is it not?

A. The top one is a band, yes.

Q. You call that one a band, okay, so that band here that you called, it would be equal in fragment size or -- enough to call it a match with the top band of Linda Daughney?

A. Slightly smaller.

Q. Slightly smaller?

A. Excuse me, it might be slightly further so it's slightly larger.

Q. Well, this is the female --

A. I wouldn't call that.

Q. You wouldn't call that?

A. No.

Q. Would that be equal -- would you call that a match, a visual match, these two?

A. Again, this band here migrates slightly further than this band here.

Q. So you wouldn't call that a match?

A. No. No.

Q. No, you wouldn't call that a match. Okay. Now we at least know what kind of visual difference that we need that you don't call matches. You can go to the next slide, Doctor.

A. This is the second probing, or reprobing, of the membrane for locus D17S79.

Q. The reprobing of this, was this just for the benefit of maybe clearing up some --

A. The reprobing was essentially to show that the bands that were seen in the upper quadrant with the original probing were from the previous hybridization in the original probing.

Q. You wouldn't try to call a match on this autorad between lanes 3 and 19, would you?

A. Yes, it is possible for the original, not -- you can see the band in lane 135 there --

Q. Can you see the bands there?

A. -- and 135 there. It's better in the original.

Q. I see where the bottom band should be, but each to their own whether there's one there or not.

A. Again you will notice that there is, in this particular autorad, there's no indication of any band as you would suggest in --

Q. No, because the exposure must have been a little less length of time, was it, or the same length of time?

A. The exposure here is eight days. It's actually quite a bit longer than the original exposure would be.

Q. This exposure would have been longer than the original?

A. The original was six days. This is an eight day exposure.

Q. So it appears to me that the other one was darker, more intensity?

A. That is correct.

Q. It's because of the --

A. The stripping and reprobing.

Q. The stripping, that you're losing your DNA?

A. You're losing small amounts of DNA with each subsequent stripping and reprobing.

Q. It didn't take much to remove what may have been a band, or what I thought may have been a band?

A. In my opinion it was not a band.

Q. Non-specific probing?

A. It was -- I wouldn't even -- it would be non-specific binding. It was just background.

Q. Is there any way an operator could manipulate the results that they want by length of time they exposed the amount of DNA they put in, the amount of times they restrip it, take DNA off? If you wanted to remove a band completely, say you run this and you found the band and you wanted to remove it completely, one of these, let's take the good intensity one. Would that be possible to remove it completely and then run another probe and look as if it was never there? I'm not saying you would do that, I'm just asking if it was possible?

A. Okay, if I understand this correctly, if someone took this particular locus and saw these two very intense bands, stripped it and manipulated it and then reprobed with that same probe and leaving the rest of the membrane?

Q. Leaving all the rest the same except removing one of these bands. Would that be possible?

A. The only way I could think that would be possible would be to actually cut out that area of the membrane and remove it.

Q. Or put, maybe, a chemical to -- would a chemical destroy it, the ability of it to -- for the homing probes to find it?

A. It would be very difficult to treat the membrane with a chemical that would be band specific. It would distort -- make a mess of the entire membrane. I'm not aware of any way --

Q. No, just if -- I was wondering if you lose band intensity by stripping and maybe by washing, you know, could they accidentally come off some other way?

A. No, the stripping process removes DNA, a slight amount of DNA with each subsequent stripping. It sort of depends on the amount of DNA there. The loss across the membrane is equal. It is not specific to any one area of the membrane. The loss is just a very slight loss throughout the membrane. It's only a very slight loss. I'm not trying to indicate that you lose --

Q. During the washings -- during the washings, too, of the membrane is it possible for whatever you lose, the intensity that you lose in some bands and fragments, is it possible that it could be removed from one area of the membrane and lodge onto another area?

A. No, it isn't.

Q. Okay, we can go to the next probe, Doctor?

A. This is the first probing of the locus D16S85.

Q. I understand your interpretation of this probe was that it was a little too faint to call?

A. To a certain extent it's a little too faint to call. Actually, the slide in this particular case enhanced some of the smudges and bands. This here on the original looks like two smudges coming together. (Witness points out area on exhibit.)

Q. It appears to me, Doctor, that -- if you go back to

the last one that you said you would call, there was lots there?

(Witness changes slides.)

Q. Do you see something in this area which you call a band? On this one, and I think the quality is the same on the original, and you say this one is good enough to call. But now flip it ahead to the one, D16, and I can see that much clearer than I can see on the other one and this one is not good enough to call? I'd like to know --

A. The reason, as I explained --

Q. Where's the boundary line as to what you call a match and what you don't?

A. The slide representation of this enhances those smudges so that they can be seen better. The slide representation of the previous probe was less contrasting and you couldn't see the bands on the slide as well. What I'm looking for is defined band, and here there is no defined band if you look at the original. There's a bit of an odd-shaped smudge there and a bit of an odd-shaped smudge here in lane 135.

Q. Okay, let's go back again to the D4. You're not calling this one because it's too faint. Let's go back to the D4 again.

A. D4?

Q. Yes. It's back one.

A. D17 is back one.

Q. Oh, is it 17? Okay?

A. The call was originally made on this one.

Q. Okay, the call was originally made on this one.

Now, I'm going to ask you, this you can't call a match because you say you wouldn't call this a match because you say this one is slightly below this one?

A. That is correct.

Q. You've already stated that. How can you call this smudge a match if that lower band is way over?

A. Because one looks at the center of the density, the center of that particular density.

Q. You look at the center of that density and the center of that density? And you can tell that one is no more lower or higher that the center of this density and that density? You can see that with your eyes from back there?

A. Not from back here. I wouldn't call from the slide, I would do it from the original.

Q. But from the autorad? We will have to take your word for it, Doctor. Okay, we'll go on, then.

That one we've already dealt with. Please go to the D10?

A. This is the second reprobing, D16, which we did not make a call.

Q. Which you did not make a call. Again, it's too faint? You can't tell?

A. In this particular case I'm just being conservative.

Q. Okay, we will go on to D10?

A. This is probing with locus D10S28.

Q. Maybe before we go on to this one, we had better go back to D16S85. I missed something. I believe this is a probe also where originally in 1989, is this the one here, or is this the '91?

A. This is the '91.

Q. Okay, let's go back to the '89. You called, I believe in your original interpretation of this match, you called three bands in lane 2, is that right? Do you recall?

A. I believe I scored three bands.

Q. Yes, you scored three bands in lane 2, and this thing here you scored as a band, is that correct?

A. That was to check and make sure it was a stripping problem.

Q. That was to what?

A. To ensure that it was a stripping problem, just like these other two bands were here.

Q. Yes, you knew that these were a stripping problem, but you didn't interpret this as a stripping problem in 1989, so you called three bands in that lane?

A. No, no, I interpreted it as a stripping problem. I scored it just to ensure that it was the same value. It is from the locus D17.

Q. So even though you knew it was a stripping problem, and it wasn't a band, you still scored it, is that what you're telling me?

A. To ensure that it was.

Q. To ensure that it was?

A. Yes.

Q. How do you ensure it's a stripping problem by scoring it?

A. To see if it's the same size as the band in the previous hybridization.

Q. Is there anything in your notes about that?

A. No.

Q. There's nothing in your notes about why you scored that as a band, is there?

A. No, I don't put anything in my notes about why I score anything as a band.

Q. Let's look at lane 14.

A. Lane 14 is exhibit 110, male fraction of the body swab reportedly from Donna Daughney.

Q. Do you see any bands in that lane?

A. There's an extremely faint band right there. (Indicates)

Q. Right, you scored a band in there? Right?

A. I believe I might have.

Q. VD-7 -- VD-70, rather?

A. Yes, I have scored one band in that lane.

Q. At 1603?

A. That is correct.

Q. Do you know whether or not you scored a lane in that band in the 1991 probing? (sic)

A. I don't recall.

Q. Let's have a look at lane 17 while we're at this one, which is 134.

A. One thirty-four, male fraction of vaginal swab reportedly from Linda Daughney.

Q. How many bands do you have in that lane?

A. There's a faint smear similar to a band right there. (Indicates)

Q. That one there? (Indicates) Okay, we can go on to the next one, now. This would be the 1991 one?

A. Yes.

Q. Where you had three bands in lane 2 in 1989, now you have two?

A. That is correct because we're confirming the fact that the third band was from the previous hybridization --

Q. A problem with stripping?

A. Inefficient stripping.

Q. What do you have in lane 14, now? That's 110, male fraction from Donna Daughney? I show you VD-83 which is the computer sizings for this probe, lane 14?

A. No bands detected.

Q. No bands? You had a band there in the other probe and this one it, again, disappeared? Correct?

A. There was a very faint band there. Again, with slight loss of DNA from the membrane due to stripping, it is not visualized in this particular --

Q. So that one wasn't a problem with stripping?

A. No.

Q. Now, in lane 17, how many bands would it have?

A. Seventeen.

Q. One thirty-four?

A. One thirty-four is the female fraction of the vaginal swab reportedly from Linda Daughney. Again, there seems to be a very faint band.

Q. Now, in your sizings in VD-83, your sizings for this probe, now you show two bands in lane 17 where you only showed one band on the previous one. Surely the second band didn't show up because of loss of fragments from stripping?

A. Just a cleaner background.

Q. Pardon?

A. Cleaner background.

Q. Where is the second band?

A. You can't see it on the slide.

Q. You can't see it on the slide?

A. There's a very faint band there. (Witness indicates on exhibit.)

Q. This right there? Right there?

A. This was just for my purposes of looking at that band to see if it was comparable to anything else I could see in that position. It's not something that you could call a match on.

Q. Well, it looks pretty comparable from what I see on the original autorad and here. I see that very little faint smudge here you're calling a band.

A. No, that is not--

Q. Are you calling that a band because you see a band over here and you know it belongs to the same person?

A. That is not the smudge I scored.

Q. So therefore you're calling that a band? That's not the smudge?

A. No.

Q. Okay, Doctor, I believe we can go on to D7Z2.

A. D7Z2.

Q. D7Z2 is the next one?

A. To do what? We started on D10, but then we went back.

Q. Oh, that's right. Now, all these lines in here, up there on top, is that degradation again, or just non-specific probing?

A. This probe is a very sensitive probe and that may be the result of two things. One would be a very slight partial digest, or the washing procedure allowed some of the DNA in those samples, there's much more DNA in some of these samples to bind homologous sequences that are not precisely the locus in question.

Q. I notice in lane 3 there's faint black marks which you score as bands continually. What do you call this now?

A. That, since there's nothing above that, I would call degradation products.

Q. Degradation products?

A. And they do, and with this particular probe, appear more like bands.

Q. Could that be an indication, or would anybody -- could anybody else interpret that as improper digestion?

A. No, because normally with improper digestion one would end up with larger fragments at this point. This is indicative of diagnostic. With this particular probe, D10S28, one gets a series of bands rather than smears as with other probes.

Q. Okay, Doctor, now we can go on to D7Z2.

A. This is an exposure for D7Z2, a two day exposure.

Q. Do you always get the multiple bands in the lanes with these probes?

A. With this particular probe, yes.

Q. With that particular probe?

A. It depends on the exposure time, but there is a series of bands beneath the fragment size. This is 2731, the only sequence band for this particular probe, and one gets a series of bands, smaller fragments, and there are often larger fragments. Some of these fragments are, in fact, polymorphic. We use this only for the monomorphic fragment that was identified and sequenced, 2731 base pairs.

Q. Well, as I understand the D7Z2 band, it has a specific sequence and it binds to a band of equal length and of specific sequence?

A. That is correct.

Q. Is that right?

A. That is 2731.

Q. So all these other ones that we see here, they would have the same sequence but just different lengths? Would that be appropriate?

A. That would be appropriate.

Q. They would all have to have the same sequence as the D72?

A. It would be the same sequence or very closely homologous to that sequence.

Q. Is there any reason why the probe would show up the band it's supposed to show any more that it should show the ones like here? I think you've explained earlier that the intensity, probably your largest band fragment sizes would show more intensity because there's more DNA there? Did I understand that correctly?

A. That can be the case, yes.

Q. As it does here, you know, it shows up good here and it shows up good here, but why wouldn't it show up in here also? If you have enough DNA to show here, there should all be fragment sizes that size up here, too, shouldn't there? Why wouldn't it show?

A. In that particular lane you're looking at, there are -- again, this slide has too much contrast to it on the original. If you look at the original on lane 135, there are faint bands up here and below here, as can be seen from the original.

Q. Why wouldn't they be the same intensity? It's the same quantity of DNA?

A. Oh, by no stretch of the imagination are they the same quantity of DNA. Look at the intensity of that band compared with that one.

Q. Oh, no, not with -- I'm not talking about between lanes. Within a lane.

A. Within a lane? That band, the 2731, is the most intense band in this entire lane.

Q. Why does it show up more than the others?

A. Because the copy number of that particular fragment size is much greater.

Q. So does that mean the other lanes are not the same sequence?

A. They are very closely related sequence.

Q. Closely related sequences but not the same?

A. They do not have to be identical.

Q. So you're apt to end up with something similar to your other probes, your polymorphic probes, where they will bind to something that is similar to their own?

A. As Dr. Waye explained, you're not binding probes to the exact identical sequence. There can be slight variation in that sequence, and it's not the purpose of the test.

Q. And when there is a slight variation in sequence, they will still bind to that fragment although that fragment is a different length?

A. No, because under the conditions that we run this test, it will only bind to the closest homologous sequence in that individual and that is the particular locus of interest. If one wanted to do that stringent conditions, of course, one would pick up a whole series of bands. But we're only picking up sequences that it binds most stringently to

and those are the most commonly or the most homologous sequences. They have the least difference and therefore for that particular locus they are identifiable.

Q. As I understand it, this probe is used again to indicate whether or not there was band shifting?

A. That is correct.

Q. And to see if the lanes are running the same speed?

A. That is essentially correct. It also indicates to the accuracy and precision of the gel test and the numbers that were generated. One can see here that when one compares one lane to the next, there is no evidence of any band shifting or lane shifting. When one also measures, this using a computer to see what size this particular fragment is, and that way one can test the accuracy or the precision -- and the precision, of the test. If it falls --

Q. Actually, if I understand correctly, you're using this probe running the gel to test the degree of inaccuracy of the system?

A. No.

Q. No?

A. It's a measure of our precision and accuracy.

Q. A measure of your precision and accuracy?

A. That is correct.

Q. And precision and accuracy in what?

A. In being able to say that this particular band size is close to its real size.

Q. Right, now you know -- well, sometimes you're out by, say, six percent?

A. No, we are not out by six percent.

Q. Well, at least 5.2?

A. What one can have across several gels, and across gels within the same gel, one can have a band size that brackets the accurate known size of the fragment and it's within 5.2 percentage.

Q. Right, and when you put the computer sizing on, they'll be within 5.2 percent?

A. No, the comparison of one lane to the next will be within 5.2 percent. The difference here is that it has to fall within the range of the actual value of the monomorphic.

Q. Okay, now, Doctor, according to the standards you set earlier, I would see that band being slightly lower than this one. Is that normal? I mean, when you run your D7 probe, would that be normal to have one slightly lower than the other?

A. It's very slightly lower.

Q. Yes, it is? So you wouldn't call that a match, but yet you don't call this band shifting?

A. No, what I do is I go to the computer to see how different the computer scores the centers of those bands, and I don't have the computer sheet here, but if I remember correctly, these are all very close.

Q. Now, you said there's no band shifting here. Is that because you didn't observe any visual band shifting or is it because all the computer sizings are within 5.2 percent?

A. There's no visual band shifting in the sense that --

Q. I thought you said there was -- you wouldn't normally call that a match?

A. It may look here as though that's tailing up a little bit and this is lower. That is within my tolerance in a visual match.

Q. That's within your tolerance even though visually you can see a difference, it's within the tolerance showing that there's no band shifting?

A. Well, there's the appearance of the difference here as I mentioned before. You have a tailing up of the band. It slightly goes up and this one comes down. But if one looks at the center of this, it's within tolerance of the visual match.

Q. I am just wondering, Doctor, you're using what appears to me would be going to measure the degree, what, in precision and in accuracy? How did you describe that again?

A. The measure of precision and accuracy.

Q. The measure of precision and accuracy, so therefore it will also measure imprecision and inaccuracy?

A. Measurement in precision can be defined and has been defined, in fact, using this particular probe.

Q. What I find puzzling, Doctor, is you're using the same measuring tool, the same system, to measure its own inaccuracy and that doesn't make any common sense to me. Could you explain how you can measure the inaccuracy by something that is inaccurate?

A. We're measuring the measurement in precision because we know the size of that particular fragment. It is known as to the sequence, therefore we look at the value that we achieve, using a computer to see what it gives as that fragment size. That is a measurement in precision. It's the difference between what we observe and what we know to be a fact.

Q. Now, I understand that all these are exactly the smae length, the same amount of base pairs, 2731, right? We know that some gels will -- some lanes might run a little faster or slower than others. Do we know that for a fact?

A. That can happen with certain contaminants.

Q. And the idea of this test is to see if the lane is running faster or slower. If you take lane 3 and lane 19, you want to see if they're running the same speed because they're quite a distance apart, and this helps you accomplish that, does it not?

A. That is correct.

Q. But when, in fact, the lanes will run different speeds, by merely putting in a known measurement length to see how fast they are running, that is sufficient to measure the inaccuracy?

A. I'm not sure I quite understand the question.

Q. You've got something running 27 -- this one is 2731 base pairs?

A. That is correct.

Q. You don't know what speed it's going to run, no way of telling that, so the only way you can compare it is with another lane to see what speed that lane is running?

A. It runs at the speed the fragment the size of 2731 should run in that particular gel.

Q. And in that particular lane?

A. A fragment of a given size will run at a given speed in a particular gel system.

Q. Consistently?

A. Well, that is the whole point of doing this measurement in precision because you can find that

some gels, I think in this particular gel, all these fragments are slightly larger than the known sequence fragment lane of the monomorph.

Q. So why do you get such a difference when you go from gel to gel?

A. The difference from gel to gel is just the different make-up of those particular gels. You run gels different times, different days, slight differences in the agarose or the salt concentration will change the way these things migrate, and that is part of the measurement in precision of this test. and that's why we measure it using this particular monomorph.

Q. So what I understand, then, if we have a known DNA fragment, say, in any one of your probes, say your D10 probe. We have a known DNA fragment and you run it in one gel and it comes out to, say, 3,000 base pairs, for instance?

A. It would never be that far off, I don't believe.

Q. No, I'm not saying 3,000 from -- I'm talking about your D10 probe. You may have a fragment length of 10,000 -- or 3,000 base pairs?

A. Yes.

Q. Okay, we'll let on we've got the D10, so we have a fragment length 3,000 base pairs. We run our D7 and we come out that it's 2731 right on, okay? We run the same DNA sample. We run it in a different gel, the same DNA sample in different gel, the same probe. We get -- you should get, again, if you got in your D7, 2731 base pairs, showing it right on, that fragment length should also come right back out at 3,000 base pairs?

A. No.

Q. No?

A. Because you're assuming that the computer is going to give you the exact same base pair number every time you scan the same gel and that is not true because there is part of the measurement and precision process is the fact that the computer cannot give you the exact same base pair number every time it scans the same blot.

Q. So are we saying that the 5.2 percent matching window is there because of computer error?

A. No.

Q. Inability to measure the same thing the same all the time?

A. No, because that is -- it only accounts for part of that measurement in precision.

Q. So what you're trying to do is measure all the imprecisions and inaccuracies of the system as a global --

A. It gives you a feel for the total amount of imprecision that one could have in the whole match, yes.

Q. You're using the same system to measure its own error?

A. We are using this system and by determining the size of these particular fragments that we see in our gels and comparing the known true value, that is how we determine the measurement in precision.

Q. You mentioned you use this probe also to measure band shifting, or to see if band shifting occurs?

A. Yes.

Q. How would it indicate that band shifting has occurred? How would you be able to tell band shifting has occurred?

A. Band shifting is generally a visual thing in the first place, but if there is band shifting in this lane, what one would expect is that there would be a significant visual difference and size difference in one band as compared to the next lane, or in adjacent lanes in that same gel.

Q. If there is a visual difference, say if this band here is -- there's a little visual difference but it's within the matching window. But if we saw this one a little lower, then all the bands in all the other polymorphic probes should, again, be a little less in value than the ones in this lane?

A. That is correct. It could also be lower or higher.

Q. Lower, yes, it wouldn't matter.

A. It doesn't matter. A shift can occur in either direction.

Q. It would all have to be in the same direction?

A. Yes. They would all be in the same direction because what essentially happens is everything, all the DNA in that sample is shifted in one direction.

MR. FURLOTTE: It may be appropriate for a break, My Lord.

(Accused escorted from courtroom.)

(Court Recessed 10:50 a.m. to 11:05 a.m.)

(Accused Present.)

COURT: Mr. Furlotte, you were going on?

Q. Okay, Dr. Bowen, I believe that brings us to the next slide.

A. This next slide is just another exposure for locus D7Z2.

Q. Okay, let's go to DYZ1.

A. This slide is for the locus DYZ1.

Q. Now, I would assume since this is, again, a monomorphic probe with 3564 base pairs?

A. It exhibits the monomorphic band that's 3564 base pairs in males.

Q. So it would be correct to assume that this one also could be used to measure band shifting as the same principle as the D7 probe, except that you won't have bands in every lane? But otherwise all the other principles that work for this one will --

A. That is correct. I'm not sure of the exact base pair sizes, 3564. It's in that range, so we don't have the exact sequence for the HaeIII cut.

Q. If you wanted to measure your system precision or imprecision accuracy you could measure the shift in -- with this probe and compare it with the shift of the D7 probe and they should be consistent, should they not? If you're going to have a two percent shift with the D7Z probe, you should have a two percent shift with this one in the same lane?

A. Not necessarily because we're not talking shift here, we're talking imprecision.

Q. Imprecision?

A. In determining the size for that particular fragment. Again, the computer will scan this blot and if you scan it ten different times, it will give you certain measurements in precision, so it is not a strict -- if you see a two percent difference with the DYZ1, one should see a two percent difference with the monomorphic probe. The other thing is that the shift throughout the gel is not necessarily the same.

One can often have larger shifts at the top of the gel with a band shift, lesser shifts in the middle of the gel, and again larger shifts in the bottom of the gel. It's not a consistent degree of shift. That is why we do not use a monomorph to adjust for a band shift because it will not tell us exactly how to adjust for all portions of the gel. But what it does is indicate a band shift.

Q. Okay, then, well, because it's not a continual degree of shift even for monomorphic probes, it would definitely hold true it would not be consistent shift for polymorphic probes?

A. That is correct.

Q. So therefore if you had -- take, for instance, a two percent shift for the D10, the fragments in the D10 probe, you could have a four percent shift for the fragments in the D17 probe?

A. A shift is outside the measurement in precision, so it would be greater than five percent.

Q. Let's talk about inside the measurement precision of 5.2 percent. It wouldn't be uncommon to have a two percent shift for the D10 probe and a four percent shift for the D17 probe?

A. We're not discussing shifts when we measure the measurement in precision.

Q. Well, okay, let's discuss measurement in precision. That would be common, a common factor?

A. It is possible that, yes, one will see a difference in the amount of measurement in precision between various bands and various positions of the gel.

Q. As I understand it, whenever you run a different gel with samples from Mr. Legere, and this was the

difference in fragment sizes between gels, some of them were considerable, 5.2 percent, some of them?

A. In the second gel that we've described, there is a difference of 5.2 percent with one fragment in one of the hybridizations. That is the maximum --

Q. That is the maximum?

A. -- with that gel.

Q. Is that just measurement in precision or is that, maybe, --

A. That is measurement in precision because as we've stated previously, we have detected empirically throughout our data base that we can have a difference measurement in precision of up to 5.5 percent between gels. What we've done is taken 99 percent of those values which was 5.2 and gave it a more conservative match window.

Q. Why do you have greater measurement imprecision between gels than you do within a gel, lane for lane?

A. With the monomorphic probing? Because you're comparing samples done under slightly different conditions. You do not have the absolute precise same conditions in each gel as you do in the gel.

Q. But since your monomorphic probing fragment lengths are all the same size, your marker lanes are -- your markers are the same in each gel, and don't you measure the length of your polymorphic fragments in relation as to how far up the markers it travels rather than from the top of the gel?

A. The difference in the gels is represented by the fact that the marker lanes migrate slightly differently as compared to the DNA in the sample of the degradation -- There's a slight difference

in the way they migrate and the way you measure them and that is part of our measurement.

Q. So I understand that whatever is in -- what's in these marker lanes?

A. These marker lanes are DNA. It's a yeast DNA that has been cloned and you get a set fragment size for several fragments. It's yeast DNA.

Q. Yeast DNA?

A. And some of the fragments, this one and some of the lower fragments, are part of the vector, part of the material, the plasma, that is used to grow up this particular yeast DNA.

Q. And they have particular fragment lengths?

A. That is correct.

Q. Okay, now, am I to understand you to say that if a marker had 3,000 base pairs and a polymorphic specimen DNA sample had 3,000 base pairs, that they would run at different speeds through the gel even though they're different -- even though they're the same length?

A. The conditions are set up that they run as close as possible and that is what we are measuring here. If there is a very slight difference in the way those two run, and the reason that they run differently is the fact that there is very, very, very small amounts of DNA in these marker lanes. We're talking about picograms of DNA as opposed to nanograms of DNA run as polymorphic markers. So if there's a slight change in the gel, it will affect the marker lanes slightly, more than the polymorphic bands.

Q. Okay, I don't think we -- there's no other slides in there, is there?

A. There are the slides for the second gel.

Q. I don't believe we'll need that.

(Witness returns to the witness stand.)

Maybe I can have a look at the D7Z2 probe for the second gel?

MR. WALSH: The second blot?

MR. FURLOTTE: The second blot, yes. Again I wonder, in the first blot we saw all the extra bands and you gave the explanation of them. Why is it that we don't see all these extra bands in this one?

A. As we see here, we have the monomorphic band showing, There are extra bands in the original, but the slide has taken too much contrast. You just can't see them. You can see some of the bands up here, but if you look at the original you can see the ladder of bands.

Q. I believe you also mentioned that you sometimes see the second band in about ten percent of the individuals?

A. That has been reported to me by Dr. Fourney that it's around ten percent.

Q. Now, again, these two samples are both of Legere. Why does he not have two bands in both samples?

A. He does.

Q. He does?

A. You just can't see it in the slide.

Q. Okay. I think that will be all. I understand you were the hair and fiber man at the forensic lab before you started doing DNA testing?

A. Yes, I was a hair and fiber specialist, yes.

Q. Did you take part in the testing to come up with the figures one in 4,500?

A. No, I did not.

Q. Now, you mentioned from the reports that you got you thought that the body swabs for Linda and Donna Daughney that was checked in the Sackville lab and that was found to have been semen on it?

A. That is correct.

Q. Are you also aware from the reports from Sackville that -- you're aware that the hair, item number 16, that was found on Father Smith's leg, that that was analyzed and found to be similar to Mr. Legere's?

A. Microscopic examination indicated that it was similar -- consistent with Mr. Legere's.

Q. Which would have been one in 4,500? Now, would you -- do you have your calculator with you?

MR. WALSH: Mr. Furlotte said -- the last statement was "Which would be one in 4,500," and I don't know if that was a statement that he expected the doctor to comment on?

MR. FURLOTTE: Dr. Carmody admitted that in his testimony so I --

MR. WALSH: No, Dr. Carmody didn't and Dr. Carmody is not a hair and fiber specialist. Perhaps if he wants to he could put that question to Dr. Bowen, but I don't want to leave the impression that Dr. Bowen accepted that statement Mr. Furlotte made. It wasn't in the form of a question.

COURT: Well, let's give Dr. Bowen a chance --

MR. FURLOTTE: Duff Evers made the statement in his first week. Are you aware that there's literature out there, tests conducted by the R. C. M. P., that found that hair samples such as was taken from

Mr. Legere, that the probability of somebody else having that hair out there would be one in 4,500?

A. I'm aware of that literature, yes.

Q. Can you calculate the frequency that one could expect two people to be in the same place at the same time, or similar hair, as Dr. Carmody did, with the other figures?

A. No, I cannot, because you're assuming that there's some variable that I can say that two people were at the same place at the same time. There's no time factor there.

Q. There is no time factor?

A. No.

Q. How does that differ from using the product rule with the DNA sample?

A. The product rule --

Q. How would that differ from Dr. Carmody and his Dr. Lewontin sharing the same birthdate? He would use a product rule for that. What would be the difference?

A. You only have one variable there. You have two variables. You have two people sharing the same type of hair. I believe that is what Dr. Carmody calculated. He cannot calculate that two people having the same hair being in the same place at one time.

Q. No, he can't calculate that. Let's say if they were in the same place at the same time. What would the figures be? There's no evidence before you that these two people with the same hair sample were in the same place at the same time. But I want you to calculate it on the proposition that they were.

MR. WALSH: Look, again, Dr. Bowen is not -- or at least he hasn't been declared to be a statistician or a population geneticist. I'm wondering if this is a proper field for Dr. Bowen to be delving into?

MR. FURLOTTE: He's using the product rule to calculate these figures in his field. He's done it for me on the tests when I asked him to compare the different fragments in the human cell line, and it's just a matter of going through the simple procedure again.

COURT: I'll leave it to Dr. Bowen to determine whether he can help you.

DR. BOWEN: May I make two comments? First, I do not feel qualified to make calculations of that type. The other comment is that for my forensic hair comparisons I never used a number such as one in 4,500. My comparisons were done on the fact that these samples were consistent with one another and in my personal experience, that consistency was found in less than -- somewhat less than one percent of the population.

Q. When you would appear in court and give such evidence that you found the exhibits were similar, hair samples were similar and consistent with an accused person, you were never entitled in court to say that it even probably came from the same person, were you?

A. I would state that it was consistent with having originated from the same individual.

Q. Right, and you could not even state in court that it probably came from the same individual, let alone proof beyond a reasonable doubt?

A. Certainly not with the hair comparisons, a microscopic comparison.

Q. Doctor, would you take your calculator, please, and multiply 4,500 by 4,500? What is the figure?

A. The number is one in 2.25 million.

Q. If you were to use those figures alone and your calculations that one in a million would be enough to prove beyond a reasonable doubt that somebody was guilty, surely --

MR. WALSH: Again, I object. Mr. Furlotte is delving into this whole issue, the Court touched on it yesterday about beyond a reasonable doubt. Mr. Furlotte wants to get the witnesses to talk about the probability of guilt versus the probability of what we're attempting to do here and to show the probability of two forensic samples matching.

COURT: Yes, well, we're not concerned with guilt here. We are only concerned with comparisons. I think it's not fair to ask a witness to express opinions on reasonable doubt, guilt --

MR. FURLOTTE: I think the answer is obvious, anyway, My Lord. I don't have to pursue that.

COURT: It is more a matter of argument.

MR. FURLOTTE: My Lord, if I may indulge the Court, I would ask for an early dinner hour. I believe I have a lot of material I have to go through and I would like to finish with this witness today, and I want to make sure that I touch on the important parts.

COURT: What time are we now? Quarter to twelve. I think that is fair enough. I think we would all probably very much like to finish with this witness this afternoon and --

MR. FURLOTTE: I expect that I will be -- I can do that. I expect I will be less than an hour with the witness.

COURT: Less than an hour you think you will be?

MR. FURLOTTE: Yes.

COURT: That would be good. How much time do you want, until half past one, say, still or --

MR. FURLOTTE: Half past one should be sufficient.

COURT: Well, let's do that.

MR. WALSH: My Lord, if I may address the Court on next week? I have some more information. This morning we've been on the phone. It would appear that at least tentatively, to forewarn Mr. Furlotte of how the Crown intends to proceed, and the Court, the way it is looking that Dr. Fourney will testify first thing Monday morning. Dr. Waye will be, hopefully again, we haven't confirmed with Dr. Waye yet, but what we would like is to have Dr. Waye follow Dr. Fourney. We hope that we can -- and again, we are estimating that perhaps we could finish these two witnesses, both cross -- I can't speak for Mr. Furlotte, but I'm hoping with a cushion that we could finish by Wednesday evening on these two witnesses, both direct and cross, and recall, and Dr. Kidd would be available for Thursday and Friday of next week. I hope -- I've told Mr. Furlotte at the break briefly what our plans were and hopefully we can work around that particular scheduling. I know it is not written in stone, My Lord, but we believe it will facilitate all parties.

COURT: Yes, has Dr. Kidd recovered?

MR. WALSH: Yes, he's back this morning. According to his secretary he feels much better and he's -- we're making plans for him to fly in sometime later on Wednesday for purpose of testifying on

Thursday and Friday.

COURT: This sounds reasonable with you, Mr. Furlotte?

MR. FURLOTTE: It sounds workable.

COURT: Let's recess until half past one and then if we do that, you say about an hour, half past two or so? You will have a little re-examination?

MR. WALSH: Yes, little is the appropriate word, My Lord, at this point anyway.

COURT: Then we'll all be away home by quarter to three. Eternal optimist, I am.

(Accused escorted from courtroom.)

(Court Recessed 11:45 a.m. to 1:30 p.m.)

(Accused present.)

Q. Dr. Bowen, I believe I had requested from you a copy of all the notes that were made in the conducting of these tests?

A. Yes, you did.

Q. And you provided me a copy with all your notes?

A. At that time, yes.

Q. Now, I notice when you conducted your first probe, D2S44, that you made a preliminary report of your findings and you forwarded that to the R. C. M. P., is that right?

A. That is correct.

Q. I don't see anything in your notes where you interpreted any of the other autorads after completion. Did you make any notes? When you completed the autorad, D1S7, why is there nothing in there as to what your interpretation of it was?

A. It's not a common practice, actually, to issue any reports after the first or second probing.

What we normally do is issue a report that is a final report on all our findings.

Q. That's to the R. C. M. P.?

A. That is to the R. C. M. P.

Q. But why not even in your notes, in your lab report? There's no mention in your lab reports at all, your notes that you're going through as you're taking the test, as to what your findings were?

A. Because the final interpretation is done at the very end.

Q. And you mention that Dr. Waye had, before the very end, I believe you said Dr. Waye had come in and checked over the autorads and to see what his interpretation would be?

A. That is correct. At one stage he did look at all the autorads.

Q. There's nothing in the lab reports or the notes to indicate that interpretation?

A. No, there is not.

Q. Were there any made?

A. No, there were not.

Q. So the only time those autorads were interpreted was some time in November or December of 1990?

A. No, they were interpreted as an on-going, as the case was on-going. Nothing was ever recorded until the final interpretation was developed.

Q. Is that standard scientific procedure?

A. As far as I'm concerned, one interprets the autorads. The fact that I didn't make a note in my notes does not detract from the interpretation.

MR. FURLOTTE: I have no further questions.

REDIRECT EXAMINATION BY MR. WALSH:

Q. Yes, Dr. Bowen, Mr. Furlotte had you do some calculations at the very outset of your testimony, I believe, this morning. Do you remember that?

A. Yes, I do.

Q. What, if any, scientific value would you put to the validity of those calculations in terms of what we're trying to determine here?

MR. FURLOTTE: I object, My Lord. He's not an expert either in statistics or in population genetics.

COURT: I'm just not clear on what --

MR. WALSH: Mr. Furlotte had him do some calculations, I believe it was, this morning.

COURT: I don't think very much came of them, did they?

MR. WALSH: Well, I just wanted to --

COURT: One over 4,500 was multiplied by one over 4,500 --

MR. WALSH: -- and I wanted -- yes --

COURT: -- and the result was one over 2.25 million, but I don't remember very much more.

MR. WALSH: All right, fine, My Lord, I just wanted to determine whether or not there was any validity to the actual calculations that the Doctor could see to what we were doing here, or what we are trying to assess here.

COURT: My recollection isn't very firm on just what was done, but if you have any explanation you want to give, Dr. Bowen?

WITNESS: I don't believe that they had any validity to what I'm expressing in terms of frequency for these occurrences in the DNA patterns.

Q. In answer to one of Mr. Furlotte's questions you mentioned a Dr. Weir. Would you tell us, please, fully who is -- his full name and who he is and

what stature, in your opinion, he has in the scientific community?

A. Dr. Bruce Weir is a professor of statistics, I believe, at South Carolina State University. I'm not sure if it's South Carolina or North Carolina. I'd have to check. He's a very eminent person in his field.

Q. And what field is that?

A. Statistics.

Q. Mr. Furlotte asked you some questions with respect to the time differences between the application of one probe before the application of another probe. You had given testimony about the lab being in renovations and a number of reasons why there were time differences between the applications of the probes. Do you remember that?

A. Yes, I do.

Q. Would you tell the Court, please, whether or not a time difference between the application of one probe to the application of another probe, whether or not that in any way affects the validity of the results obtained?

A. No, it does not.

Q. Mr. Furlotte mentioned that one in 4,500 and asked you about whether, when you were a hair and fiber specialist, whether or not you ever quoted those particular figures or relied on those figures. You indicated that you didn't. Is that my understanding?

A. That is correct.

Q. Would you explain, please -- could you explain that particular report? I think it's Gaudette and Keeping and what you understand about that report and its --

A. The report by Gaudette and Keeping was a fairly large study on comparisons of hair from different individuals. The frequency that he derived from these studies was that significance of a hair match between two Caucasian individuals, this is scalp hair, was one in 4,500.

Q. And was that report ever challenged in any way?

A. Yes, it has been challenged.

Q. Have you ever relied on it?

A. No, I have not.

Q. Mr. Furlotte asked you a question about -- I'll refer you to the third blot, the one that has item number 16, the single root hair taken off, or purportedly taken off Father Smith's leg, and you indicated -- and Mr. Furlotte asked you a question with respect to what, if any, comparisons you made to other samples with this number -- the pattern that is displayed in item number 16. Do you remember that?

A. Yes, I do.

Q. Doctor, from your experience can you tell us anything about the practicality of determining the origin of a single root hair?

A. Well, forensic purposes, one obviously tries to achieve a match between two individuals. A single root hair found at a scene does not necessarily mean that it had anything to do with the particular matter in hand. It could have been there from any source.

Q. Why is that?

A. Because people do transfer hairs from one to another throughout the day. It's a common event.

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

COURT: Thank you very much, Doctor. That finishes you, then, I guess as a witness, at this stage in any event.

(Witness Stood Down 1:50 p.m.)

COURT: You have nothing else you want to go on with this afternoon as part of your case?

MR. WALSH: No, My Lord. Again, we've found it a little firmer over the lunch hour. Dr. Waye will be available, he will be coming in late Monday night so he'll be available for Tuesday and Wednesday, or whatever periods of time Mr. Furlotte wants to continue his cross-examination of Dr. Waye. Dr. Fourney will be coming in Sunday night, so he'll be available Monday morning, and Dr. Kidd we expect will be coming in Wednesday and he'll be available for Thursday. Just one point for the record, Dr. Bowen will be flying back to his lab. He will exchange or hand over the original autorads and the notes that accompany them to Dr. Fourney so Dr. Fourney can bring them down and keep control of them throughout next week so they are available.

I've spoken to Mr. Furlotte about that and I understand he agrees to that procedure to have these available, but we don't want to, obviously, lose the continuity and the chain of continuity of that.

COURT: Are these the ones that are actually in evidence?

MR. WALSH: No, these are the originals that are being displayed on the lightbox. You may want to have them available next week, but they're Dr. Bowen's property, so to speak, since he generated them, and

he's going to change them over or exchange them to Dr. Fourney and Dr. Fourney will take custody of them with the consent of Mr. Furlotte. Whether Dr. Fourney will be able to stay all of next week we're not quite sure, that is after he finishes testifying. In the event that he is required to go back to the lab, Dr. Bowen will come back down and take custody of the autorads and be present throughout the rest of the hearing.

COURT: Did I understand that Dr. Waye, does he finish before Dr. Kidd comes on, or does he have to be recalled for some purpose after --

MR. WALSH: No, he could be recalled before Dr. Kidd. He was to be -- his purpose of the recall from the Crown's point of view was after Dr. Bowen's testimony, and Dr. Bowen has finished testifying now, so --

COURT: It rather looks as though next week would finish up the Crown's end of the DNA and then we would have a week's break and before Dr. Shields was called on Monday, the 27th, or whatever date it is; the 27th.

We will recess now until Monday morning at 9:30.

(Accused excorted from courtroom.)

(Court Recessed at 1:50 p.m. to 9:30 a.m. on Monday, May 13, 1991.)

Continuation of Voir Dire Proceedings on May 13, 1991 commencing at 9:30 a.m.

(Accused present.)

COURT: This is the continuation of the voir dire. We are still missing Mr. Sleeth, I guess. He's still tied up, is he?

MR. WALSH: I haven't spoken to Mr. Sleeth, My Lord. I'm not sure; I can only assume he is.

COURT: Mr. Walsh, you have another witness?

MR. WALSH: Yes, I do, My Lord, and perhaps if you would indulge me just before I call my first witness. There were a couple of matters I would suggest are more in the nature of housekeeping. Last week when Dr. Fourney testified, he referred to some slides and if you remember, My Lord, the reproductions that I entered into evidence were not in colour and the slides were coloured. I have the colour reproductions and what I'm going to suggest is that I would enter the colour reproduction and perhaps what we could do is -- I believe one of them, for example, is the black and white reproduction is 63. I could add the colour reproduction as 63-A and we could staple it together if that was agreeable.

MR. FURLOTTE: That would be fine.

MR. WALSH: My Lord, I have a colour reproduction of what is now entered into evidence as VD-63 and I would move that that be marked as VD-63A.

COURT: You could staple them together, Mr. Pugh, and put the coloured one on top, perhaps.

(DOCUMENT MARKED AS EXHIBIT VD-63A)

MR. WALSH: I have, My Lord, what is a colour reproduction of what is now entered in evidence as VD-62 and I would move that that be entered as VD-62A.

(DOCUMENT MARKED AS EXHIBIT VD-62A)

MR. WALSH: I have, My Lord, what purports to be a colour reproduction of VD-59, and I would move that that be entered as VD-59A.

(DOCUMENT MARKED AS EXHIBIT VD-59A)

MR. WALSH: I have what purports to be a colour reproduction of VD-60 and I move that that be entered as VD-60A.

(DOCUMENT MARKED AS EXHIBIT VD-60A)

MR. WALSH: I believe that's it, My Lord. I can double check that at break time to make sure we've covered them all. The Crown is prepared to call its first witness. Call Dr. Ron Fourney.

DR. RONALD FOURNEY, BEING CALLED AS A WITNESS AND HAVING BEEN DULY SWORN, TESTIFIED ON THE VOIR DIRE PROCEEDINGS AS FOLLOWS:

DIRECT EXAMINATION BY MR. WALSH:

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

A. Ronald Mitchell Fourney. I'm section head of research and development for the Royal Canadian Mounted Police in their DNA typing laboratory which is currently called biology section.

Q. Dr. Fourney, I'm going to show you this particular document. Would you look at it and tell me whether you can identify it?

A. Yes, this is my c.v.

MR. WALSH: My Lord, I'd move to have this entered.

(DOCUMENT MARKED AS EXHIBIT VD-90)

Q. With the Court's permission, I would ask if I could lead Dr. Fourney through his c.v.

COURT: Right.

Q. Dr. Fourney, you have a Bachelor of Science in Biology with honours from Queen's University, is that correct?

A. Yes, I do.

Q. You have a Master of Science in Biology from Queen's University, is that correct?

A. Yes.

Q. And you have a PhD in Biochemistry from Memorial University in Newfoundland?

A. Yes.

Q. Dr. Fourney, I note under academic achievements and awards that you have a National Cancer -- or had a National Cancer Institute of Canada Research Fellowship, is that correct?

A. Yes, that is correct.

Q. Would you explain, please, what, if any, relation that particular fellowship or that particular type of work would have to DNA and/or DNA typing?

A. Yes, after I finished my doctoral training I went into a post-doctoral research program and I was awarded an N. C. I. C. Fellowship which was specifically awarded to study the relationship of cancer-causing genes in families and I used specifically the DNA typing procedures that we currently use now in the DNA application for forensic identity.

Q. Which kind of procedures would they be?

A. They would range from the extraction of DNA, quantitation, quality assurance of the DNA, the

running of southern gels, for instance, a restriction digest, and the probing of these patterns and the assessment of the patterns with respect to families in order to derive some form of molecular genetic relationship with respect to cancer predisposition.

Q. Would you use the RFLP technique in this regard?

A. Yes, exclusively.

Q. This particular position, it dealt with, I take it, human DNA?

A. Oh, yes, it was human cancer patients.

Q. In that particular regard, how many RFLP tests would you have conducted while you were such a Fellow?

A. It's sort of like asking a dentist how many teeth he's looked at. I would say I've looked at thousands of gels, probably.

Q. I note from your c.v., Doctor, under research and academic positions, and please tell me if there is any overlap, I note here that you were a post-doctoral Fellow Molecular Genetics and Carcino-genesis Laboratory, W. W. Cross Cancer Institute at Edmonton, Alberta?

A. Yes, that's correct.

Q. Is that the same work that you just discussed?

A. Yes, in fact, during my stay at the Cross Cancer Institute I was an N. C. I. C. Fellow for part of my training. I was an Alberta Cancer Board research scholar for the remaining part of my training. The initial part of my studies involved developing -- looking at cancer-prone families using the RFLP technology. The second part of my

training was the development of new diagnostic procedures for the assessment of cancer.

Q. Using DNA typing?

A. Yes.

Q. Would you tell me, Doctor, please, whether or not any of the work that you did at that point, whether or not that has been followed up or adopted by anyone in the fields, or is being used by anyone?

A. Absolutely. There's a number of publications stemming from my post-doctoral research. The lab that I actually left has developed a major breast cancer screening program which is one of the areas of specialty I was involved in and the current diagnostic procedure, I think, is actually being used clinically now.

Q. The procedure you formulated?

A. That I was part of a team formulating this technology, yes.

Q. I see, Doctor, that you were also a research advisor in nucleic acid detection on membrane supports for Gelman Sciences Incorporated of Ann Arbor, Michigan. Would you explain what your role was there and what, if any, relation that would have to DNA typing?

A. Basically, Gelman Sciences is one of many companies that provides biotechnology supplies to Molecular Genetics Laboratory. One of the prime supplies that they actually provide are membranes. It's the membrane that we use for binding the DNA in our RFLP analysis, and I was involved with testing some of their membranes and to write up and develop the technology that they currently have published as

their protocol for alkaline blot or transfer and hybridization procedures.

Q. And this alkaline blot or transfer or hybridization procedures, what application would that have to the RFLP typing?

A. It's exactly what we're currently using at the R. C. M. P. labs now, with some minor modifications, of course, but generally this technology is pretty well the same.

Q. Doctor, I see also that you were a molecular genetics specialist for the R. C. M. P. Central Forensic Laboratory in Ottawa. During that period of time what, if anything -- what was your role, what were your duties?

A. I was one of the two molecular genetic specialists initially hired and we were given --

Q. The other being Dr. Waye?

A. Dr. John S. Waye, yes. We were given the agenda to develop and implement DNA typing procedures and program for the R. C. M. P., and during my initial ten year first year with the R. C. M. P., Dr. Waye and myself pretty well established our initial data base. We developed many of the procedures that are currently being used now, and we documented these procedures in a series of written manuscripts that have been peer reviewed and submitted to journals.

Q. And I see also that you were for a period, approximately a year, in charge of operational support at the Molecular Genetics Section of the R. C. M. P. Central Forensic Laboratory. What were your duties and role there?

A. Well, actually the duties and role changed very little from my initial year. The only feature there would be that we had more individuals involved in the program and besides actually doing the work myself, I now had the -- I had to also direct the research and program of those other individuals under me, so I became in charge of what we, at that time, called operational support. It was essentially research and development for the existing DNA typing procedure.

It's also a program that is used to troubleshoot and to alleviate any problems that may occur in the actual forensic application of the DNA typing, and this would include such matters as unusual samples that have to be processed for DNA analysis. It can also include aspects of quality control and quality assurance.

Q. When you say troubleshoot, what -- how does that apply?

A. Well, generally it is very hard to predict the nature of the samples that come into our laboratory. The forensic nature of samples are very diverse, consequently we're constantly looking at samples that we might not have seen before and will have to develop a valid protocol in which to treat those samples, and before that actually gets released into the operational network, we'd have to justify it using various test cases and research, which is my major responsibility at the R. C. M. P. lab.

Q. What, if any, role would you have with respect to consulting or providing advice to others in the lab that are actually conducting the RFLP typing test?

A. In terms of the operational section?

Q. Yes?

A. Dr. Bowen is in charge of operations and generally we meet on a routine basis and discuss any problems that could exist in operations or troubleshoot concerns that we may have had to make sure that the operation is running smoothly with the best type of results, so it's a constant interaction between operations and operational support, or research and development as it is now called. That, I guess, is one of the advantages of having your lab next door. We share many of the same facilities and often we would know if something is going to be a concern from the research point of view long before it ever gets into the operational network.

Q. That would lead into your title, section head, research and development?

A. That is correct.

Q. That stems from being in charge of the operational support, is it?

A. Yes, essentially I probably associate it with the actual technical aspect of the science used in the R. C. M. P. labs more closely than any of the other individuals. Once it's released into operations, of course, Dr. Bowen assumes that responsibility. In my particular section I have a number of individuals that report directly to me and conduct specific projects under my guidance.

Q. I see also, Doctor, that you are an adjunct professor in the Department of Biochemistry in the Faculty of Medicine at the University of Ottawa, is that correct?

A. Yes, that's correct.

Q. And you teach courses in biotechnology, molecular genetics. Biotechnology and molecular genetics, what kind -- how does that apply to DNA and human DNA typing?

A. Well, I'm one of a number of lecturers who teach students the procedures and protocols and the basics behind the RFLP DNA typing procedures that are currently used at the R. C. M. P. lab.

Q. And these are medical students you are teaching?

A. They could be from a diverse number of disciplines, primarily biology and medical students -- biochemistry students, I should say.

Q. Doctor, you have a number of publications. First, perhaps, you have a number of professional associations. You are a member of the American Society of Human Genetics?

A. Yes.

Q. Does that apply to DNA -- does that have any application to DNA, DNA typing?

A. Yes, it is basically the background behind many of the diagnostic tests and the various molecular genetic principles that are being developed now stem from recombinant DNA research.

Q. And the Canadian Society of Forensic Science, you are a member of that as well?

A. Yes, I am.

Q. And does that have application to DNA and DNA typing?

A. Oh, yes, DNA typing is firmly entrenched in forensic science in both Canada and the U. S.

Q. You are also -- it notes here under professional associations that you are a member of TWGDAM, the Technical Working Group on DNA Analysis Methods,

"A North American forensic organization evaluating and developing the standards in molecular technologies for forensic applications.." Can you explain? You are a member of that particular organization?

A. Yes, I am.

Q. And what is that organization attempting to do?

A. Essentially, TWGDAM is an organization that is sponsored by the F. B. I. and we meet routinely approximately three times, maybe four times a year, I guess, amongst those laboratories currently participating in DNA typing throughout North America. I'm one of the two representatives, the other being Dr. Bowen, for the R. C. M. P. at the technical working group. During the course of our meetings, we will discuss the application of DNA technology in forensics, new developments in the technology, the statistical assessment and various aspects of data basing and generally it's a working relationship amongst -- I guess there might be 26, 27 labs now participating throughout North America.

The ultimate goal behind this association is to develop a generalized standard of protocol of DNA typing that has very high reliability and validity throughout North America, while at the same time, remaining standard such that results are comparable from lab to lab.

Q. Now, Doctor, you are also a member of the Editorial Board of Biotechniques, the Journal of Laboratory Technology for Bioresearch?

A. Yes.

Q. What, if any, application would that have to DNA or DNA typing?

A. Well, generally biotechniques is one of many journals that specifically deal with the application of DNA technology and being an editor, reviewing editor, I routinely peer review articles for that journal and make comments with respect to the size and consistency of results on those articles.

Q. And those articles that you peer reviewed, they included the RFLP technique, aspects of the RFLP technique?

A. Oh, yes, all aspects of DNA typing.

Q. You are also a member of the Canadian Society of Forensic Science DNA Committee?

A. Yes.

Q. Now, you have a summary, Doctor, you say, "A committee formed under the auspices of the Canadian Society of Forensic Sciences whose main purpose is to address issues and set guidelines of quality assurance, methodology, proficiency testing and standardization in DNA Typing for forensic sciences in Canada." Is that a fair summary of the role of the DNA committee?

A. Yes, it would be a fair summary.

Q. Doctor, you've also noted under here that you've been a moderator and the chairperson of various meetings. One, you were the moderator of the International Symposium on Human Identification Data Acquisition and Statistical Analysis for DNA Laboratories, Promega Conference in Madison, Wisconsin, is that correct?

A. I have been a moderator twice, in fact. The first meeting that occurred, I believe, in '89, and just recently, I guess it would be April -- March of this year, I was also a moderator in that meeting.

Q. What issue or what types of things do you deal with? Does it have any application to DNA and DNA typing?

A. Definitely. Basically, just the most recent meeting besides being a moderator, I also gave a paper and it was strictly dealing with the forensic application in DNA technology from, not only a forensic point of view, but we had members from the American Armed Forces give a talk. Some of the -- there's a Swiss doctor who also is involved with genetic identity using DNA protocols, so pretty well this entire meeting is set up to look at some of the concerns and questions and present new information with respect to DNA analysis.

Q. And who, Doctor, would attend that kind of meeting, all scientists, all forensic scientists?

A. A great majority of the scientists attending these meetings are certainly forensic scientists. Anyone who is interested in forensics and the application would certainly go to these meetings. There's also a fair number of lawyers that attend these meetings as well.

Q. Doctor, you're also a chairperson of the DNA Mini-Symposium, the Canadian Society of Forensic Science in Edmonton, in 1989?

A. Yes.

Q. And that, I take it, dealt with the forensic aspects of DNA typing?

A. Yes, that was actually the first time that the

Canadian Society of Forensic Science actually set up a small mini-symposium dealing specifically with DNA analysis and forensics.

Q. And you are also a chairperson and coordinator of the DNA Mini-Symposium, Canadian Society of Forensic Science, in October of 1990?

A. Yes, that was a larger symposium. There was certainly a lot more interest and I was tasked with coordinating, once again on the Canadian Society of Forensic Science, a symposium where people who are interested in the application of this technology can meet and discuss the results of their own research as well as hear others.

Q. Doctor, I note as well that you've just come back from a conference in Riverside, California, is that correct?

A. Yes.

Q. And you had some participation in that conference. Could you please tell the Judge about that?

A. Yes, I was, once again, asked to represent the R. C. M. P. to discuss the application of RFLP analysis, both its potentials and limitations with respect to forensics at the Riverside conference. There was a great number of speakers at that conference, both from the legal side as well as from the research side, and scientific sections.

Q. Was there a cross-reference of those people from across North America attending that conference?

A. Yes, that particular conference was very well attended and I was quite surprised at the number of members from the legal community that had attended that particular conference

Q. Would that have included lawyers and judges?

A. Yes, in fact, not only were they attending, but many of the people that were actually giving the talks, the speakers themselves, there were both prosecution as well as defence lawyers giving talks on DNA analysis, and several prominent judges who have played a role with respect to DNA typing and its acceptance in North America.

Q. Doctor, I note again you have several publications, or many publications, I should say. I just touch on a few. Could you tell us, please, I note here you have a paper, "A simple and sensitive method for quantifying human genomic DNA in forensic specimen extracts," a paper that you co-authored along with Dr. Waye and several others? Does that apply to DNA and human DNA typing?

A. Yes, that's actually our method of quantitation and one of the steps that we take to evaluate the amount of human genomic DNA that is present in order to go through the RFLP or VNTR analysis.

Q. I believe that paper is actually filed as an exhibit in this particular hearing. Another paper, Doctor, I see you co-authored with Dr. Waye, "Agarose gel electorphoresis of linear genomic DNA in the presence of ethidium bromide: band shifting and implications for forensic identity testing." You were an author of that particular paper?

A. Yes, I was.

Q. That, again, is entered in this particular hearing. You were also a co-author with Dr. Waye of the "Identification of complex DNA polymorphisms based on variable number of tandem repeats and restriction site polymorphism." Again, I believe

that's entered in this hearing. That has to do with RFLP typing and the forensic application at the R. C. M. P. laboratory?

A. Yes, these papers are all stemming from our initial year of development that Dr. Waye and myself participated in.

Q. And along with -- you also co-authored with Dr. Waye and Dr. Bowen in the "Forensic analysis of restriction fragment length polymorphism: Theoretical and practical considerations for design and implementation." Is that what's known as the Promega paper?

A. That's the first Promega paper. There's going to be a second Promega paper as well.

Q. You also are an author on the fixed bin paper?

A. Yes, I was collaborator in the writing and formatting of that particular paper as well as numerous other individuals, I might add.

Q. You have given -- I see also, Doctor, that there's been a number of abstracts and presentations that you have made. A number of those abstracts and presentations deal with human DNA, human DNA typing?

A. Yes, they do.

Q. In particular, forensic application?

A. Certainly in the last three years they have.

Q. You have attended conferences in various parts of the world involving forensic DNA typing, am I correct, Doctor?

A. Yes, that's correct.

Q. Would you please tell the Judge where you have gone and what kind of meetings these would be?

A. I've been to a number of conferences. It's difficult to actually remember the number.

Q. I see one here, Doctor, and I'll show you.

A. Yes, that was a meeting that occurs every three years where it's an international meeting of forensic associations, and generally it's a large meeting and it's well represented throughout the world. At that particular meeting there is a great number of individuals from right across just about every forensic lab that would actually be doing any kind of application of various disciplines would have attended that meeting, including DNA analysis. And I might add, at that particular meeting a large section of the actual meeting was devoted to DNA typing.

Q. Doctor, in what field of science do you belong, general field of science would you consider yourself belonging to?

A. My doctorate is in biochemistry.

Q. And biochemistry has applications for DNA and DNA typing?

A. Yes, biochemistry is essentially the -- is the science dealing with chemistry of a living organism and the structure and function of the components of that organism. Certainly within the cell are nucleic acids and nucleic acids are part of -- there's a division, there's DNA and RNA, and if you are a biochemistry student studying nucleic acids, you become a molecular biologist. Essentially, molecular biology would be a sub-discipline of biochemistry.

Q. Doctor, at the R. C. M. P. laboratory have you had any experience with respect to actually doing forensic typing yourself?

A. Have I participated in the case work?

Q. Yes?

A. Yes, I have some of my own cases, of course, but generally what they would prefer me to do is utilize the expertise that I've acquired along with my research team to help other individuals that are in operations so that they can achieve successes on some of the more unusual case work.

Q. Are you familiar, Doctor, with the issues involved in the forensic application of RFLP typing as it applies to the courts in Canada and the United States?

A. Yes, I am.

Q. Have you ever actually attended any court proceedings in relation to RFLP typing, DNA typing?

A. Well, I testified in this court and I was also consultant to the Crown on several cases, the first few cases, in fact, with the R. C. M. P. was taken to court with respect to DNA analysis.

Q. That would be the McNalley case and Bourguignon?

A. Yes, the first case would be McNalley in '89 and the first murder trial, actually, was Bourguignon which was -- I guess the trial itself was January of this year.

MR. WALSH: My Lord, at this time I'm going to offer that Dr. Fourney be declared an expert in the field of biochemistry and in the area of DNA technology and testing procedures, and forensic DNA typing.

COURT: If one were to say biochemistry and DNA technology and testing, wouldn't that cover the RFLP aspect?

MR. WALSH: It may, My Lord. I just was being specific in terms of the area of DNA technology and testing procedures and forensic DNA typing. Certainly, you pointed out that DNA typing could be included under the umbrella of DNA technology and testing procedures, but I wanted to emphasize the fact that he has experience in forensic DNA typing. It will become important should the Court be assessing the relevant experience of experts in terms of weighing their opinions on certain matters.

COURT: Do you have any questions, Mr. Furlotte?

MR. FURLOTTE: I have no questions.

COURT: Well, I think Dr. Fourney's expertise in the fields mentioned has been adequately demonstrated and so I declare him an expert for the purpose of this trial in the fields of biochemistry, DNA technology and testing procedures and forensic DNA typing.

MR. WALSH: Yes, My Lord, thank you.

COURT: You also had something added about RFLP, or RSP or whatever they are.

MR. WALSH: No, forensic DNA typing is fine, My Lord. I'll try not to overdo it. Dr. Fourney, would you please tell the Court, you're in research and development, is that correct?

A. yes.

Q. Does research and development have anything to do with quality assurance?

A. Yes, of course.

Q. Would you tell us, please, first of all what is quality assurance and what role do you play in this

aspect for the R. C. M. P. lab?

A. I think I should start off by defining what quality control is. Quality control is steps taken by a laboratory to ensure the reliable and accurate results are performed. Quality assurance is the evidence or documentation that, in fact, quality control has been carried out properly.

Q. Again, what role do you play at the R. C. M. P. laboratory with respect to quality control and quality assurance?

A. It is one of my principal requirements in my position to ensure that adequate quality control and quality assurance is maintained at all times in the laboratory, and that the operational side of the laboratory retains a very high quality control product to which we use for DNA analysis, and that the results obtained through the protocols, procedures, and various items that are used within the laboratory all meet such a high quality of standard that we know that our results are reliable.

Q. Doctor, I'm going to show you this particular document here. Would you look at it for me, please, and tell me whether you can identify it?

A. Yes, this is in fact one of the initial guidelines drafted by the technical working group for DNA analysis on quality assurance programs for RFLP analysis in forensic labs.

Q. Did you have any involvement in the actual drafting of these guidelines?

A. Yes, I was part of the group that was responsible for drafting these guidelines.

Q. And this was to apply to -- this is the TWGDAM group?

A. That's correct.

Q. And this particular guideline, or the heading of this is "Guidelines for a quality assurance program for DNA restriction fragment length polymorphism anaylsis"?

A. Yes, I'd like to point out that this is the initial draft and there is a subsequent second draft which has just recently been released and covers some new avenues of DNA analysis, and I was also a member of that committee.

Q. When you say new avenues of DNA analysis, what are you referring to?

A. In the near future we'll probably be looking towards a technology called polymerase chain reaction, for instance, and the new guidelines also include that particular specific technology.

Q. For the purposes of this case, PCR would not have an application, would it?

A. No, for the purpose of this case it has no application.

MR. WALSH: I would ask that this particular guideline be entered.

COURT: This will be VD-91.

(DOCUMENT MARKED AS EXHIBIT VD-91)

COURT: I'm assuming here, as I have done earlier, that copies of these reports and so on have been given to Mr. Furlotte?

MR. WALSH: Yes, My Lord, with notice. I have here --

COURT: VD-91.

Q. Yes, My Lord. I refer you to this particular document. Would you tell me what that document is, please?

A. There's actually two documents in here.

MR. WALSH: Excuse me for a second, My Lord. I guess there are. Somehow, My Lord, I had another document bound at the same time. I believe the document has already been entered into evidence, another document, and I just ask for the Court's indulgence for a moment. Perhaps we'll start over, Doctor. Would you look at this document and tell me what it is?

A. Yes, this is the quality assurance document that has been prepared by chief scientist, Pat Allain, for the R. C. M. P. and it specifically covers the quality assurance program that we currently have in place at the R. C. M. P. laboratory. It's specifically drafted along the guidelines of the TWGDAM document, but it makes a special -- basically it's drafted under the R. C. M. P. manual of quality assurance that is already present in most of the forensic disciplines that the R. C. M. P. have.

MR. WALSH: I move to have this entered, My Lord.

COURT: That would be VD-92.

(DOCUMENT MARKED AS EXHIBIT VD-92)

Q. Doctor, again I'm going to show you VD-91 and VD-92 and I'm going to ask you if you would please tell His Lordship how these particular documents apply to the DNA testing laboratory. I note for example that the latest, VD-92, is dated in -- 91, it's dated February 18, '91, and I would like to know how these particular documents have applied or whether or not they in fact have applied to the R. C. M. P. lab and how they've been applied?

A. Initially the technical working group for DNA analysis drafted a guideline which was considered a minimal guideline of which a lab practising DNA analysis would have to maintain in order to have accurate, reliable and valid results. This document was the first document drafted, and subsequent to that it became required by the R. C. M. P. to draft a document that would encompass the actual TWGDAM document, but meet the format that the R. C. M. P. manuals already had in place.

Q. Now, the R. C. M. P. manuals that are already in place, they would apply to?

A. All disciplines, and specifically it addresses special concerns and relates back to other manuals that are already in place by the R. C. M. P. such as training manuals, for instance, so that it builds upon preceding guidelines for other disciplines as well as other aspects of forensic science within the R. C. M. P.

The person that coordinated this effort was chief scientist, Allain, and I was one of several participants in a subcommittee at the central forensic lab where we analyzed the two documents here, had several drafts formulated and this was the final draft of that, final copy, which our lab is currently using as their quality assurance guideline.

Q. Doctor, we had evidence previously that the lab opened approximately in October of '89, if I may use the colloquial 'open for business'. Would there have been any guidelines in place at the

time, say for example, October of 1989, quality assurance?

A. Well, certainly the TWGDAM guidelines and being tied closely to the drafting of these documents, we would be aware of any changes that were occurring or going to occur in the future, so I would say that our laboratory has always practiced fairly high standard of quality control and quality assurance.

MR. WALSH: Mr. Clerk, I'm looking for VD-42, 43 and 44. I will refer you to what's been marked on this hearing as VD-42. Do you recognize that document?

A. Yes, this is our first DNA typing protocol manual that was drafted by myself, Dr. Bowen and Dr. Waye.

Q. And VD-43?

A. This would be an amended document taking into account newer developments and procedures.

Q. VD-44?

A. This is the current document that we have in place that is called our DNA typing protocol manual, and in this particular document there is a great amount of detail has been added to aid in the training of our forensic scientists in the DNA program.

Q. Doctor, could you tell me what impact those protocols would have with respect to the testing done in this particular case, whether any of those protocols would have had an application to this case?

A. Yes, Doctor Bowen would have followed whatever the current protocol was at that particular time for the RFLP analysis that he had conducted.

Q. Any of the changes in the protocol between the three of them, would any of the changes invalidate the protocol that would have been previously followed?

A. No.

Q. Could you please review with us, Doctor, what controls were in place at the R. C. M. P. DNA lab to ensure that the lab uses top quality materials? That comes under quality assurance?

A. Yes, one of the aspects of quality assurance we have to address is to make sure that at all times we're using the best materials which we can get a result that we know would be a reliable result and valid, and there are a number of different components to the DNA typing procedure that have to be evaluated. For instance, membranes, this is what the DNA actually binds to and it's important to have a good quality membrane. Not all membranes are alike, and in fact, we're very specific on the membrane that we choose to do our DNA analysis on and we will actually look at the lots of membrane and run a number of validation studies on these membranes to make sure that before it's released into not only the research lab, but into operations that it will give us consistent results.

Other aspects of quality control with respect to materials include such elements as the restriction enzyme that we use. Here, again, we look at lot specific enzymes from one particular manufacturer and we will evaluate its ability to cut the DNA properly, consistently. We look at the agarose, that's the actual material that forms

the gel where the DNA components are run electrophoretically and separated. There's many different types of agarose. Once again, we're very specific on the brand and grade of agarose. The probes that we actually use to do our hybridization, these are lot-specific probes. We often require a small amount of the lot to be sent to us where it undergoes fairly rigorous examination both in population blots and research blots. There's a number of test procedures that we actually use to make sure that it will bind to what we want it to bind to, human DNA, that it will give a consistent result. All these things are tested prior in the research and development section of our laboratory under my direction before they're actually released into operations.

Q. What, if any, concerns do you have about any of the materials that were used in relation to, and noted in any of the protocols?

A. Well, in any procedure we see improvements, of course, and with new developments we will shift our technology, and it's important to recognize that quality control has to shift with respect to new developments in technology and the specific forensic nature of our samples. So we're very flexible in our quality control program to look at newer and better procedures and materials to use.

I would say that the materials that were used by Dr. Bowen for this case would be the best that we had at that particular time.

Q. Could you review with us, please, apart from the material, the quality of the materials that are

actually used in the RFLP typing test, would you tell us something, please, review the controls that are actually used in the application of the technique to ensure accurate results?

A. There is a series of controls, of course, that are used, controls being known steps or tests that will give a result that is predictable such that if you get the wrong result, you know that that test is not reliable. Consequently, controls are an integral part of any of the procedures that we use. For instance, in the actual gel itself, the running of the RFLP technology, we would have a male and female cell line control. This is simply DNA that is uniform that we have run many, many times. We know what the established typing pattern will look like. We know the sensitivity of the probes to be expected. If we do not get the required result, then we know that that particular test is invalid.

We would also have the cutting of the DNA, for instance, by the enzyme. We would have a control in there to assess whether or not it is cut properly. There's a series of steps within any of the protocols we use that will allow us to not only predict what to expect, but if we do not get the expected result, we can certainly troubleshoot and find out why it hasn't worked properly, and generally, for instance, if a sample might not have been digested properly or that is cut into small fragments suitable for RFLP analysis, that quickly becomes evident in what we call a test gel which assesses the actual restricted pattern, the fact that these fragments have been cut up into small pieces. If that

hasn't occurred, then the predefined pattern that we would see in this gel would give us a result that was inconsistent with a sample that has been digested properly.

Certain steps are taken, then, to go back and repeat that procedure so that the DNA is cut properly.

At all steps that we can, it is documented as well, both in the actual notes of the investigator but also in certain forms that we use, stepwise procedure so that we know in the order we've taken to produce a result and the result that was actually attained. Often the reports are supplemented with photographs, for instance, showing the test gel that has been digested properly. The actual analytical gel that is the gel where the actual DNA typing result has been conducted on, that it has been run properly, the material itself is in the lanes, and also, the gel itself would contain markers, for instance. These markers are integral to the actual measurement of the bands and the actual pattern of these markers give a consistent, uniform associated molecular weight and if something has gone wrong we'll immediately know about it.

Q. Doctor, are you familiar with the quality assurance programs and quality controls used in other forensic laboratories, either in Canada or the United States?

A. Yes, very familiar.

Q. Could you, perhaps, give us some comparison in terms of controls as they compare between the F. B. I. and the R. C. M. P. system?

A. I would like to think that we both have a very high standard of quality assurance and control, and that many of the controls that we use, although they may not be the exact same DNA, they would give the same results and tell the investigator whether or not an experiment has gone wrong, for instance.

Each forensic lab that participates in DNA analysis has a very similar type of protocol so that they can evaluate the performance of their testing procedures.

Q. Is there anything that, perhaps, the R. C. M. P. lab do somewhat differently?

A. There's a few --

Q. In terms of controls?

A. In terms of controls?

Q. I'm thinking in particular, Doctor, we had testimony and His Lordship said he never wanted to hear the word ethidium bromide, but I'm going to ask you where that would fit into the scheme of things?

A. Well, actually ethidium bromide is a minor component. Essentially, this is a dye that technically inter-collates. Essentially, it means it binds DNA and causes a colour fluorescence so that you can visualize the DNA pattern in a gel. Generally this is done under UV fluorescence and you can photograph the pattern, so it allows you to look at the DNA to make sure the pattern is properly run and that the DNA has been cut properly.

Some labs in the U. S., for instance, and other parts of the world actually add this particular dye prior to the electrophoresis of the gel.

In our particular case, we add it only after the gel has finished running or the electrophoresis is over. The practical reason for this is actually a concern of health because ethidium bromide is a known mutagen and most mutagens are carcinogenic. I particularly don't like my laboratory personnel involved with such a dangerous substance, to start off with. If you control a small amount of this material too, it's better for the safe elimination of the material, so economically it's important that you only generate a small volume of this material. If you add it to the gel at the beginning, you're going to end up with liters of material to dispose of as opposed to a few, say, 200 microliters.

Q. Apart from the carcinogenic --

A. -- 200 mils, I should say.

Q. -- concerns, what, if anything, did your lab notice about its actual application in the technique and the use of technique?

A. In our particular protocol using the tris borate EDTA buffer system, it was evident that ethidium bromide present in the gel would cause aberrant pattern such that there would be a tendency for shifting to occur.

Q. What if anything else do you use in your system that is not used in, for example, the F. B. I. system?

A. There's a series of probes that are not used by the F. B. I. They have a certain routine that they follow that works very well for them. We use a probe D10S28 or TDQ7. Now, that's been investigated

by Dr. Budowle's research group at Quantico and they certainly have data bases on it, but the fact that it's not used at the present time by their Washington lab as the case were doesn't mean that -- I don't consider that a major change in their protocols.

Q. You've investigated D10S28, have you not?

A. Oh, yes. At the very early onset of our DNA program, there is a number of probes that were available for evaluation. In the beginning, actually, most of these probes were right from the person that identified and cloned these, so these were research laboratories long before many of the commercial labs got involved with the production of these so-called forensic probes.

We had a number of these in our lab and one of the first things that I was involved in was to actually look at all these probes with respect to DNA typing and to evaluate them in order with respect to their consistency, their sensitivity, their application generally in DNA analysis. One of them was TBQ7.

Q. D10S28?

A. D10S28, yes, that's correct.

Q. Are you familiar with the -- I'll refer you to the summary chart here, Doctor, VD88. Are you familiar with the probe shown here, D2S44?

A. Yes.

Q. D1S7?

A. Yes.

Q. D4S139?

A. Yes.

Q. D17S79?

A. These are all common probes.

Q. D16S85?

A. Yes.

Q. D7Z2, that, we understand, is called a monomorphic marker?

A. Yes, that's in fact another change in the procedures that we use that some labs have chosen not to use, and that would be a difference.

Q. What is the purpose of a monomorphic marker? Does it add to the system or detract from it?

A. Oh, it certainly adds to the system. The monomorph allows us to assess the measurement precision within a gel because it gives a consistent pattern after it's cut. After DNA is cut with the restriction enzyme, HaeIII, we expect to see a fragment at 2,731 base pairs, so it immediately allows us to investigate whether or not the gel is run properly and allows us to quantitate the measurement precision of that particular size length -- or that particular lane with respect to the size of the marker.

The other thing that D7Z2 does as well that I find very practical is that it allows you to assess whether or not the DNA has been cut properly, so it's an extra test thrown in there that confirms proper restriction digest, for instance.

Q. To leave ethidium bromide, one final question. By applying the ethidium bromide at the end of the electrophoresis, do you consider that taking something away from the system or adding something to the control of the system?

A. In our particular case, it has the advantage that it allows us to use, certainly in the tris borate EDTA system without any apparent shifting, so it certainly adds to it.

Q. Now, we heard testimony last week, or the week before, with respect to slot blot quantification and I understand that that's something that was actually developed for forensic use at the R.C.M.P. laboratory?

A. Yes, in fact, Dr. Waye and myself were involved with that as well as a number of investigators with the F. B. I. laboratories.

Q. And has that been picked up by other laboratories?

A. Yes.

Q. Is it being used by other laboratories?

A. Actually, it surprised me at the last meeting that I attended at Promega the number of labs that are using a slot blot quantitation procedure. This we thought would be a difference at the beginning, but it seems to be a favorite protocol now for evaluating small amounts of human DNA, and it certainly is becoming more prevalent.

Q. And the use of the sex typing probe, DYZ1?

A. That's an extra test that we like to perform as our lab. It gives you a bit more information with respect to the nature of the sample, whether it be male or female, and also it has the advantage that after cutting with HaeIII, it acts as a monomorph as well because you expect to see a fragment at 3,565 base pairs. So once again, it gives you the ability to tell whether or not the sample has been run properly.

Q. Doctor, I'm going to ask you some questions, please, with respect to validation, validation studies. Perhaps if you would, first of all, tell His Lordship and the court what you understand by the term validation or validation studies and how it applies to quality assurance and the program at the Ottawa lab?

A. Any lab in general carrying out clinical diagnostics or forensic analysis has to have a valid set of procedures. Validity in a scientific sense essentially means that you're going to get the right answer. Reliability means that you're going to continually get the right answer.

In order for a test to be considered valid, we have to examine its performance such that we would run a number of samples over and over again to look at whether or not what we expected to have happened actually did happen. If it involves a new extraction procedure, has it worked, for instance? Is it a valid procedure? Will it give you consistently high molecular weight DNA for analysis? Any step before it is turned over to an operational laboratory has to be checked and rechecked so that we know it will perform properly, and that I would consider as a validation type study.

Q. What, if any -- how did the R. C. M. P. approach validation of their particular system validation studies?

A. Well, we were very fortunate when we started into our DNA program because it became obvious that the undertaking to develop a DNA analysis program for the R. C. M. P. was going to be quite a major step,

and at the same time, the F. B. I. were also partaking in the development of their procedure. So early in 1988 we drafted a formal document with the F. B. I. such that we would share and collaborate all aspects of DNA analysis pertaining to the forensic application.

As a consequence of that, we even preceded TWGDAM with respect to setting up standards, for instance, and much of the validation work for our program was actually performed in conjunction with the F. B. I., and in many aspects, the F. B. I. performed, for instance, what we call the environmental insult studies. These would be what happens to DNA when it's exposed to such things as common household items, gasoline, bleach, et cetera. In turn, we chose to look at other aspects of validation such as, for instance, one of the ones that we're particularly interested in is luma light. This is a fluorescent light that is used to detect biological fluid.

We ask simply the question, "Does luma light have any effect on stains, for instance, for DNA analysis," and we ran a series of studies there to show that it had no effect. Many of our validation studies are done in conjunction with our training program because one of the last features of any of our candidates who are going to be trained as molecular genetic specialists, they have to do what we call a mini-research project which is conducted under my group's advice and consultation. Many of the validation studies that we have performed have been done by our training person as

well as our own research and development teams.

Q. Dr. Fourney, are you familiar with the criticisms that Dr. D'Eustachio levelled at the F. B. I. validation studies in, I believe it was the Yee decision in the United States?

A. I certainly read the Yee report and I've seen some of his criticisms, yes.

Q. Do you know whether or not the F. B. I. have responded to any of those criticisms in any fashion in terms of actually preparing other -- doing any further work?

A. Yes, in fact, there's a publication that's going to be in September's issue of Journal of Forensic Science where they have pretty well covered most of the criticisms.

Q. That were -- ?

A. That were brought up in the Yee decision. It's a very extensive study of over 1,600 samples, I believe, of various environmental insults including temperature, soil conditions, fabrics. Everything was looked at with respect to the validity of DNA analysis and the actual summation of that paper was clear that a test performed for DNA analysis under various unusual conditions that you'd expect forensic samples to undergo, either had no result or proved to be a reliable result. In other words, if it gave a result, it would be the expected pattern that would be seen from a, say, a standard that had no insult given to it.

In other words, you could look at it and determine whether or not a match has occurred.

Q. What is the biggest problem with respect to environmental insults and the forensic contamination? What is the biggest problem that it caused in terms of DNA or obtaining sufficient DNA samples?

A. I would certainly rank one of the concerns would be degradation, and, of course, degradation with respect to DNA come from a number of different avenues. For instance, just the addition of soil to DNA stains or, for biological substances, for instance, blood and soil mixed together. For some reason it prevents adequate extraction of the DNA.

So in general, most of the studies I've seen relate to the recover of DNA itself.

Q. Okay, assuming, Doctor, in your opinion and based on your experience and your readings of others' studies, if for example, hypothetically, your slot blot quantification revealed -- and your quality control of your yield gels revealed that you have extracted high molecular weight human DNA; in your opinion what effect would environmental insults have on the actual test procedures in comparing -- and in comparing band patterns?

A. That would be minimal, or no effect at all. You would have to obviously look at each particular case in turn, but it's been my experience that if you get high molecular weight DNA, you can certainly get a reliable band pattern. It's very unusual to get a DNA pattern that is different from that expected from the controls.

Q. What, if any, concerns would you have with respect to the actual restructuring of the DNA within the cell as a result of environmental insults?

A. Well, certainly from my own experience in cancer diagnostics, I know that, for instance, DNA exposed to UV light causes what we call thymine dimers, and that's a structural alteration of DNA pattern. So that would be one change that could occur.

Another aspect that I'm becoming more and more aware of is certain unusual fabrics have fluorescent dyes associated with coloration of the material. Some of these dyes carry a stain or a dye not unlike ethidium bromide, and this dye can actually bind to the DNA and cause various shifting. But each one of these particular cases you have to look at on a case-by-case basis because it's very difficult to know in advance whether or not it would have any effect on this.

And even if it has an effect, you can often go back to the DNA itself and recover the DNA without any kind of material or stain associated with it.

Q. Doctor, I'm going to show you -- perhaps I'll show you this particular document and ask you to look at it for me?

A. Yes, this is a paper that is currently in press for the Journal of Forensic Science and it entails, essentially, the studies of contamination of environmental insults that the F. B. I. conducted for validating RFLP procedure.

Q. This is the document that you've actually referred to as the most recent study?

A. Yes.

MR. WALSH: I would move to have this entered, My Lord.

(DOCUMENT MARKED AS EXHIBIT VD-93)

MR. WALSH: The heading on the document, My Lord, is DNA analysis by restriction fragment length polymorphism of blood and other body fluid stain subjected to contamination and environmental insult. Now this is a document that I've just received in fact late last night. I gave it to Mr. Furlotte the first thing this morning. It is in press for September, 1991, in the Journal of Forensic Science.

COURT: Do I understand, this is the F. B. I. document you referred to earlier which, you said, covers the Yee criticisms. What did you mean by 'covers'? It answers, or it explains?

A. There are certain concerns that the Yee report had with respect to controls, for instance, that the F. B. I. might not have had in place, or the precision of their measurement, and certainly this study has gone back and either supplemented the original study with new research or, in fact, reformatted the original research so that it could be seen that it actually was covering or providing the information that was missing in the original Yee report.

Q. I'm going to leave that with one final question. You had mentioned in your testimony that your conclusions, or the conclusions that you've seen, relate to whether you can get a result at all or a correct result. Am I interpreting that properly?

A. I'm not sure what --

Q. Okay, you had said something previously in your testimony with respect to the conclusions that you can draw from what environmental insults can do?

A. From this paper.

Q. Yes?

A. Yes. I think if you read the abstract of the paper it clearly talks about the fact that you either get a result that is reliable, that is, it will match the standard, for instance, that hasn't been exposed to the environmental insult or contamination, or you simply don't get a result.

Q. Because of why? Why wouldn't you get a result?

A. Presumably because of lack of DNA.

Q. Meaning you wouldn't be able to recover it?

A. Either you're not recovering the DNA or it's of sufficient low molecular weight or it has degraded to the point that you will not get an RFLP typing result.

Q. Doctor, I'm going to ask you what role if any you played in determining the match window presently used by the R. C. M. P. DNA system, and if you have played a role, would you explain your involvement in how the window was determined?

A. Yes, one of my major avenues of research at the R. C. M. P. was developing what you are calling a match window. Essentially what this really is is a means of evaluating measurement precision of the entire system. The bottom line of our technology is to run bands, DNA fragments or bands, out onto a gel and to assess whether or not they are going to match or not match.

The concern we have, and any lab has, with respect to match window is how deviant can a match be with respect to being the same or different and still be considered a match, and this addresses strictly the ability of your system as a whole to

run the fragments out onto a gel, the extraction of the DNA, etcetera, and the final product, more or less. You have to assess whether it's not reliable -- whether it's reliable or not. What we did was to develop a measure of a precision, so to speak, so in other words, if this band is a match, what size is the band? How altered can it be and still be considered a match?

We went into it in two different modes. One, we used pristine blood samples of which DNA was extracted. It was run onto gels, and it was probed with the monomorphic probe, D7Z2, and we simply asked the question, how often does the band that we were supposed to see at 2,731 base pairs actually deviate from the 2,731 base pairs. And if the samples are essentially the same, you would expect no deviation. The fact that all of us shared this monomorphic band, a very simple and easy was to assess measurement precision was simply to take our data base samples. These are 600 or 700 samples, for instance, and probe them with monomorph and across the data base we would ask the question, what is the average size of band we would see with the monomorph. From that, we would know what the deviation would be to expect, and if I can refer to my notes, I can certainly give that information to you with respect to monomorphic precision.

Q. On the pristine samples?

A. Yes.

Q. With your permission, My Lord?

COURT: Yes.

A. The initial assessment of this monomorphic band was conducted on 594 samples and we found that after assessing all these fragment sizes, that essentially deviation from the expected 2,731 base pairs across all 594 -- 99.7 percent of all the samples we measured, that is, 592 out of 594 were plus or minus 2.6 percent, I have here.

So essentially that would tell us that virtually all the samples but one were within the match window of what we call 5.2, so plus or minus 2.6. Then we proceeded to actually go through and look at it in a more detailed manner, and it became evident that in actual fact, if you -- Across the actual gel, for instance, if you measured the monomorph between existing flanking lanes, the average deviation was 13 base pairs from the actual 2,731. This would being to slightly increase as you had more lanes separating the samples. For instance, adjacent lanes were 11.4 base pairs, lanes that were separated by one lane was 13.4 base pairs, by two lanes was 15, by three lanes was 18.5 base pairs.

The actual size difference is probably more meaningful than the actual mean size difference and across the entire data base flanked by the same markers, so that would be any of the samples we measured between two existing size standards, the maximum deviation we saw was 2.9 percent from the expected 2,731. The maximum difference we saw across all lanes on the same gel was 3.2 percent and if you take into account intragel comparisons, between gels and within a gel, we can accomplish all measurements within 99 percent if we used a

maximum difference of 5.2 percent.

Q. Now, that was with respect to these pristine samples, what you referred to as pristine samples?

A. Yes, these would be samples that we would expect not to deviate because of environmental insult. Essentially they were collected by various blood banks, delivered to the R. C. M. P. lab and we extracted the DNA from these samples.

Q. What, if anything, Doctor, did you do with respect to forensic case work samples?

A. Well, the other aspect that becomes very important is we're not dealing with pristine samples, obviously, from a forensic point of view and we wanted to know, for instance, what was the measurement precision that we would expect to see on the average case sample, the forensic sample that we have no control over. How would it fare up with respect to deviation.

Q. What, if any, conclusions did you draw from that?

A. Well, what we actually did in this particular case was we analyzed our first ten cases, the first ten R. C. M. P. cases, and we did a match comparison band by band between what we considered to be the control DNA substance and the fragment generated from that, and the substance, the DNA fragment, generated from the forensic substance, the unknown. Essentially, we made 502 pair-wise match comparisons and asked the question, "What was the maximum deviation we saw from the known measurement versus the unknown forensic material?"

Within -- out of 502 comparisons, we found that if we used a match window of 5.2 percent, 99 percent of all our declared matches would fit, so that is

497 observed events. If we used a 5 percent match window, that is, a maximum deviation of 5 percent, 98.6 percent of our samples fit. Three percent match window, 94.4 percent; two percent match window, 86.1; and one percent, 61.4 percent.

Q. How does it compare, Doctor, with other -- you said you were familiar with other laboratories, forensic laboratories. How does that compare in terms of other forensic laboratories?

A. Our match window is plus or minus 2.6, or the entire window would be 5.2. It's very comparable to that found in most forensic laboratories. The F. B. I. match window is five percent plus or minus 2.5. I think Metro Dade in Florida is five percent as well. Many of the forensic labs in North America are in the five percent range.

Q. What, if anything, can you tell us about the precision associated with having 86.1 percent within -- 86.1 percent of your samples or comparisons within two percent? What, if anything, does that tell you about your system?

A. I think it tells us that we actually have a system that's performing extremely well.

Q. Do you have a slide? I believe you do have a slide, Doctor, of --

A. Yes, I've sort of made a diagramatical representation of this, and if it pleases the Court, I can certainly show that.

Q. I show you this here. Is this the slide that you're going to show?

A. Yes.

Q. Perhaps if you would put it up on the machine, Doctor?

(Witness does so.)

Q. All right, Doctor, what I have in my hand here is a paper reproduction of what's on the screen, is that correct?

A. Yes, it is.

Q. I would move to have this entered as an exhibit, My Lord.

COURT: VD-94.

(DOCUMENT MARKED AS EXHIBIT VD-94)

A. This is just basically an easy way of looking at our match comparison. What we have are 502 band-wise comparisons. These were generated in the central forensic lab, actual case work. They encompass all types of forensic samples including hair, stains, blood, semen, so a wide variety of actual forensic material. From the established standards or known control that was given to us from that what we had to make a match, we found that of all 502 comparisons, if we used a maximum deviation from the known sample, 5.2 percent would certainly account the fact including all 99 percent of 502 comparisons. But if we use plus or minus 2.5 percent, that is, a total window of five, 98.6 percent of our samples would fall into this category, the total window of three percent, that is, plus or minus 1.5, 94.4 percent of all these comparisons would Fit here. And even a window as small as plus or minus one percent, that's a two percent total window, 86 percent of our samples are falling into that category. What was particularly striking that the one percent, that's plus or minus .5, 61 percent of the actual comparisons fell within that category.

Q. What does that tell you, Doctor? You say it was particularly surprising. What does that tell you as a scientist?

A. Well, considering the type of evidence we're dealing with and the whole unknown elements that are facing us with respect to insults that the samples would face, we have a system which essentially is generating a very accurate determination of the molecular weight fragment size. It's almost at the limits of the sensitivity and precision of the instrument for evaluation.

Q. When you say it's at the limits, the upper or lower limits?

A. It's at the minimal limits of detection precision of our computer, for instance. You would not expect using the gel system that we have and the various aspects of our protocol to be this accurate. This provides us with a very confident feeling that when we declare a match, certainly if we're declaring it, of course, within our 5.2 percent window, we're quite confident of that result.

So from a forensic nature as well as from pristine samples, the 5.2 percent window seems to match very well.

Q. Would you, Doctor, only use measurement, the match window, to declare a match? Would you use any other factors besides the match window in order to declare a match?

A. The actual match itself, the routine that is performed, is a visual match and the expertise of the analyst and the training and the experience would come into play to tell whether or not there is truly a match there. Once a match has been

established, then it's backed up by a computerized program which allows us to make a molecular weight determination of that particular fragment. That is what I believe has been entered into previous documents in this Court from Dr. Bowen's case work.

Q. Dr. Fourney, what if any opinion do you hold about the R. C. M. P.'s RFLP system's ability to produce accurate, reliable and replicable results?

A. I think we have an excellent system and it performs extremely well.

Q. What opinion, Doctor, do you have as to the risk of a false positive, and I would define a false positive, that is declaring a pattern of bands in separate lanes or gels across multiple loci to be identical when they are not.

A. The coincidence of a false positive occurring once is a possibility. Occurring across five loci is so remote it's not even worthy of consideration.

Q. What opinion, doctor, do you have as to the risk of a false negative, and that is declaring a pattern of bands in separate lanes or gels across multiple loci to be different when they are, in fact, identical?

A. There is always that possibility. The conservative nature of our system is such that we will declare a result either inconclusive or an exclusion.

MR. WALSH: Perhaps, My Lord, if I may suggest we could have a break at this moment. I expect I'll be able to finish up with Dr. Fourney by lunch time.

(Accused escorted from courtroom.)

(Court Recessed 11:10 a.m. to 11:25 a.m.)

(Accused present.)

COURT: Okay, Mr. Walsh.

Q. Dr. Fourney, before we get into a new topic, reviewing my notes, I would like to go back and cover one area again with respect to validation studies, things of that nature. You've also indicated that you attended the most recent Promega conference. Do you know a Major Weeden?

A. Yes, Major Victor Weeden is in charge of the DNA analysis team that is working with Operation Desert Storm.

Q. Could you tell us, please, was Major Weeden at this conference?

A. Yes, actually Major Weeden presented an excellent seminar on procedures and results that he has had with DNA typing with respect to the identification of human remains after combat.

Q. What kind of conditions would he be trying to extract DNA from?

A. In this particular case, from the slides and presentation that I witnessed, they're horrendous conditions of heat, impact, explosion, et cetera. Often Victor Weeden was trying to assemble various body parts back such that they could identify who the actual victim was, and to have a proper burial.

Q. What kind of technique would they be actually applying to any DNA that they did extract?

A. They used several procedures. From what I understand, Major Weeden used an antibody finger-printing technique, for instance. They use a DNA typing analysis procedure much the same as what the F. B. I., for instance, use for our own lab.

Q. That's the RFLP technique? / A. That's correct, what we call the RFLP DNA typing procedure. They also used a newer technology involving what we know as the Amp flp PCR procedure.

Q. What, if anything, did you determine from Major Weeden's studies and work? What, if any, conclusions have you drawn with respect to the stability of DNA as to DNA molecules?

A. It's quite remarkable to see the excellent results that their lab has attained with respect to putting back together these pieces and essentially the materials that he worked with had tremendous environmental insult, heat. For instance, in combat there was one particular case of an armoured personnel carrier being hit by a Hell Fire missile. The impact and heat and the incineration of that material inside the personnel carrier was such that it was very difficult to even identify human remains, let alone to do a DNA typing on this material.

Q. Was he able to actually extract DNA and do a typing on the material?

A. That particular case I think he used a combination of both RFLP analysis as well as polymerase chain reaction. They often did tests to confirm his results.

Q. Doctor, I'm going to show you a document marked VD-64 entitled Rebin population distribution. Would you look at it for me, please, and tell me if you can identify it?

A. Yes, this would be the rebin population distribution that would have been used for case work at the time that this particular case was being worked on.

It's dated December 3, 1990; represents the Caucasian data base from members of both Vancouver area as well as Ontario.

Q. Is this the particular population distribution data that was used in the calculations of the frequencies in this particular case?

A. Yes, it was.

Q. Doctor, I'm going to show you this document here. Would you look at it, please, and tell me whether you can identify it?

A. Yes, this is a more recent rebin population distribution of the same data base with the exception of five individuals that were removed from it.

Q. Okay, and who actually did this particular document that you have in your hand? Who prepared it?

A. This was prepared by myself.

Q. How many pages does that contain?

A. Six.

Q. What application would that have to the item marked VD-64? What, if any, comparison can you make?

A. It would be an update to this previous document.

Q. And the update would consist of doing what?

A. Essentially, we took out five individuals. After doing the bin frequency and analysis of this data base, we became aware in January that there was a possibility of duplication within the data base, and this could be for several reasons, one of which could be that individuals contributing to the data base that would be donating blood at the time may have donated twice. It could also be possible, and

it certainly became evident from talking to members of the Red Cross, that there are also identical twins that often give blood, and we could essentially in there have two individuals giving blood but essentially give the same DNA typing pattern. So in order to be very conservative, we removed these individuals from this data base.

Q. When you say there could be twins giving blood, is that in Canada generally or in a particular area?

A. I became aware that it occurs routinely in the Ottawa area in particular and through personal communication it was conveyed to me that there was approximately twelve sets of identical twins that routinely gave blood in the Ottawa area.

Q. And you have gone through the data base and the rebin distribution and have taken out any duplicates?

A. Yes, this would represent a more accurate assessment of the bin frequency.

Q. What, if any, difference would this have in relation to the use of the previous document, VD-64?

A. The results would be identical, almost identical, I should say. There would be very insignificant differences.

MR. WALSH: My Lord, at this time I move to have this document entered.

COURT: VD-95.

(DOCUMENT MARKED AS EXHIBIT VD-95)

MR. WALSH: My Lord, 95 has six pages. I don't know whether you wish to identify it further. There are six pages stapled together.

COURT: It's an update of VD-94 -- no, VD-64.

MR. WALSH: Yes. It's an update on the rebin population distribution for the Caucasian data base.

A. Yes, it should be realized that at the R. C. M. P. labs as well as many forensic labs, as we gain more information we will be releasing updated versions, whether the information is a little bit more accurate or there are simply additions to the data base. Our data bases will grow and we'll have to amend the actual rebin population distribution.

Q. What, if any, effect would this particular update have on the validity of the results or the significance that Dr. Bowen has assigned to the matches he declared in this case?

A. In my personal opinion, there would be no change.

Q. Doctor, what, if any, role do you have, or did you have, or do you now play with respect to the compiling of the R. C. M. P. data base for DNA typing -- data bases probably is the correct word.

A. I played a major role in coordinating the actual obtaining the samples, running the samples with respect to organizing the individuals within my team. The original data base is actually processed by Dr. Waye with some help from our technical staff. Since then we have had a number of data bases and it comes under my particular direction.

Q. What kind of data bases, how do you divide your data bases at the R. C. M. P. lab? I'd ask you to speak up just a little, Doctor.

A. How do I divide the data bases?

Q. How are they divided? Are there any groupings in relation to race or --

A. Yes, we have several different data bases at the

present time. We have a Caucasian data base which represents individuals from the Vancouver area. We have an Ontario Caucasian data base which is a composite of members -- blood donors from the Ottawa area. The large majority of these individuals actually come from the Kingston area and there are three large blood donor clinics operating in the armed forces bases in the Kingston area.

Q. Now, this pertains to the Caucasian data bases?

A. That's correct. We have other data bases as well. We have a Native Indian data base and that has been generated from samples obtained from individuals in a prenatal clinic that was developed under the direction of the Red Cross, and these would be Native Indians in the northwestern Ontario region. We also have a Native Indian data base comprising individuals from British Columbia.

Q. Doctor, I'm going to show you this document that's been marked VD-58. It's a two page document. Would you look at that for me, please, and tell me whether you can identify that?

A. Yes, this is a document that I prepared, mostly for information purposes for our technical people as well as the operational staff so that they would have an understanding of how the data base was compiled and the actual individuals that were in the data base, and it details the number of samples, when the samples were received, where they were received, and the nature of the race, for instance, Caucasian.

Q. And is this document an accurate reflection of the Caucasian data base as it presently exists?

A. It's certainly an accurate reflection of -- this is dated December 3, 1990 and would be an accurate assessment of the first data base that was used in this case, and there would be a few individuals in this data base, five, in fact, that would be removed and then it would be an accurate reflection of the second data base that was submitted.

Q. That is reflected in VD-95, the most recent update of the --

A. Yes, those individuals have been removed from that document.

Q. Apart from that, is it an accurate reflection of the Caucasian data base?

A. Yes.

Q. In existence at the R. C. M. P. laboratory?

A. Yes, it is.

Q. Doctor, could you tell us, please, the manner in which the data from the Caucasian data base, how it was actually gathered? How did this take place?

A. In the Caucasian data base the samples from the Ontario area were obtained anonymously from the Red Cross located in Ottawa, and these samples would come in as a consequence of blood donor clinics. We would be called that the samples were available and they would be delivered to us. It should be completely understood that these samples are all anonymous and we have no way of really retracing the identity of these samples. This is a prime requirement under the Red Cross charter. The samples that are actually obtained from Vancouver were gathered for us under a specific contract that Dr. Lorne Kirby coordinated, and they

were obtained from the Vancouver area, I believe also primarily from females, and those particular samples were processed with respect to DNA according to our procedures and they were all run in our lab.

Q. Doctor, can you tell me, please, what if any instructions, or what if anything did you want from the Red Cross and from Dr. Kirby? What would you ask the Red Cross for? What are you specifically requesting of them?

A. We would specifically ask for no duplication. We would ask for a specific quantity of material so that we could run a number of gels, for instance, plus have some blood in reserve if we had to go back to look at these samples. We would request that they be processed, or I should say stored in EDTA tubes so that it would preserve the integrity of the DNA as much as possible, and as much as possible, they would record the racial characteristics of the samples, in other words, Caucasian. In the Vancouver case, they did this by actual identification as well as by surname.

Q. Could you tell us, please, in the forensic scientific community or in general scientific community, how is collection of samples in that fashion, how does that compare with collection in other places?

A. It's very much the same manner of collection. One thing that becomes ultimate in all these samples is to preserve the anonymous nature of the samples so that, really, prevent people from tracing back any particular sample to an individual. This is primarily for legal purposes as well as for ethical issues.

Q. Do you have any concerns with respect to the reliability of the data bases in terms of their representation?

A. No, I think they are very accurate representation of the Canadian population.

Q. What would you base that opinion on, Doctor?

A. By the actual population distribution of Caucasians, for instance, in Canada.

Q. What about the mention that part of your data base was from Kingston?

A. Yes, I believe it's -- I'd have to check my notes, but I think it's 524 samples.

Q. I'll refer you to VD-58.

A. Five hundred and twenty-six samples were from the Kingston area. These were obtained from the Canadian Red Cross blood donor clinics operating in the Canadian forces bases in that region, and this most likely represents the best way to obtain a fairly uniform population distribution of Canadian Caucasians because what became illuminated by the people we talked to, the Kingston region, certainly the armed forces base, is very cosmopolitan with respect to the various provinces that were represented there. I believe you have some documents?

Q. Yes, I'm going to show you a couple of documents. You may want to refer to the ones you consider more appropriate. I'll refer you to item 62-A, 63-A, 60-A and 59-A. You may want to refer to any or all of those documents explaining your opinion with respect to how representative this data base is. Just if you could speak up just a little bit?

A. Yes, VD-60A, the Canadian population by province, represents our most recent census, 1986 Canadian census, where the total population is segmented into various percentages in terms of provinces, and you'll find here, for instance, that Quebec and Ontario is represented by 25.8 percent for Quebec and 35.9 percent with Ontario. The actual military personnel and their dependents that would be present in the Kingston area, Quebec group would be 20.5 percent and the Ontario group, 33.0 percent.

Q. Who actually prepared those charts?

A. These charts were prepared by myself. It becomes immediately convincing to me, and I believe to the Court, that the representation of a military personnel and dependent covers all provinces at approximately the same ratios that would be found with the Canadian population breakdown. The only difference that you would note here is that, if anything, the military personnel and their dependents are biased towards having more members in the Canadian military in Kingston that are represented by the Maritime regions, that being New Brunswick, Nova Scotia, Prince Edward Island, and Newfoundland. So it would be the military personnel dependents would probably reflect more of the -- slightly biased on the Maritime component of the population as opposed to the actual breakdown within the Canadian provinces.

Q. Do you have an opinion as to how representative the R. C. M. P. Caucasian data base is of New Brunswick, in particular?

A. I think there would be another figure that covers that, but it would be -- it would certainly be well represented within the Kingston military population. As you can see from here, the actual breakdown, if I read it correctly off the graph, it's approximately six percent -- here we go, New Brunswick would be five percent represented in the military personnel dependents in Kingston and it's 2.8 percent total population in Canada, so if anything, there's over-representation of individuals from the New Brunswick area, presumably. These samples being anonymous, we certainly can't say specifically that any one province would be left out. I would like to think that each province would have members from that would contribute to blood donor clinics equally.

Q. Why is that, Doctor?

A. I can't foresee any reason for any particular province having individuals that don't want to participate in blood donor.

Q. What, if anything, does that have to do with randomness or random sampling?

A. I would think it represents a fairly good population proportion of the Canadian -- in a micro sort of way, military personnel encompasses what we would expect to see in Canada.

Q. Would you consider the collection of the data bases, of the Caucasian data bases in the manner that you've actually described, to be a random collection?

A. I would think so.

Q. Why, Doctor, was the formulation -- how does the size of the Caucasian data base of the R. C. M. P.,

how does that compare with other forensic laboratories?

A. It's probably one of that largest in the world.

Q. Why was it important to obtain a Caucasian data base in Canada for Canadians, for the Canadian worker?

A. We wanted to be completely aware of any deviation from the expected results that Canadians, Caucasians for instance, would have with respect to allele frequencies such that we wouldn't be in error, for instance, of assessing the wrong frequency because we used, for instance, the population data base for Switzerland. In general from my own personal opinion as well as from evidence that I've seen in many meetings, and certainly at TWGDAM, I'm generally impressed with the fact that Caucasians overall have a very similar portion of RFLP frequencies.

Q. I believe, Doctor, you have two slides on the machine in relation to this particular question associated with why Canada needs a Caucasian data base? Is that correct?

A. Yes, I can show those.

Q. Please?

A. I think it's important to recognize the fact that any DNA lab should have the population data base with respect to the area that it's going to do an analysis, so each country probably generates its own data base. What this slide shows is a general profile of the Canadian ethnic groups that comprise Canada.

Q. Doctor, if you could stay back here by the microphone, I think it might be easier to pick up. Right here is fine.

A. As you can see from this particular diagram, 95.7 percent of our Canadian population is actually represented by Caucasians. The other groups would be of much smaller representation, so we are primarily concerned with the analysis of Caucasians and that's one of the reasons why we would choose to look at a Caucasian data base first and develop a Caucasian data base, and secondly, you would want a very good representation. This would be unlike other countries, for instance, where, for example in the United States in certain regions of the country, you have a wide number of individuals such as Hispanics, Negro, et cetera. We certainly -- primarily our country is composed of Caucasians.

Q. Doctor, before you move on I'm going to show you what purports to be a paper reproduction of what you have on the screen. Is that an accurate reproduction?

A. Yes, it is.

Q. Who actually prepared this slide that we're now looking at?

A. Once again, it was prepared by myself from research that has been derived in our own lab with Census Canada 1986.

Q. Relying on your reference to Census Canada, is that an accepted manner of looking at that kind of data to support some of the conclusions that you draw?

A. Yes, it is, and until there is a new census I think it's an accurate assessment.

MR. WALSH: I would move to have that entered, My Lord.

COURT: You'll have to wait one more month.

WITNESS: We'll have to do everything over again. No, actually we don't expect it to change that much.

COURT: That would be VD-96.

(DOCUMENT MARKED AS EXHIBIT VD-96)

WITNESS: I have a second slide.

Q. Before that, Doctor, maybe we could just get this out of the road. Is this an accurate reproduction of what you have on the screen?

A. Yes, it is.

Q. It's entitled Canadian Caucasian profile geographical origin. I would move to have that entered, My Lord.

A. What I've tried to show here --

COURT: VD-97.

(DOCUMENT MARKED AS EXHIBIT VD-97)

Q. Go ahead, Doctor?

A. What I've tried to show here as accurately as I could is the breakdown if you remember the large percentage of the Caucasian population. They would be represented from these geographical origins. As you can see, the British population comprises the greatest percentage of Canada, followed by the French, and then you have various other groups, mostly European, that would comprise the Caucasian population in Canada.

I think what the main feature of this slide would be to recognize the fact that the British and French population distribution here of the Caucasians would be what you would expect to see, in general terms, in the New Brunswick population, for instance. So there's nothing unusual with

respect to this breakdown and what we would expect to see in New Brunswick.

There are some smaller ethnic groups, for instance, that may not be present in New Brunswick, but certainly the Caucasians we would expect to see would be from either British or French ancestry to the major degree.

Q. How is that division represented in the C. F. B. Kingston profile?

A. Once again, we would expect to see, with the participation of the blood donors at those particular clinics, they would probably pretty well represent this particular profile. In Canada we're generally dealing with the Caucasian population. The other data bases we have specifically are derived from Native Indian groups, for instance, for specific questions we wish to address with respect to substructuring.

Q. Dr. Fourney, have you had any population geneticist look, in particular, at your Caucasian data base?

A. Yes, we have. Actually, it's one of the more exciting features of my position is to work collaboratively with some of the better population geneticists in North America. I'd like to think that certainly Dr. George Carmody is very good in participating with looking at our data bases. We've also sent our data bases to the F. B. I. and their people have analyzed data bases. Dr. Bruce Weir who has written a number of publications involving population genetics and specifically is now looking at questions concerning VNTR polymorphisms and allele frequencies also has our data base.

Q. What was the purpose of actually sending your data base to someone like Dr. Weir?

A. First of all, I think it's very important information. From an academic point of view, it's certainly interesting and worth looking into, so from the pure science I think it's exciting research. In our particular case, from our forensic application, it's important that we have someone look at our data base to tell us that it actually will do what we want it to do, represent the allele frequencies within the Canadian population.

Q. Doctor, what have you done or participated in to hold out the R. C. M. P. RFLP typing system and/or the data base to general scientific scrutiny? What kind of things have you participated in or are you aware that the lab has actually done?

A. Our program has written a few papers about our data bases and the forensic applications. We also participate to a large extent at meetings throughout North America talking about our DNA analysis and data bases, including we've also participated in Australia where we presented our data bases in poster format. So it's very important that people see our data and review it and give us feedback, tell us what they think about one, the procedures we use and the actual data itelf, whether or not it's a reliable and valid data base.

Q. What about the RFLP technique and the way it complies with the R. C. M. P.? Has that been held out to scrutiny as well?

A. Yes, I'd like to think that it's very highly regarded. We certainly participate in a lot of

collaborative studies. We have numerous individuals who are very interested in our procedure and I've sent out publications to those individuals. One of the aspects of writing papers is that we get reprint requests, for instance. These are interested individuals who are reading the literature and want to know more about the findings we've had and the studies that we've completed.

We also have members of other laboratories visiting our program and taking part in training and research activities. These would come from a variety of fields. From a forensic point of view we have the F. B. I. have been up a few times to do work in our lab and we've also gone down to their labs to conduct research and DNA analysis verifications and studies, et cetera. We've had members from other state forensic laboratories such as Illinois participate in research at our lab.

From the academic community, we have university individuals looking at our procedures. From the government programs we have Agriculture Canada. We've dealt with helping them establish a DNA typing protocol for their animal and livestock studies. Health and Welfare Canada has got our protocol procedures and are looking at the various techniques and protocols that were used for their diagnostic division that is being set up there under the direction of Dr. Remi Aubin.

We also have a great deal of interest from the Canadian Red Cross. We've had a post op from their research group in Ottawa train in our lab to use the procedures that we currently use for bone marrow transplant recipient programs so that they can better identify people to give bone marrow transplants to donors after chemotherapy. And they particularly like our procedures because they're very sensitive, they're very accurate, and they're very reliable, and they use this protocol, or they're hoping to use this protocol -- they're still in training right now -- to not only screen for potential recipients and donors for their bone marrow transplant program, but also to evaluate after transplant has occurred whether or not it has been successful. If there has been remission for the cancer, they want to know what component of the cells have contributed to the cancer, whether it came from the donor or the recipient, and often the techniques that are used require very sensitive detection and analysis of the DNA patterns and they're hoping to use our procedures for that.

Q. Doctor, have you had any involvement with respect to the case specific evidence, that is, the case of the Queen versus Allan Joseph Legere, and tests conducted in this case?

A. Yes. I would have been the reviewer at the R. C. M. P. lab for this particular analysis.

Q. And the actual analysis, who conducted the actual analysis?

A. The case was conducted by Dr. John Bowen and I would have gone over Dr. Bowen's work and looked at his results and his conclusions.

Q. I'll show you, Dr. Fourney, what's been marked in this hearing VD-54. Would you look at it for me, please, and tell me whether or not you can identify it?

A. Yes, this is the forensic laboratory report that Dr. Bowen had generated.

Q. Are you familiar with that report?

A. Yes, I am.

Q. I will show you, Dr. Fourney, VD-55; VD-55 is dividdd into two sections. The first part is preceded by two pages with typing on it identifying lanes and substances contained within lanes that's headed gel number one membrane number one, and it's followed by a series of autorads. The second part refers to a paper with typing on it referring to gel number two membrane number two with a number of lanes mentioned and substances contained within those lanes followed by a series of autorads. Would you look at this for me, please, Doctor, and tell me whether or not -- and they purport to be duplicates of originals generated by Dr. Bowen. Would you look at that for me, please, and tell me whether you're familiar with those autorads?

A. I would be familiar with the originals of these autorads.

Q. You have those originals in your possession?

A. Yes, I do.

Q. And they were transferred to you by Dr. Bowen?

A. Yes.

Q. Over this weekend?

A. Yes.

Q. This past weekend, I should say?

A. That's correct.

Q. And VD-56 is, again, a booklet divided into two parts. The first part refers to gel number three membrane three. It's a single sheet of paper with typing on it and it contains lane numbers with what is contained in each lane followed by a series of autorads, and the second part is headed Miscellaneous Known Samples on a single sheet of paper followed by a series of autorads. Would you look at that for me, please, and it purports to be duplicates of originals generated by Dr. Bowen in this case. Are you familiar with those?

A. Yes, I would be familiar with the originals.

Q. You have actually reviewed the original autorads generated by Dr. Bowen in this case?

A. Yes, I have.

Q. I refer you to page five of that particular report. I'm going to read a section to you if that's agreeable, and I'm also going to refer you to VD-88 which is this particular chart here. This chart purports to be a summary of the first blot, what has been identified in court as the first membrane gel -- first gel, first membrane. In Dr. Bowen's report he states: "For the DNA typing profile obtained from Exhibit 1I" -- this one here -- "D4S139 matches that of Exhibit 56A-69A." Are you familiar with that particular call made by Dr. Bowen?

A. I would be familiar with it after reviewing the autorads again, but --

Q. Okay, do you have an opinion with respect to the calls that Dr. Bowen made in this particular report?

A. Yes, I'm familiar with the report and I would agree with the calls that were made in that particular report.

Q. Okay, fine, that's probably the best way to approach it. When we say calls, what are we referring to? What do you understand when I use the term 'calls'?

A. From my understanding of what you mean, the declared matches, the inconclusive results, and the positive results with respect to the monomorphic probe and the sex-typing probe.

Q. So you agree with Dr. Bowen's conclusions with respect to all the calls he made with respect to the first blot?

A. Yes, I do.

Q. Are you familiar with the statistical significance that Dr. Bowen has assigned to each of the inclusions that he made, the visual matches that he made?

A. Yes, I am.

Q. Backed up by computer quantification. Could you give me your opinion with respect to statistical significance that Dr. Bowen has assigned to the matches?

A. I would have independently calculated the same statistical matches.

Q. Doctor, are you familiar with the second blot, what's been called in this proceeding the second blot, and that is the blot containing what is purported to be two known standards of Allan Joseph Legere? Are you familiar with that blot?

A. Yes, that would have been blot 89-OL-1191. May I refer to my notes?

MR. WALSH: My Lord?

A. By the second blot, I assume you must mean 89-OL-1191-13?

Q. That's correct.

A. Yes, I'm familiar with that.

Q. And what, if any, conclusions did you draw with respect to the results exhibited on that particular blot and compared to the blot 89-OL-1191-6?

A. I would agree with the particular calls, so to speak, that Dr. Bowen has made.

Q. Do you have any reservations with respect to the opinions that Dr. Bowen has set out in his report marked VD-54?

A. No, I think they are fair and accurate results.

Q. Could you explain to the Court, please, what you actually did to review Dr. Bowen's results and his tests? Would you explain how you went about it?

A. After the completion of the tests in December, I independently reviewed the autorads. I went through them quickly to assess any particular problems that may have occurred, then I went back in more detail and examined each particular autorad with respect to the matching, the actual measurement calculated for the bands that were present on the autorad, and I would do the actual calculations on the matched comparison results.

Q. And your findings with respect to the method in which the -- or your findings with respect to how the RFLP technique is applied by Dr. Bowen?

A. It would be applied if I had done the result -- the same analysis myself.

Q. And the statistical significance again?

A. I would agree with Dr. Bowen.

Q. And the method of calculation, Dr. Bowen, I believe, indicated that using the binning frequencies and applying the Hardy-Weinberg equation and the product rule, he arrived at the statistical significance associated with those matches. Is that a fair summary of the procedure for calculating?

A. Yes, it is.

Q. Do you agree with the application of that procedure?

A. Yes, I do.

MR. WALSH: My Lord, at this time, I see it's twenty after twelve. I've come to pretty well the end of my direct examination of Dr. Fourney. I would ask if we could take our lunch break now. I could review my notes over the lunch hour to ensure that I've covered all the areas I wish to cover, and I expect for Mr. Furlotte's purposes he should be prepared to commence cross-examination very soon after we resume, My Lord.

COURT: That seems a reasonable request. We will recess now until half past one?

MR. WALSH: That will be fine, My Lord.

COURT: One question I have to ask just before we recess and that is while I've read the acronymn DNA and have heard it used many thousands of times now, and have read it in many places but I've never heard pronounced the word for which DNA is the acronymn. Will you please pronounce it?

DR. FOURNEY: Deoxyribonucleic acid.

COURT: Nucleic, with the emphasis on 'cleic'.

DR. FOURNEY: Yes.

COURT: Deoxyri--

DR. FOURNEY: Deoxy -- ribo -- nucleic acid.

MR. WALSH: It's just as well you didn't ask me, My Lord, my pronunciation would have been slightly different.

(Accused escorted from courtroom.)

(Court Recessed 12:20 p.m. to 1:30 p.m.)

(Accused Present.)

COURT: Now, Mr. Walsh, did you have any further questions?

MR. WALSH: I just have a couple, My Lord. Doctor, we were discussing before lunch VD-54 which is the report of Dr. Bowen. You've indicated that you visually looked at the autorads yourself and confirm his calls, is that correct?

A. Yes, it is.

Q. Did you also have occasion to look at the sizings that were generated in relation to the autorads?

A. Yes. Yes, I did.

Q. What, if any, opinion did you have with respect to the sizings and whether or not they confirmed your visual calls?

A. Yes, the sizing would confirm, certainly, my visual call.

Q. As well, Doctor, this morning we filed into evidence the F. B. I. environmental paper, VD-93. Have you had occasion to review the conclusions that they drew in this particular paper that are set out at pages 12 and 13?

A. Yes.

Q. And what is your opinion as to the conclusions that they drew?

A. I think they're very accurate.

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

COURT: Cross-examination, Mr. Furlotte?

CROSS EXAMINATION BY MR. FURLOTTE:

Q. Dr. Fourney, you mentioned today when you were going through your c.v., you mentioned about the work you did with cancer patients and checking DNA analysis with cancer patients, is that correct?

A. Yes.

Q. And I believe a couple of weeks ago when you testified you mentioned something about there being the DNA in cancerous tumors affected the migration rate of DNA fragments in -- is that correct?

A. I don't think that's correct, no. Not in those words, perhaps. Could you --

Q. You said there was an operation -- a genetic structural change?

A. Oh, there's a possibility, for instance, in tumor material to have an altered DNA with respect to the control tissue. That possibility does exist, yes.

Q. Could that have any effect on DNA analysis in forensic work, depending on where the DNA sample was taken from?

A. If we obtained a tumor material sample?

Q. Yes?

A. Could it have an effect with respect to DNA patterns?

Q. Yes?

A. It's possible. You wouldn't really know it until you actually looked.

Q. Could a community that had a high, say, cancer rate, could that affect the DNA profile, say, on a data base if you were going to take a data base just from this community?

A. Probably not.

Q. Probably not?

A. No. You have to remember that tumor material is different from the actual control, or for that matter, healthy material, and in general when a tumor forms, what it is, it's an aberrant pattern of growth of a group of cells, almost a clonal type growth and it grows and grows. And cancer is essentially uncontrolled growth, and presumably the type of samples that we would get from healthy blood donors would not be leukemia, for instance.

Q. What about, say, someone who has leukemia? I understand leukemia attacks the white blood cells from which DNA analysis can be taken? Wouldn't one might expect a little more common patterns among people who have leukemia?

A. Probably not because the VNTRs that we're looking at, the particular loci, for instance, that we have identified, chances are they have nothing to do with the cancerous growth. What I was dealing with in my post-doctoral research were activation genes, termed oncogenes. These are cancer-risk genes and they're quite deviant from normal control material.

Q. I understand from your testimony that you say you were initially hired by the R. C. M. P. along with Dr. Waye to set up the laboratory for DNA analysis and for forensic purposes?

A. Yes, the actual history of my hiring is rather interesting in the sense that I contacted the R. C. M. P. as far back as 1984 as a result of research that I was undertaking at Memorial University. It became apparent that you could

use this technology for species identification, and one step removed from that would be for a DNA identity in man, and in 1984 I actually contacted the R. C. M. P. and asked if they had ever considered using this for forensic purposes. And it wasn't really until Alex Jeffreys published his first paper in 1985 that the significance of this actually took into effect. During that period of time I was already conducting my post-doctoral research, so it wasn't until 1988 that I was contacted and asked if I'd be interested in becoming part of the new program that they were establishing, and it took another letter of initiation from me to ask the inquiry once again. "Would this be a program that you people are starting up?" and, "Yes, it was indeed," and after my security clearance, et cetera, I was hired.

Q. And who recommended Dr. Waye to assist you? Did that come from yourself or was that somebody else?

A. No, Dr. Waye was hired first.

Q. Pardon?

A. Dr. Waye was there first. He was --

Q. He was there first?

A. I believe, not being there when he was hired, I think he started in April and I became a member in November of that year.

COURT: Where were you then? What were you doing then?

A. In?

COURT: In '89, in '88, I'm sorry.

A. In '88 I was just finishing up my post-doctoral studies in Edmonton.

Q. Now, when you and Dr. Waye established data base, the R. C. M. P. data base, and you run some of the test gels yourself?

A. We split up our tasks. The initial data base composed of the Caucasians in the Ottawa area and the Kingston group, a lot of that work was actually undertaken by Dr. Waye, and at the same time, I was generating probe results and developing the DNA VNTR probes that we would probably use in data basing. And you have to realize that at that particular time in 1988, there weren't very many labs actually doing this and we were working with the second generation DNA technology. A lot of the initial DNA typing had been done with multi-locus probes, for instance, and it quickly became apparent that these would not be useful for forensic purposes, and we were doing research and development to establish the actual single locus probes that we use today for the data base analysis.

So in answer to your question, Dr. Waye played a large part in the initial part of the data base and I played a component more in developing the probes that would be used. I did a lot of the actual X-ray developing, and both of us, I believe, sized that data base ourselves independently.

Q. Independently? Now, when you did your data base did you also use the D7 probe?

A. Yes.

Q. And the sex probe also?

A. I can't recall. I don't think we ran the sex probe. Generally the samples that we were actually looking at would be anonymous and there is no real

purpose to running a sex probe. In some of the later data bases we actually ran the sex probe primarily to check out a new variation of a probe that we were thinking of implementing into the actual R. C. M. P. program, so some of the data base might have been run with the sex probe.

You also have to recall that having prior knowledge, for instance, that our data base was made up primarily of females. Running the sex probe would really tell us very little.

Q. But you only knew that from your source that they were primarily females?

A. Well, we were advised of the nature of these samples and where they came from, and actually, some of these blots were run with the sex probe.

Q. You didn't have the contributors' names or anything when you ran your data base?

A. No, we wouldn't.

Q. How would you identify, say, a sample with your test gel? Would you use some kind of code?

A. Yes. The tubes would come in and we would code them.

Q. How would they be coded?

A. Generally by date and numerical number.

Q. And numerical number?

A. Chronological order.

Q. Would any records be kept as to where that particular numerical number had come from?

A. Yes. The actual day it was received in the lab, where it came from, and most of the samples we can actually go back to the original blood standard. It's still there in the lab for many of these tests.

So if we had, for instance, a concern over a particular sample that might not have digested properly with a restriction enzyme, we could actually go back, pull out a sample of that blood, and prepare the DNA again and run it, or many of our samples.

Q. There's no way you can trace that sample back to any individual, I believe you stated?

A. No.

Q. You belong to the International Society of Forensic Haemogenetics?

A. Yes.

Q. You do?

A. Yes.

Q. And what about the American Society of Crime Laboratory --

A. No. The American Society of Crime Lab Directorate. That's -- generally, that's a society where the directors of a lab belongs to. For instance, our director of our lab is a member of that. I am not a member of that, so the R. C. M. P. is a participant in that way.

Q. The R. C. M. P. has a member in there?

A. Yes, that's correct.

Q. You're not --

A. No, --

Q. You're not the director of the R. C. M. P. lab, then, I take it?

A. That's absolutely correct.

Q. One of your functions, you stated, was to develop a valid protocol for the DNA typing in the lab?

A. Yes.

Q. And to set out some quality assurance program?

A. Yes, that's correct.

Q. Was there any typed up quality assurance program in effect in 1989?

A. I believe at that particular time we were using the technical working group quality assurance document.

Q. So you relied, basically, on theirs?

A. Well, it's also part of mine. I'm a member of that committee and I helped draft it. I would like to think that I played some part in drafting that document.

Q. Was there any proficiency testing going on in your laboratory in 1989?

A. Yes, before any examiner actually does a case, for instance Dr. Bowen would have had his first proficiency test prior to doing a case.

Q. Proficiency test?

A. Yes.

Q. And what would that entail?

A. Well, after -- you must remember that Dr. Bowen had some experience prior to coming to our lab in DNA analysis, and that when he joined our program in the summer, he worked with us on several aspects that we were developing, and he would have tried all the procedures. Essentially he was an apprentice with our program. We didn't have a formal training program, per se, for Dr. Bowen because of his advanced knowledge, but he would certainly have conducted a proficiency test and successfully completed that before he went into doing actual case work.

His particular proficiency test I think was administered collectively by myself and Dr. Waye and it consisted of the matching, correct matching, of twelve blood standards from our data base right from the extraction through to the actual sizing of these and they had to agree with our previously derived results.

Q. Which month did the lab open, let's say, for business and start doing DNA profiles on actual case material?

A. I guess by opening, you're referring to what Mr. Walsh has said, October 9, 1989, or pardon me -- yes, 1989. Dr. Waye would have done his first case in April of that year.

Q. April of 1989?

A. Yes, and that was a test case, really, to see how the procedures, et cetera, would stand up with respect to the legal community. So I guess if you want to call it official opening, or we started looking at case work in general, it would be October of that year.

Q. So how many -- so you're saying the test case was in April, '89?

A. You have to have an initial case some time and our first one was in April.

Q. And there was no testing done on other cases before, again, until October of '89?

A. That's -- well, we had cases that were coming in. I, myself, had a few cases that were coming in, for instance. I think Dr. Waye had a few cases as well, but in general the doors were not open until October of that year. We wanted to establish

a case work priority system, for instance, how best to serve the police community.

Q. I understand Mr. Legere started in around October 15, 1989?

A. I'm not sure I can remember the exact date.

MR. WALSH: I don't think that's the correct date.

Q. October 25 I see the first notes by Dr. Bowen?

A. It's possible. I'm sorry, I'm not in operations so you would probably have to ask Dr. Bowen when he first received the case.

Q. I understand from the article Simple and sensitive method for quantifying human genomic DNA in forensic specimen extracts that you're attempting to find out how much DNA you could contribute to human DNA and how much you could contribute to bacterial or some other form?

A. The main objective of what you're referring to called the slot blot quantitation procedure is to use a human specific, or higher primate specific, in fact, is the more correct term alpha satellite probe to detect the amount of DNA that would contribute to a successful DNA typing. It's a very sensitive procedure that can detect, in a short period of time, subnanogram quantities of DNA.

Q. If you detect it's human DNA and bacterial DNA that they were together, how would you separate it for -- or could it be separated before you run it in the gel? Or do you just have to find out if it's there for your interpretation purposes?

A. I'm not sure I understand your question. You want to know how to separate bacterial DNA from human DNA?

Q. Well, I assume when you would -- whatever procedure --

A. To actually get an accurate quantitation, you don't have to separate them.

Q. You don't have to separate them?

A. No, because the probe is specific. It won't bind to bacterial DNA.

Q. It won't bind to bacterial DNA, is that what you're saying?

A. To the common bacteria that is found in the human body it generally does not bind to it. We would do a series of validation tests. I think in that paper there's actually one of the figures. It may not be bacterial DNA, but we run routinely what are called zoo blots and these are essentially DNA obtained from various species and we would extract the DNA from the blood, for instance, of horses and different animals and actually look and try to get an estimate of how much non-specific binding occurs with our probes, and in general, the VNTR probes as well as the D17Z1 is very specific. We've enjoyed quite excellent success, and one of the highlight features of the slot blot quantitation procedure is often where we are limited to the amount of DNA that we have. If you want a precise estimate and be able to get the best chance of getting a success with RFLP typing, if you can determine the limit of 50 nanograms from your slot blot procedure, you can put all that material onto a single blot and actually get a successful result.

The alternative of this is to do a series of dilutions, spectrophotometric tests, et cetera, and that takes a lot more DNA from your very valuable

forensic specimen. Consequently, you may eat up your DNA, or use up your DNA prior to actually being able to do an RFLP analysis, so one of the highlight features of the slot blot is that it's fairly fast, it tells the amount of hybridizable human DNA, and it's quite accurate. It's very sensitive as well and has enjoyed considerable success with those labs that are using PCR, for instance.

Q. In the evidentiary samples in this case here, was there any evidence of bacterial contamination?

A. The slot blot wouldn't tell you that.

Q. What did the slot blot tell you?

A. What it would essentially tell you is how much DNA you have to work with from your material that you extracted. There's two features to this procedure. The slot blot quantitation tells you how much DNA is present, then you run a yield gel which tells you the -- it's a second back-up quantitation. This is where you take a small amount of your material and run it on the gel and it tells you a very important point, and that is the actual quality of the DNA. Is it high molecular weight DNA, for instance? If it's high molecular weight DNA, then you'll know you'll have a very *good* chance of successful RFLP analysis.

Q. Did you review these tests conducted by Dr. Bowen, these particular tests, the slot blot and the test gel?

A. I certainly saw the autorads. The slot blots, I think I saw the initial analysis. I can't recall if I've seen all the slot blot analysis.

Q. Can you answer my question whether there was bacterial DNA mixed in with human DNA in this case?

A. I wouldn't be able to tell with that particular procedure. You'd actually have to take a bacterial specific DNA probe and probe it to your material to find out whether or not there is bacterial DNA. Then you would actually have to take, generally, the specific bacteria that you have a question concerning and use the probe derived from it to get a hybridizable pattern.

If there was bacterial DNA present in the samples, it probably would not have any alteration to the pattern anyway.

Q. Is it possible that it would show extra bands?

A. Very unlikely. There may be --

Q. What do you mean by very unlikely?

A. I'm just thinking in my practical experience with the samples I've seen run and my own past experience with working with bacteria. I would think that the VNTRs are highly specific for picking up primarily human DNA, for instance. You have to lower what we call the stringency conditions of hybridization to pick up non-specific banding, and in doing so, you would afford less discrimination power on your protocol.

We use a very high stringency condition for hybridization, and this is probably one of the major separating features between multi-locus probes, for instance, and single locus probes because in general multi-locus probes use a low stringency condition such that they have a good chance of picking up non-specific banding from

homologous organisms, for instance, and that's one of the reasons we've gone to a second generation typing procedure.

Q. So your non-specific hybridization or banding could be due to bacteria contamination?

A. I'd have to look at the specific set of autorads.

Q. I thought that's what you had just said?

A. I'm sorry, could you say exactly what you just said?

Q. I thought you said that some non-specific banding is -- that's due to bacteria?

A. No, I don't think I said that, but what I would think is that most of our VNTR probes are very specific toward human DNA. There may be, I think, on the occasion I've noticed one particular probe -- I'm just trying to recall. I think it was, perhaps, one of the earlier lots of D4S139 that might have been able to pick up a quantity of bacterial DNA. But you have to realize that even if you picked up bacterial DNA, it would generate the same pattern throughout the autorad, so you wouldn't see any deviation from sample to sample, for instance.

It's not polymorphic, like it would -- like these probes are with respect to VNTR. You don't see a restriction fragment length polymorphism. When you have a contamination feature present in an autorad, you generally know it very quickly because you see a large, black band, for instance, or you see a constant band in a particular region. It's quite apparent.

Q. I show you Exhibit VD-50, Doctor, which is the experimental paper by yourself and by Dr. Waye and Dr. Bowen entitled a forensic analysis of restriction fragment length polymorphism. I probably want to refer to a few of your comments in that paper. On page 2 in your introduction --

A. That would be page 118?

Q. Maybe -- I don't know if I have the same printing or not. I guess it would be on page 117 of the report that you have, the first page and the last sentence of the first paragraph says, "Lastly, some gene products are subject to rapid degradation, inactivation, or alteration as a consequence of environmental interactions." What do you mean by alteration there?

A. Presumably one of the things that could happen in terms of alteration would be that the protein itself would change.

Q. Its what?

A. Protein. "Lastly, some gene products..." products of genes are proteins. That sentence has nothing to do with DNA.

Q. It has nothing to do with DNA?

A. That's correct.

Q. It's just a gene product, it's not the gene itself?

A. That's right.

Q. On page 119 at the top of the page you state that, "This report provides an overview of the DNA typing system utilized by the molecular genetic section of the Royal Canadian Mounted Police. Theoretical and practical considerations for the design and implementation of the DNA typing system are

discussed with particular emphasis placed on aspects of the system that addresses controversies associated with forensic applications." So I assume you do admit that there are controversies associated with the application of this procedure?

A. At the time, certainly at the time that this paper was written there were controversies, at that time, yes.

Q. Are you saying there are no more controversies?

A. I think the controversies associated with forensic application are primarily dealing with aspects of the population genetics, for instance. The actual application of the technology is valid and has been well recognized. The office of technology assessment makes that very clear. Has that been entered into court?

COURT: I think so.

MR. FURLOTTE: I'll go through the report.

Q. It says, "Recent debates have brought into question the ability to achieve genetic individualization based on the analysis of a limited number of genetic loci." They quote here Lander and Lewontin. Is that debate still open?

A. I think what you have to understand that in any scientific field there are controversies. There are people who are going to proponents of a system, there are people who are going to be not proponents of that system, and a healthy science is one that has controversy in order to be progressive. I would find it highly unlikely that there would be any science where there is no controversy.

Q. Okay, and you refer to King, here, of 1989? Would that be Mary Claire King?

A. I believe that's -- I just have to check here. Yes, I believe that was one of the early articles. It was a review editoral, actually. It was an invited editorial. It wasn't actually a paper. It's some authors who are respected in the field are invited to make their comments on particular aspects of a house science.

Q. And Landers, I would assume that was Dr. Eric Landers?

A. Yes, once again, that's another editorial in science. It's not a paper but it's a comment by Eric Landers on what his feelings were concerning DNA finger-printing. I think that was probably written around the time of the fairly controversial Castro case, and a lot of the concerns addressed in Castro are no longer concerns that are present. Certainly, the issues of specific hybridization and probe validation, a lot of those have been completely eliminated as a problem now. With good quality control, most of these problems can be solved.

Q. You state also, "Apart from quality control and technical proficiency, there are several bonafide scientific issues at the heart of this controversy." Is that correct?

A. That's certainly the sentence that's here, yes.

Q. So I understood you just -- your prior explanation is trying to slough it off as just being a problem with quality control?

A. No, no, I said one of the controversies involved quality control. First of all, in this particular sentence one has to realize that when this paper

was written, this paper was probably drafted in -- I think it came out in the '89 proceedings so it was probably drafted in late '88, 1988, so there is -- DNA typing in North America was just in its beginning stages at that particular time. So if you go on to the next sentence, for instance, these include concerns regarding the number and types of loci being analyzed. That pertains to the question of standardization more than anything else. What we were trying to develop was a standardized approach in North America so that our results would be comparable from lab to lab and it stands to reason you would want to use the same restriction enzyme, for instance, in the same probe.

Ideally, the work that you address in your own lab should be able to be reviewed by another lab who uses a similar system.

Q. At that time there wasn't a controversy as to whether or not the allele frequency population data bases are representative of the relevant populations and the validity of the statistical methods used to assess the significance of the RFLP inclusions. These were all controversies of that day, were they not?

A. I would say those were concerns by some members of the community, yes, the scientific community.

Q. Are they not still concerns?

A. To some members of the scientific community, yes, they are still concerns.

Q. To a good number of the members of the scientific community? Would that be correct, Doctor?

A. That's your personal view. I would like to think that it's not that case.

Q. Well, Doctor, in the job that you had setting up the R. C. M. P., I would assume that you want to know what's going on around you?

A. Yes, that's one of the reasons why I make a strong attempt to read the relevant literature as well as attend as many academic functions involving forensic analysis as possible.

Q. And that includes reading the relative case law and witnesses that go to court either for the promotion or to oppose this type of evidence?

A. I've read a lot of transcripts, but I like to think that I've read more scientific literature because that's primarily my role. I'm a research scientist, essentially, with the R. C. M. P.

Q. Have you read the paper by Ronald T. Acton about the substructure within races?

A. I certainly have. In fact, I talked to Ron Acton at the Promega meeting because I believe he gave a poster either at the same time that we were giving a poster and I had a good chance to talk to him and I know of his work and I saw his initial work that was done, I believe in the first international symposium hosted by the F. B. I. which would have been in June of 1989.

Q. He still have cause for concern as to validity?

A. Apparently in the area that he's looking in Alabama where he's located, he has concerns that the relevant black populations are slightly different, for instance. I think he's -- I'm just trying to remember the Hispanics that he's also looked at, and I believe he's had a few Caucasian data bases as well. But you also have to remember that Ron Acton is using a slightly different approach

than us in the fact that his bins are much smaller and there is some concern that the collapsing of these bins are, first of all, not very conservative, but also the fact that there's a question that he's trying to make a lot more out of his data than is really there with respect to the precision and accuracy of the general RFLP approach.

Q. That's what the opponents claim about the R. C. M. P. and the F. B. I. also.

A. That's a possibility. I'd like to think that one, we have, as Dr. Jeffrey Mooers introduced me at the Riverside -- or introduced Dr. Budowle at the Riverside meeting, we have the biggest bins around; and two, that probably the major criticism that faces us in the forensic circle is that we're so conservative that we're actually throwing data away.

Q. But Dr. Acton, as you stated, uses smaller bin sizes?

A. Yes, in fact --

Q. In his, but he uses the same bin size whether he's gathering the data for population data base in Chicago or Detroit. He doesn't change systems.

A. No, but he -- I believe, and I could be misinformed about this, but as recently as the Promega meeting I think his bins were approximately 100 base pairs which is very small.

Q. He's using a much more discrete system than what you are, so therefore it should be more accurate, wouldn't it?

A. Well, he's actually defined a system that could possibly be beyond the limits of the technology, so it would not necessarily be accurate, for instance.

You have to realize there's a difference between accuracy and precision. Precision is getting the same answer, accuracy is getting the right answer. Ultimately, when I put both together and get an accurate answer all the time.

Q. So is your system one of precision or accuracy?

A. I'd like to think it's both.

Q. A true politician, Doctor. I'm sure you're well aware that Dr. Eric Lander still would be considered to be an opponent, rather than proponent of this?

A. I think he still has some concerns, but I was quite impressed, actually, with the nature of a recent editorial that was published in American Journal of Human Genetics that just came out two weeks ago. I thought he was -- he's quite good in referring to our paper, the fixed bin approach, that appeared in the same journal as well as Dr. Alex Jeffreys' paper for instance.

Q. I have a list of scientists here as to who has even taken the trouble to come to court and be as witnesses and write papers against the procedure as opponents, and I have, I suppose, twenty. I have Rayne Flattery. Are you aware of her being opposed to the technique?

A. Not directly. I mean, I think I have one transcript of her work, but --

Q. Dr. Joseph Nadeau?

A. He was actually in the Jakobetz case, I believe, I believe Vermont versus Jakobetz. How do you spell that name?

Q. N-a-d-e-a-u, Nadeau? / A. I believe that's correct.

Q. He pronounces it Nadeau, I think. Dr. Paul Hagerman?

A. I think Dr. Hagerman was more concerned with the technical features, in particular.

Q. Right, which you say there is no concern with any more?

A. He was particularly concerned with ethidium bromide. I may be wrong there, but I think it was the use of ethidium bromide in the F. B. I. procedure and, of course, as you realize we don't use ethidium bromide in running our gels.

Q. You don't use it the same way, but it still could be considered on the basis of an environmental insult, as a contaminant?

A. Well, no, I don't think so.

Q. You don't think so?

A. No, because it's deliberately added to the gel after the process of the electrophoresis has been concluded.

Q. Yes, but whether a contaminant is deliberately added or accidentally added, what's the difference in test results?

A. Well, for one thing, you have a controlled situation and you know exactly what you're going to get when you deliberately add something, and in our particular case, we add a little bit of ethidium bromide after the actual electrophoresis is completed. That's simply to visualize the DNA. The DNA has actually run its course in the gel and will not move any more, so that when it is transferred to the membrane, it will be an accurate and reliable facsimile of the DNA profile in the gel, and the ethidium bromide has nothing to do with the alteration of the binding capacity of that DNA to the membrane.

Q. The tests that you did with the ethidium bromide to show how much -- I suppose what do they call it, a variation or band shift, that would occur? Exactly how did you conduct that test?

A. In that particular case, we ran a series of control dilution gradients of DNA onto gels and we had one set of gels run in the presence of ethidium bromide, so you actually -- before you actually load the samples, you're adding ethidium bromide to the buffer solution. That's the reservoir where the electrophoresis is conducted, and you're actually making the gel with ethidium bromide in the gel itself as opposed to, for instance, pouring the gel without ethidium bromide in it, without the presence of ethidium bromide being in the buffer reservoir. After the electrophoresis is completed, the gel is then transferred to a fresh buffer solution and you add a small quantity of ethidium bromide for a short period of time, which case you wash away any excess of ethidium bromide and you photograph the gel under UV fluorescence. So there's a major difference in quantity of ethidium bromide that you're adding to the gel and the buffer, and certainly the exposure time, and the fact that the DNA has run its course in the gel.

Now, you also have to realize that the F. B. I. procedure uses ethidium bromide in their gel system, but they also have slight variations in the type of agarose, for instance, that they use. They use an MEE agarose as opposed to an LE agarose.

Q. And they have a difference in their buffer solution?

A. And they have a slight difference in their buffer, yes, and presumably with the slight variations that

they have in their system, they get highly reliable results. So when you look at the entire protocol involved, for instance, in RFLP analysis, you have to look at the holistic picture, all the steps involved and what the final results would be.

Q. How did you measure the deviations in the ethidium bromide testing? What did you use for a measurement?

A. That paper was written quite awhile ago. I seem to recall we ran the monomorph, for instance.

Q. D7Z2?

A. That's correct, and we would expect to see a 2,731 base pair fragment and we would measure the deviation from that particular size range.

Q. You would measure the deviation?

A. I also think we ran a series of VNTR probes, I seem to recall, and we would measure the average --

Q. Okay, before you go on, just for my own understanding, you had measured the deviation by the D7Z2 probe and just your normal procedure, like, you take your sizings and then you figure the base pairs differentials?

A. Yes, it's run in conjunction with markers.

Q. It's run in conjunction with markers, just the same as the test run in this case here? The only thing, ethidium bromide included in the --

A. Yes, that's one of the major features of any good scientific experiment is that you try to only alter one component of the experiment at a time and that allows you to make a conclusion at the end of the result, for instance.

Q. Now, I believe you got upwards to what kind of a deviation, percentagewise?

A. You'd have to refresh my memory. I think it was in the Tris Borate EDTA buffer system, I think it was -- I could be wrong about this -- I think it was as high as 5.2 percent.

Q. And is another term for that band shifting? That would be band shifting to a degree of 5.2 percent?

A. Some people called this band shifting. Band shifting can be the result of several aspects to a sample. For instance, there's several insults to --

Q. Now, in ethidium bromide testing results when you assess as to how much of a differential is taking place with or without the ethidium bromide, would you see a visual difference also, or just go by the sizings?

A. Oh, you'd see a visual difference.

Q. You'd see a visual difference, and you go by the sizings?

A. Yes, you would use a sizing as a back-up. You have to remember with the actual ethidium bromide shift there is a sample range where you get a minimal deviation and in the actual sample application that is normally applied in forensics, in the 500 nanogram range, for instance, the effects of saturation of ethidium bromide on the sample is minimal. It's only when you're getting into the high range of concentration of DNA and the low range when you're comparing two that ethidium bromide may play an adverse result on the sample.

For instance, the F. B. I. routinely run a 500 nanogram concentration of DNA and they have no apparent shifting due to ethidium bromide.

Q. That's because they use -- you feel that's mostly because they use a different buffer solution?

A. No, I think it's because the effects of the ethidium bromide at that sample concentration are minimal.

Q. Is there any way of converting the R. C. M. P. systems to yours and you use the same buffer but don't use the ethidium bromide? Do you think you might have a much closer match window?

A. No, I don't think so. In fact, what Dr. Budowle and myself have done in the past, Dr. Budowle is the research scientist involved in the DNA typing program for the F. B. I. at Quantico research lab. We've actually exchanged samples and looked at the two systems with respect to comparison because this becomes a very important question for standardization in North America, and part of the function at TWGDAM, actually, we asked those exact questions. What effect does agarose, for instance, ethidium bromide, buffer, length of gel, type of tank that was used, et cetera; all these variations that could occur within a lab; we asked the simple question, what effect does that occur. We had three separate studies in TWGDAM which encompasses precision and match criteria, and what surprised me was just how close the actual precision and accuracy was within all the labs. It was quite astonishing.

Q. I have this question for you, when I think of Peter D'Eustachio who was critical of the F. B. I.'s environmental insult studies, is that right?

A. Yes, I think he actually phoned Dr. Waye and had a chance, an opportunity to talk to him.

Q. And I suppose part of the argument in that case was the effects that the R. C. M. P. found that ethidium bromide had in nerve system?

A. He might have made comments towards that. You could refresh my memory, but I think he had also concerns over their standards or controls that they might have run within the gels when they did that first set of analyses, and one has to recognize that the paper that Mr. Walsh has put into evidence certainly has addressed some of those concerns.

Q. What I'm concerned about, Doctor, is because you and Dr. Waye, and I guess Dr. Bowen, were concerned about what effect the use of ethidium bromide would have in your system that it might cause irregular band shifting or unnecessary shifting?

A. There's no -- it was -- we have enough situations that we can't deal with with respect to forensic samples that we don't need to add any more aggravation. The other, the actual practical concern with ethidium bromide --

Q. But my question to you, Doctor, is that ethidium bromide would cause aggravation in your system. It does not cause aggravation in the F. B. I. system.

A. Apparently using --

Q. Now, environmental insult studies have not caused aggravation in the F. B. I. system. That doesn't mean it won't cause aggravation in your system because you have to use the ethidium bromide as an analogy here to prove that you have to do your own environmental insult studies?

A. I wouldn't agree with that.

Q. Many scientists would agree with that, though, wouldn't they?

A. I don't think so. I think we also have done some of our own environmental insult studies as well and what you're essentially saying is that we should redo all our studies that the F. B. I. have done. You also have to recall that other labs participate in TWGDAM. For instance, Metro Dade, Dr. Rodger Kahn, there's a lab that doesn't use ethidium bromide, uses TAE buffer, and same agarose and everything that we use and they've done all the environmental insult studies and there's no deviation from the results that the F. B. I. have had.

Q. That's in their lab?

A. Why would our lab be different?

Q. Well, because you can't achieve the same results in your lab as the F. B. I. achieves in their lab.

A. How are the results different?

Q. The ethidium bromide test is one.

A. I'm not sure I follow you.

Q. Well, if the ethidium bromide as a contamination affects the migration rate through your system and it doesn't affect the migration rate in the F. B. I. system --

A. At the high range and at the low range, both systems, there's an effect. At the actual forensic concentration that is applied in a routine case, there's no effect, and in fact, Dr. Budowle and myself have done studies where we looked at variations in the two microgram range down to about -- I think we went down as low as 50 nanograms

or maybe it was 100 nanograms, and the ethidium bromide, whether used it or not, had no effect on the actual displacement. It's only in the high and low range, and those studies I conducted with Dr. Budowle at Quantico.

I think the whole issue with ethidium bromide is one that people dwell on and, in actual fact, it can be considered a red herring. In Tris Borate EDTA systems, I think they're just as reliable as Tris Acetate EDTA.

Q. Dr. Fourney, it's been claimed, I believe in at least one of the later cases to go to court, that in actuality there's more opponents in number going to court and testifying against the admission of this evidence, say scientists, than there are proponents. Are you aware of that?

MR. WALSH: If I could find out where that's said, I would much prefer, My Lord. I'll form it in the way of an objection, but if Mr. Furlotte would indicate where that statement is made and who made it before Dr. Fourney is required to address it?

COURT: I would think it would be an awfully hard thing to assess. I don't know whether somebody connected with a judicial system would have to make an assessment like that, or a law society or --

MR. FURLOTTE: Well, it would be somebody who is keeping records of all the cases and the witnesses going to court, I would imagine.

COURT: I don't think, really, it demonstrates anything. You know, if it is a valid statement, whether it demonstrates anything. I don't think it demonstrates anything really. There are an awful lot of

plaintiffs' actions fail, you know, in a civil suit where a plaintiff may call fifteen witnesses and the defendant may call one, or perhaps none at all. You know, the number of witnesses that you have isn't indicative of --

MR. FURLOTTE: Or like the Crown calls five and the defence calls one?

COURT: That's not going to win for the Crown in any case.

MR. FURLOTTE: I should hope not.

COURT: It is the merit of the argument, the merit of the evidence in any case. However, the point you're trying to make is there are a lot of scientists or a lot of people in the scientific world who have reservations, who either have reservations or at least are prepared to say they have.

MR. FURLOTTE: I guess when they use the term "generally accepted" in the scientific community, I guess, the evidence I'm trying to bring out that will -- what do you mean by "generally accepted"?

COURT: But if you took all of the people who may have testified, perhaps, against. They all may have a variety of reasons why they would oppose DNA testing. You know, the numbers aren't conclusive one way or the other. I would tell Mr. Walsh the same if he were asking a similar question of a witness. But if the witness has any knowledge on this point or any observation to make, you're free to do it now.

WITNESS: I think it was pointed out in Jakobetz where they made a comment that the validity or reliability of a protocol or procedure is not made by a nose count I think that's exactly what they're attributing it to is the number of one side versus the other side. It has nothing to do with the actual science.

COURT: I like your expression "nose count". I must use that in some civil case.

Q. Doctor, the ability to -- or I won't say the ability, the reliability to use this system and to calculate the frequencies, I would admit for your purpose that it is probably generally accepted in the scientific community of forensic scientists. Could you agree with that?

A. The ability to calculate the frequencies of VNTRs?

Q. Yes?

A. I would think so, yes.

Q. That's amongst the forensic scientists. Now, what about the scientists in general, in your population genetics?

A. I think you'll have an opportunity to ask Dr. Kidd that this week, actually.

Q. Do you know Dr. Daniel Hardlt is against the use of this in establishing the figures?

A. Establish -- what exactly is he against?

Q. The formation of the -- the validity of the data bases that are founded by the F. B. I., and no doubt other laboratories?

A. So what you're saying is that he doesn't think that DNA procedures can give you a positive match? Is that what you're saying?

Q. I'm saying that Dr. Daniel Hardlt says that the F. B. I. cannot even identify its own F. B. I. agents on retesting data.

A. I think they're probably looking at fairly old information and that presumably means their -- they had a number of different data bases that they were using. Could you be more specific?

Q. Well, Dr. Hardlt criticized the F. B. I.'s procedure and their results, I suppose it would be more than anything else, in the formation of their data base whenever they did their rebinning procedure, that they weren't able to obtain the same results. It wasn't reproducible.

A. I don't think they're the same tests that were performed, or it wasn't the same samples, or the same procedure might not have been run the same way. So you're essentially asking me if you run a procedure differently with different results, am I surprised that you would get a different result?

Q. I don't believe -- as far as your understanding, you believe it was run differently with different people?

A. Oh, I know so. Once again, I believe you could check Jakobetz, page 28, and you will note that the C1 and C2 data base there actually used a different binning mark -- they used different markers, bin markers, and they actually supplemented their samples. I can't recall how much, but ten or twenty percent supplement with actual new samples because for some reason, the samples that they had previous had degraded or they weren't present in the -- they had used up the samples, what have you, but, so they weren't exactly the same samples and they used a different marker system to actually calculate the bin frequencies.

So perhaps there were some minor variations in that. The other thing is that I think they also, and you could check this, possibly the F. B. I. on this, but I think they ran their gel slightly longer, and one of the concerns they had, for instance, in the initial data base is that they

were getting a few more homozygotes than they should have. By altering the concentration of DNA was also changed. They went from, I believe, either four micrograms to two micrograms or two micrograms to one microgram. Whatever the net effect of that, when they re-ran that with a smaller concentration of DNA, they were able to start to resolve double bands -- or single bands into double bands, and that would account for some of the variation that they saw in the initial data base. So there were slight differences.

Q. Why would that change variation in the bin frequencies?

A. No, I think --

Q. If you're going to measure a fragment length, it should be the same length regardless as to which system you use, shouldn't it?

A. Yes. It didn't change the bin frequency. What it changed was the homozygote count or what is more correctly termed single band patterns versus double band patterns.

Q. So as far as you're aware, it didn't change bin frequencies?

A. As far as I'm aware, I think there were some changes in bin frequencies in those two studies, yes, but they are also different studies. It wasn't a replication of a previous experiment.

Q. Are you aware that because -- or maybe I shouldn't say because of the concerns of Dr. Hardlt, but the R. C. M. P., or the F. B. I. actually did a third rebinning and did their tests all over again a third time?

A. I think they've probably done four, actually.

Q. Four, actually?

A. And I think you'll also find that their data base is no longer 250 people like it was in that particular Yee decision that you're referring to. I think their data base today is probably even larger than ours. I think it's close to 1,000 Caucasians, for instance.

Q. I thought you said you had the largest in the world?

A. Well, I could stand to be corrected at this point because according to Dr. Budowle, they are constantly adding more samples and we could be close second. We certainly have one of the larger data bases. I'd like to think that we had the largest data base, but once you get past 600 individuals, then you have a fairly representative population.

Q. There's also Dr. Richard Lewontin is against the R. C. M. P. or the F. B. I. or any of you using the product rule?

A. I think he has some concerns. He filed a report with Yee and some of those concerns are probably being addressed as we speak. With regards to Dr. Hardlt, now, are you saying -- is he against -- are you suggesting that he's against DNA finger-printing with respect to positive identification?

Q. I believe in Dr. Hardlt's report he suggested that the F. B. I. are incapable of identifying their own F. B. I. agents, so therefore they couldn't identify anybody else. So, yes, in those regards he was probably against it.

A. So he would be against the positive identification of DNA typing being used as a positive identification?

Q. As effectively as it is today?

A. That's in direct controversy to his recent book that he's written addressing the fact that he thinks that DNA typing is a very positive identification means, and it's going to be a very strong forensic application for this procedure.

Q. If it's done properly?

A. Well, he just makes reference --

Q. Does he have that qualification in there?

A. I would make that qualification in anything. If anything is done properly, then it's a lot better than if it's not done properly. Any clinical test will fail and give you a non-valid result if it's done improperly, even a simple pregnancy test will fail.

Q. Isn't that the same opinion of all the scientists in the scientific community, that some day you will be able to do it right, but today you can't?

A. I think the general opinion of the scientific community is that any test that is done properly will give you valid and reliable result. That -- I would agree with that. Whether or not some scientists disagree that that time has occurred with DNA typing, I'm not in that opinion, no.

MR. FURLOTTE: Maybe we could have a break at this time, My Lord?

COURT: Without pinning you down, do you sort of see yourself getting through with this witness this afternoon? I'm not pushing you at all.

MR. FURLOTTE: No, I don't think I'll be through with him this afternoon.

(Accused escorted from courtroom.)

(Court Recessed 2:55 p.m. to 3:10 p.m.)

(Accused present.)

Q. Dr. Fourney, I'll go on to read from VD-50, the article that you authored.

A. This one here?

Q. Again, at page 119, to continue, I'll just repeat the last sentence that I had read to you. It says, "Apart from quality control and technical proficiency, there are several bonafide scientific issues at the heart of this controversy." Now I'll continue. "These include concerns regarding the number and type of loci being analyzed." That is still an issue in the scientific community?

A. I don't think so.

Q. You don't think so?

A. Certainly in North America we adopted the HaeIII restriction endonuclease and --

Q. Aren't there many scientists who feel that there should be eight to ten probes being used rather than four or five?

A. I don't see why.

Q. You don't see why? okay.

A. We currently have --

Q. I didn't ask you what you saw, I asked you what other scientists saw.

A. We have seven probes in our system.

Q. You're aware that other scientists are of the opinion that they should be using five to ten probes? Are you aware of that fact?

A. I'd have to be shown it, I think.

Q. So you're saying you're not aware of that fact that

other scientists are of that opinion?

A. What I'm saying is that I would have to see in what context that had been said. There are certain reasons why --

Q. Doctor, these are your words that I'm reading.

A. Um hmm.

Q. It's not somebody else's opinion that I'm reading when I say that the concerns -- these include concerns regarding the number and types of loci being analyzed. What did you mean by that?

MR. WALSH: Objection. Mr. Furlotte has put a question to him about whether or not he's aware that other scientists suggest that there should be five to ten probes used. Now, Dr. Fourney would like to know the context and where that was said. Now, unless that's in the document, I think he should at least tell the Doctor where he got this statement from or is Mr. Furlotte making this up at break?

Now, I think it's important that he actually refer to it.

COURT: Well, we're sort of getting our questions a little mixed up. As a matter of fact, I think you asked, Mr. Furlotte, did you not, some scientists feel there should be from five to ten probes used. Instead of what, because there are seven being used here, and, you know, it makes the question sort of meaningless. But what are your --

MR. FURLOTTE: Two probes here are not being used for identification purposes. You are using five for identification purposes in this case?

A. There are six probes there for identification.

Q. In the office of technology assessment report, did

Dr. Lander state that he figures eight to ten probes should be used for identification purposes?

A. I've read that report but I can't remember the exact specifics. Perhaps you could show it to me, or --

Q. Okay, that's fair. I just want a fair answer. Also concerned about the criteria used to define an RFLP match. This is in your paper?

A. Yes, --

Q. That concern?

A. You would have to define the match, yes.

Q. Yes, and the degree to which allele frequency population data bases are representative of the relevant populations. That's also a concern?

A. I think that's --

Q. And you stated as a bonafide scientific issue?

A. The concern there would be are you using the relevant data base for the particular case that you're working on.

Q. But it is a bonafide scientific issue? You identify that as being a bonafide scientific issue?

A. These are all issues that we discussed in this paper, and that some of these --

Q. Doctor, I don't like to ask you to answer yes or no, but I would like an honest answer here, if that's an issue?

A. To which allele frequency population data bases are representative of the relevant population?

Q. Yes?

A. Yes, I think it's important to know the population that you're dealing with.

Q. And also it is an issue, a bonafide scientific

issue is the validity of the statistical methods used to assess the significance of RFLP inclusions. That is also a bonafide scientific issue?

A. Yes, I would say the statistical issue involved with frequency would be an issue that is a concern in the general population of scientists. But once again, you have controversies on both sides, and without it I don't think we'd have any science.

Q. Page 137 of VD-50, the top paragraph you state, "In theory independent DNA samples from a single individual should yield identical RFLP profiles. In practice, however, there are factors which can cause slight alterations in the electrophoretic mobility of genomic DNA such as the RFLP pattern of one sample is shifted relative to the pattern of a second sample for the same individual." You state, "This phenomenon hereafter referred to as band shifting can greatly complicate the interpretation of VNTR comparisons, or for that matter, any comparative analysis of RFLP profiles." Is that right? Band shifting can complicate the interpretation?

A. Certainly, if you have band shift, it could cause a complication, yes.

Q. And the second -- the third sentence of the next paragraph on page 137 you state, "If band shifting can be confirmed, it must be determined which of the patterns has shifted and which fragment sizes will be used to query the data base to determine the significance of the match. Of equal importance are those situations where the VNTR profiles are a visual match for it could be argued that the patterns

are, in fact, different and that band shifting has resulted in a false match." So you state that you can obtain a false match through band shifting?

A. You can possibly get a false match on one probe with a band shift.

Q. On one probe?

A. That's correct. Now, we're talking about a false match.

Q. Okay, right. Now, if you could do it on one probe, why can't you do it on two probes, if there's a possibility there for one?

A. I think that's a real question for, possibly, a statistician or someone who works at probabilities, and my feeling is -- my personal experience would be that I would highly -- I think it unlikely that you would get a band shift as a positive match for two probes. Certainly with three, much less.

Q. Okay, much less with three. Okay, if you got a match on five probes and if you say there is a possibility of a band shift creating a match in one probe and you've got five, could you have one wrong out of the five? One false match out of the five probes, and we really only have a match on four of the probes?

A. So basically a band shift on one single profile that was, what, positive or negative?

Q. Does it matter whether it's a positive shift or a negative shift?

A. Well, basically if you have a shift on one of the probes that are clearly evident it's a band shift, for instance, and you have a match on the other four, then that particular single probe would probably be deemed inconclusive.

Q. So that particular probe would be deemed inconclusive?

A. The results from that one test. Each test, you see, is an independent test.

Q. Right, but if you're going to have a shift on one probe, you know, if your DNA is such a quality, I should say, that it's going -- you're going to have a shift on one probe, would you not have a shift on all of them?

A. I would predict that, yes.

Q. And the shifts would not be consistent on all of them? They'd vary for each probe?

A. Yes, you're probably right.

Q. If you've got a three percent shift on, say, probe D2S44 on your high molecular weight band, the D1S7 high molecular weight band might have a shift of one percent? Is that correct?

A. I would think that if you had a band shift, it's consistent, and that it's quite apparent, actually. The monomorph would tend to tell you right away whether or not a band shift has occurred.

Q. And how much?

A. Yes. You could certainly get some kind of measurement away from the actual predicted 2,731 base pairs.

Q. So if you were away by three percent on the monomorphic, say you had a plus three percent, you may end up with a plus one percent on the D2S44. You may end up with plus four percent on the D4S139?

A. I don't think there's any evidence to suggest that.

Q. Could you use the consistent measurement of three percent?

A. No, we certainly -- we are unlike some labs that use monomorphs to adjust for band shift. We prefer if band shift has occurred and we conclusively have

made the tests properly and we conclusively made the call that there was a band shift, then we would deem that inconclusive. So we would not adjust for band shifting if that's the question you're asking. I believe some labs such as Lifecode may, in fact, do that.

Q. If you saw band shifting for one of the probes and because of the band shifting -- and it was inconclusive for one probe because it wasn't safe to interpret it, and we know that band shifting -- you just can't get band shifting for one probe and not the others, then wouldn't it be appropriate to deem them all inconclusive?

A. As a scientist, certainly a research scientist, if I was a band shift I would want to ask the question, why the band shift actually occurred, so I would look for the reasons behind that band shift. If you had a band shift in a sample that was clearly visible, you would probably throw that particular lane, for instance, that sample out for that particular test.

Q. Would that go for the same thing if you -- suppose it fell outside the matching window?

A. That if one particular probe fell outside -- or one band fell outside the matching window?

Q. Yes?

A. We would, what, throw the entire set of results out?

Q. Well, do you have any standards for such situations in your lab?

A. Oh, you wouldn't throw the entire set out, no. You've got to remember that the initial procedure that we use for evaluation of a match is a visual --

It's based on the experience and the expertise of that person analyzing the results. There are cases, for instance, at the top end of the gel beyond our base pair binning marker, for instance, that once it's outside that limit, we can't do anything with that. But it doesn't exclude the results of any of the bands that are within our detection lengths.

Q. No, but you could get results that shows that, maybe for one probe you're outside the limit and for another probe you're well inside the limit?

A. there are certainly variations within the gel and with respect to the deviation you could expect. Some of these are practical things like concentration of DNA, and in my personal experience with looking at raw data, essentially in our particular case, the forensic samples we've matched as the slide I showed this morning, 99 percent of those samples are within our 5.2 percent window. There's a few that are out, but very few. I think -- I have to look at my notes, but I think there were maybe two or three that were outside that out of 502.

Q. Outside the?

A. Five point two percent, and those would be inconclusive results.

Q. Which case was that, this two or three outside the 5.2 percent?

A. The actual cases that those were?

Q. Yes, you're not talking about this case?

A. No, no. I don't know what case that would be. That would be a question that we'd have to go back through our notes and I think it was one of the first cases that we did last year, for instance.

Q. Now, in those cases that wouldn't be outside the five percent matching window for all the probes, would it, just one or two?

A. I recall the details of that. I seem to recall that it was primarily at the upper end and it was most likely the D4S139, for instance which basically it's a very sensitive probe and you can get a high concentration radioactivity associated with any one fragment, and one has to be careful, for instance, to do what we call a variation in the autoradiographic exposure. That simply means to expose the X-ray film for a shorter period of time so if you have more radioactivity there, you're going to get a blacker spot. In order to make a definitive statement, you want to get as much resolution as possible, therefore you would use a shorter exposure so that there's less silver grains being hit by the radioactivity to cause the exposure.

Q. Are there any standards set within the forensic scientific community as to what to do whenever you have one or two of the probes falling outside the match window? Or is that just left up to the individual lab to make whatever they want of it?

A. That's been discussed at TWGDAM on several occasions and generally if your results indicate, for instance, that you have three or four probes that are clearly a match, not only visually but within the match criteria and often many of our matches are within plus or minus one percent, you would certainly not throw those results out because of another probe, for instance, that may be in the higher region of the gel that has shifted outside the marker range, for instance.

You would probably call it inconclusive.

Q. Could a contaminated sample and, say, a fast lane offset one another or throw it out of balance enough to create a false positive?

A. What do you mean by fast lane?

Q. Well, I think in the examples you are given about -- the ones in your direct examination, you mentioned about how your polymorphic probe, it would vary across the gel, the degrees would vary across the gel?

A. You mean going from the positive to the negative electrode?

Q. No, not necessarily going from positive to negative, but I believe in the monomorphic probe you give an example that maybe in lane two it was plus one percent and then as you go further across the gel it might increase?

A. Yes, I see what you mean. In other words, as you get further away from the flanking marker, for instance, there's a slight increase in the imprecision. Yes, that's possible. You get that, I mean, we know from our own measurement, but it's very close. I mean, we certainly are talking about eleven, twelve, thirteen base pairs. That's very accurate.

Q. Yes, it depends on the size of the fragment, too?

A. Yes.

Q. That's on the --

A. That happens to be on that particular one.

Q. Would that be due to, say, measurement imprecision or would that be due to just maybe the speed of the gel picking up as you go across it?

A. No, I think it would be probably due to just measurement imprecision.

Q. Why would that exceed consistently as you go across the gel?

A. Because of the log molecular weight properties of the electrophoresis and DNA analysis.

Q. And you would also agree that one must be able to exclude the possibility of band shifting among the samples used to compile population data bases?

A. You certainly wouldn't want to use a sample that was evident of band shifting, no.

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

A. None.

Q. None whatsoever?

A. But we have an equal guarantee that it doesn't exclude them, either.

Q. No, right, that doesn't mean there's nobody there just because you don't know if there is.

A. That's right, a negative conclusion is not worth much.

Q. But you are drawing in your conclusion that because in the Kingston army base or whatever it is, forces base, that the Maritimes are probably double their ratio as to the general population of Canada?

A. Am I making the conclusion that's the case? I know that's the case.

Q. You know that's the case?

A. The director of personnel for the Department of National Defence has compiled that data for us. I know the number of individuals in that base, and

I know what the percentage of them are representative from the provinces.

Q. And the percentage from New Brunswick on the base is what?

A. Whatever it was in that figure. It was defined as military personnel and dependents, I believe. It could be 5.2, but I'd have to check.

Q. So there's a good chance that there's actually nobody from New Brunswick in the R. C. M. P. data base?

A. Perhaps you could define --

Q. When you look at the few people that you choose from?

A. What's a good chance?

Q. How many samples come from Kingston?

A. Well, I think there is -- just trying to recall, now. We have 524 samples, or 526, whatever was in that report. I think from what I recall there is approximately 5,000 members in the armed forces community there.

Q. Approximately ten percent of the people -- you may have gotten samples from about ten percent of the people on the base?

A. It's possible. Anything is possible.

Q. Consider the French and the English, say people from England and France, to be different races?

A. Do I consider them different races?

Q. Or are they?

A. I think technically, and once again you'd probably have to refer to a population genetics text, but a race is considered to be a subgroup of individuals, a subpopulation within a larger population that has more similarities than differences.

Q. I'm just considering, you said the Canadian Caucasian data bases, in Caucasians, are mostly people from France and England?

A. Originally their origins would be from France and England, probably, yes. What's interesting there is when I was reading the Census Canada, I'd like to know how they draw the conclusion that the British are different, say, from the Irish, et cetera. From a strictly technical term in population genetics, I would find that hard to believe, but from a country of origin for Stats Canada, it's probably a very valid criteria.

Q. I see that VD-91, the guidelines, I have Exhibit VD-91 which is the guidelines for quality assurance program. I show you that and address a few comments in it, requirements. See if we've got the same page numbers here.

A. That's hard to see --

Q. Two sixty-two up top?

A. Yes.

Q. Okay. See here the paragraph page 263 it says, "These guidelines represent the minimum quality assessment requirements for DNA RFLP analysis and are intended to serve only as a guide to laboratory managers in establishing their own quality assessment program for DNA RFLP analysis." And the R. C. M. P. belongs to this group?

A. Yes.

Q. The R. C. M. P. lab? I notice one of the minimum requirements -- I can't find it now. Hang on a second. In paragraph 5.3.3 on page 269 under population studies it says, "Establish population

distribution data in different racial groups for restriction fragment bands detected by a given restriction enzyme DNA probe pair." Now, would that require you to do population studies and compare them between the English people and the Canadian Caucasian data base and or population and the French?

A. No.

Q. Why not?

A. Because I think race in this particular term, I would consider aboriginal populations, for instance, to be a distinct race.

Q. A distinct race?

A. Both, well, for reasons of geographic origin as well as culture.

Q. We have evidence in Exhibit VD-65 which was presented in court by Dr. Carmody where he did a comparison of the frequency distribution for the probes in Legere's case, and he found a distinct and statistically significant difference with binning frequencies in France than in for the F. B. I.'s data base or Florida's data base, or Minnesota's data base. As a matter of fact, for the Canadian data base it was one in 59, and in France it's one in 34. That's for probe D2S44. And again, for probe D10S28, Canadian data base is one in 108 and in France, it's one in 54. Now, why do you think the French population of Canada who is descended basically from France might not be the same as the people in France?

A. I guess that would probably concern me except that at the Promega conference I was in in February - March, I had an opportunity to speak to the

gentleman that compiled that data who was from France and he explained to me that they had so few data points that it really wasn't considered yet to be what he thought would be a reliable population size, and he was basically going to increase that significantly.

I could be wrong, but I believe there's something like 80 data points, perhaps, and they literally took them from various areas and he's now repeating that study. So I'd be very anxious to see the --

Q. Doesn't that make you curious that just maybe there might be a difference in Canada?

A. Well, as a scientist I'm always curious. As a research scientist, I think it's exciting in some ways because if there is a difference, then I'll probably have a paper for nature or science. But I wouldn't expect there to be a difference and --

Q. But as a scientist --

A. -- sadly enough, after talking to Leo Laverne at the Montreal lab which is actually compiling this type of statistics in a fairly large format, they have well over 500 samples now. We also are going to get an opportunity to look at those samples and, to date, from what I understand from George Carmody that the differences that are detected between the Caucasians and Leo Laverne's data base and ours, in particular with D2S44, for instance was one of the probes you mentioned, are not truly significant.

There may be some alterations in the frequencies, but the net result I don't think would be very much different.

Q. But doesn't such information establish besides a curiosity -- or doesn't it establish a scientific duty for you to study this probability?

A. It's my scientific duty to study anything that I find curious. If I was to write a grant in Canada, and had to have it peer reviewed with respect to proposing the situation that there would be a difference in the VNTR polymorphisms between French Canadians and English-speaking Caucasians, for instance, I would probably be turned down for that grant because there would be an awful lot of preliminary data such that I'm sure you're going to hear from Ken Kidd and others that wouldn't support that.

Q. So basically because it would take too much time and too much money to obtain this information, we just ignore it?

A. No.

MR. WALSH: That's not -- I don't know where that came up.

A. Certainly not --

MR. WALSH: That's --

COURT: Let's hear the comment.

MR. WALSH: I'm sorry, My Lord, my objection was that Mr. Furlotte was -- he turned around and said basically, and what he is saying, I didn't recognize it as being anything, and part of any answer that Dr. Fourney had given. I was just objecting on the basis that it was misleading to state it in the fashion that he did because he implied that it came from Dr. Fourney.

COURT: What he's asking Dr. Fourney to do is comment on this suggestion that perhaps those circumstances lead to the conclusion which Mr. Furlotte has just expressed.

Your answer is no, I suppose?

A. I'm trying to remember the question.

COURT: Yes, can we have it again?

Q. Basically you said you'd be turned down from a grant to do this study, to compare the English and French Caucasian in Canada, because it would take, what, too much time and too much money?

A. No, because primarily that certainly the granting societies in Canada, M. R. C. and N. C. I. C. -- or N. C. I. C. and others, they only grant those proposals that are deemed relevant and good with respect to actually being possible. So they would think it would be highly improbable, and therefore they wouldn't fund it. That would be my honest opinion.

Q. You don't know that. You didn't ask them that, though, did you? You've never approached them, did you?

A. I know of people in the States who have in similar situations, in the American granting sectors.

Q. We're not talking about the Americans here, we're talking about Canadians. Americans aren't going to fund our projects.

A. No, but they're not even funding their own projects with respect to what you perceive to be true and different Caucasian data bases. I think what's more significant is possibly to look at, certainly, the Native Indians of Canada. I think they are, certainly, a distinct society.

With all the information I've seen worldwide, presentations, the various meetings I've attended, Caucasians are pretty well similar.

That should be made with respect to the VNTR polymorphisms. They are all highly polymorphic.

COURT: You mean your use of the expression "distinct society"?

Q. If you use the same buffer as the F. B. I., do you think that might narrow your matching window?

A. I don't know. I do know that the buffer that we use, the Tris Borate EDTA, is considered to be a much better buffer, buffer having the ability to maintain the pH within your electrophoresis system; and from personal communication with the British Home Office, Dr. Peter Gill who is in charge of that DNA program, he informs me that they have tried the different buffer systems and have actually found that they prefer the TBE buffer which is what we use over that of TEA.

Q. Would you say the F. B. I.'s system is more efficient?

A. Could you define efficiency?

Q. Well, because they have a smaller matching window?

A. How is that more efficient?

Q. They come to their matching window by running their samples and their tests not on pristine samples like the R. C. M. P. did --

A. -- that's only --

Q. -- and they used the ethidium bromide and they still came up with a smaller window?

A. Perhaps you missed the point I made this morning. That was just part of the measurement precision study was with pristine samples. We also have 502 bin-wise -- or match-wise comparisons with forensic samples.

Q. Did your match window change any?

A. Did you remember the slide?

Q. Did I remember the slide?

A. Yes, the slide that I showed was on the 502 comparisons, 99 percent of them were within 5.2.

Q. Yes, 98.6 percent. What did you establish your match window on?

A. Well, they're both --

Q. The case samples or --

A. They're essentially both the same.

Q. Potentially both the same?

A. No, I said they're essentially both the same.

Q. Essentially both the same. So it doesn't matter whether you're using pristine samples or contaminated samples?

A. No, I think you have to do both the studies.

Q. What benefit is the use of the monomorphic probe to the R. C. M. P. when the F. B. I. says that basically they don't need it?

A. What benefit is it to the R. C. M. P.?

Q. Yes?

A. Well, it's a very efficient probe on which we can detect measurement in precision. It's also a probe that allows us to determine whether or not a restriction digest has worked properly. It's also a probe that's highly sensitive and it confirms yet again the presence of human DNA, and in fact, in conjunction with DYZ1, presents very good evidence for the fact that one, you have human DNA in there, and secondly, it can actually augment the studies with DYZ1. I think it has a lot of potential. In fact, many of the labs that are

participating in TWGDAM are, in fact, using DY22.

Q. And the F. B. I. still doesn't?

A. You would have to ask the F. B. I. why they don't use it.

Q. Does that make their system less efficient than yours?

A. Well, once again, I don't think it has anything to do with efficiency. Efficiency is the ability to produce a result that is just as valid and accurate faster.

Q. Well, I call, maybe, efficiency as part of proper interpretation of an autorad. The less chance you can make a mistake, the more efficient it is. On that basis, is the F. B. I. system less efficient than the R. C. M. P.?

A. Well, if you pardon the question, I think you're using efficiency wrong. Efficiency is two people doing the same task and one can do it much faster with less problems.

Q. Okay, let's go for the word accuracy.

A. Does it make our system more accurate?

Q. Yes?

A. No. It's just an additional test that we could have left out, but in the fact that it adds more information that we consider valuable, we use it. So by actually doing an additional test, we're adding to our information, we're not detracting from it.

Q. Does it give you greater interpretation powers moreso than the F. B. I.?

A. Interpretation powers. I'd have to think about that.

Q. All I've been hearing, or a lot of what I've been hearing in this hearing, is how great the D7Z2 is and I want to know how great it is.

A. It's great.

Q. It's great? But it doesn't improve your system any over the F. B. I.'s?

A. It has the advantage of being able to run an additional probe to confirm your accuracy and precision. The other thing D7Z2 has which very few other probes have, and this is important to recognize, is that the actual fragment, the 2,731 base pair fragment, has been sequenced. The fact that you've sequenced this probe means -- this fragment means that you've taken it apart into its individual components and you know the exact size of that fragment. Unlike the other probes that are present in your gel, we don't know the exact size, but the D7Z2 is an internal standard, a control, where the exact size is known.

Q. Now I'll ask you, so what?

A. So what?

Q. It doesn't improve your system any. If the F. B. I. doesn't need it and it doesn't improve your system on interpretation or the running of the gels, so what if you've got a monomorphic probe that tells you the exact size of the bands? It's got nothing to do -- it has no regulation on band sizes of the other probes.

A. It's an additional test which I think is very valuable.

Q. Tell me the value, Doctor.

A. I just did.

Q. Because it has an exact number of base pairs, 2,731?

A. It gives us a precise measurement of our results within the gel, and you can do this after a gel has been restripped and reprobed numerous times. It's very sensitive as well.

Q. You're saying it measures your imprecision?

A. It gives us one test for measurement precision, yes.

Q. How does the F. B. I. measure their imprecision?

A. I think they do it by actually evaluating runs over and over again of the various VNTR profiles, and then they would take the average or probably the medium value of those.

Q. Which would be much more accurate?

A. Why would that be more accurate?

Q. Because then you're running the different probes over and over again to see what difference you're getting in results. I've been told because of the different gel changes, changes across the gel where one lane might run faster than the other and where band shifting might have a different effect on one different fragment size than another different fragment size and you couldn't run the three percent, say, band shift on your D7Z2, you couldn't use that three percent consistently for all the different band sizes because there's a variation in them. But they don't know how it varies or why it varies, so it would appear to me that the F. B. I.'s system would be much better because at least you're comparing identical -- supposedly identical fragment sizes.

A. That's something that we do anyway. It's done every single time you run a gel. You have control DNAs, for instance, of known sample integrity, for instance, the saline DNA that we run, and they're included on the gels and we measure those as well. So in fact, what we're doing is what the F. B. I. do plus one additional test.

Q. Which has a lot of value but you don't know exactly what?

A. I'm sorry, I --

Q. Except to help you measure your system imprecision?

A. I told you three reasons why we use D7Z2.

Q. You didn't tell me the reasons, you told me the results you get from running it. That's not the reasons for running it.

A. I'm sorry, the logic is lost here.

COURT: Do you want to ask it again? Rephrase it in some way, Mr. Furlotte?

Q. All right, you tell me the three reasons you run it again?

A. Well, it gives you a precise measurement.

Q. Of which lane?

A. Of every lane that --

Q. Or of which probe, I should say, precise measurement of which probe? This probe here?

A. It tells you that you have a fragment that's going to be expected to have a HaeIII major band at 2,731. The second reason, as you'll recall, is that it's human specific so it's able to detect human DNA, and the third reason is that it allows you to make some kind of conclusion with respect to the proper restriction. If a DNA sample, for instance,

is not restricted properly, you get an aberrant D7Z2 pattern. It's just an additional test which we find very useful for those reasons.

Q. Take this lane B and lane C for an example, okay?

COURT: On VD?

Q. On VD-45. We'll say that this is the known substance, known sample, and this is evidentiary sample, unknown, and if your D7Z2, if lane B when you run your D7Z2 shows it as 2,731 base pairs and lane C shows it as plus three percent, could you use that plus three percent either to adjust to make a match or adjust to --

A. No, we would never use the variation in monomorph to adjust for match. Match is made with the actual VNTR pattern, the fragments itself. In actual fact, we're comparing those samples together so that it's never used for an adjustment of a match. It's simply there to confirm whether or not a shift has occurred.

Q. But in your difference in sizings, if you come out with this exactly the same size, 3,000 base pairs, when you run your D7Z2 probe you find maybe a three or four percent difference in the lanes with your D7Z2 probe?

A. I don't think I've ever seen that.

Q. It's not possible?

A. Anything is possible, but I think it would be highly unlikely. A shift in the monomorph would certainly -- I'd expect to see a shift in the other VNTR patterns. If it was a noticeable shift, you would certainly see it.

Q. Do you ever expect to see shifts in the monomorphic probe, say one lane is plus five percent, the other lane it's -- well, no, we won't go with five. We'll just go with two or three. Say one lane, plus three percent and the next lane right to it might be minus three percent?

A. Would I expect to see that?

Q. Would you expect to see something like that?

A. I don't think it would be common. One of my questions in that respect is that I would certainly look at the preparation of the sample and see if it had any salts or something associated with it to account for a slight variation in electrophoretic mobility. The other thing it simply could be due to is the monomorph is extremely sensitive in terms of it takes very little amount of DNA to develop a major band density on the autoradiogram and you have to be very careful in making a correct exposure so you can size that. It's more difficult to size a thicker, darker band than it is a smaller.

Q. Okay, if your monomorphic probe, you run this and you have this one measured plus two percent, then the other one measured minus two percent, is that what's called reverse band shift? If you've got one plus and the other minus?

A. I don't think I've ever heard the term reverse band shift before.

Q. You've never heard reverse band shift, phenomenon reverse band shift. It means shifting in reverse directions.

A. Reverse band shift, that specific term I've not heard, no.

Q. Have you heard about band shifting in opposite directions?

A. It's not been our experience in our lab.

Q. I'm not talking about your personal experience.

A. I'm just trying to think, though. I've never seen it so it's hard for me to make that kind of conclusion. I'd have to see the example.

Presumably if you've looked at enough samples you would have a feel for the type of band shifting you'd expect and perhaps there is an unknown contaminant out there that could give you a band shift in opposite directions on two separate lanes, of course. But in our situation at the R. C. M. P. we've been very fortunate. We haven't seen that much band shifting.

Q. On VD-93 which is the latest paper done on environmental insults by the F. B. I., I believe you stated that that paper covered most of the concerns of Dr. D'Eustachio's criticisms?

A. I think the purpose of it being written was to address some of the concerns that was the result of the Yee decision, for instance.

Q. I notice on direct examination you said most of the concerns. Which concerns did it not direct?

A. I'd have to actually be told in Dr. D'Eustachio's report what his concerns were.

Q. You don't know?

A. I remember some of them.

Q. So you don't remember the ones that it didn't address?

A. You'd have to refresh my memory with Dr. D'Eustachio's report.

Q. Well, I just saw a copy of the F. B. I. report today so I haven't had time to go over it any great deal.

Again, I believe the report, VD-93, does state on page 12 --

MR. WALSH: I have a copy here, Mr. Furlotte, I will give to the witness.

Q. It states under the conclusions, second paragraph, it says, "This study was not designed to consider all possible contaminants or environmental insults but a number of extreme conditions were tested to evaluate the robustness of the RFLP typing system." Is that correct?

A. That's certainly what it says.

Q. Was there any testing here done for smoke contamination, extreme smoke conditions?

A. Probably not. I don't recall reading that in here, no.

Q. You did read the report, I assume?

A. Oh, yes.

Q. Okay, so when you say probably not, is it because you don't remember?

A. I don't remember specifically anything dealing with smoke contamination.

Q. You didn't review the F. B. I.'s new study on environmental insults, did you? You just read the paper?

A. I read the paper and --

Q. Did you review the data -- the autorads or anything?

A. Actually, they were presented at one of our technical working group meetings at the F. B. I. TWGDAM meetings by, actually, the first author, Dwight Adams.

Q. One of Dr. D'Eustachio's criticisms on the first environmental study, that there was on two occasions band shifts were ignored. Do you know whether or not band shifts were ignored on this study?

A. I don't think there were any band shifts.

Q. You said you don't think there were any band shifts?

A. I don't recall any. It was a very well done study and --

Q. Did you view the autorads yourself to know whether or not there was band shifting?

A. The actual autorads were shown by an overhead projection to the entire audience.

Q. And you don't think there was any band shifting?

A. They looked very good to me.

COURT: Mr. Furlotte, if you haven't read that report, why don't you leave it until the morning.

MR. FURLOTTE: Until morning.

COURT: Rather than try to do it now. Go on with something else.

MR. FURLOTTE: Sounds like a good idea. I believe you stated in forensic samples that the biggest problem is with degradation, that it prevents accurate extraction? Didn't you state that on direct evidence?

A. I'm not sure if those were my exact words, but one of the problems we find in forensic DNA analysis is the ability to get intact DNA, yes, that's true, and the fact that you don't have intact DNA would imply that it's certainly degraded.

Q. Partial degradation can cause a shift in mobility, can it?

A. It's possible.

Q. And it's moreso less detectable where there is low molecular weight DNA being tested?

A. It's more detectable?

Q. Less detectable.

A. You have two opposing forces on a gel. The bottom part of a gel, the distance covered, is such that it represents a smaller number of base pairs so there's, presumably, higher resolution. The top part of a gel you have technically less resolution but your bands are more tightly bound or they're a tighter line, so you sort of have two opposing forces in different parts of a gel.

Q. What has that got to do with my question?

A. You'd have to repeat the question, I guess.

Q. Are you less apt to detect degradation on low molecular weight DNA?

A. Are you less likely to detect degradation on low molecular weight DNA, the fact that you have low molecular weight DNA is degradation.

If you take a gel and run it and you just ethidium bromide stain that gel, for instance, without probing it and you see the majority of your sample at the low end of the gel, that tells you that you've got a problem. That is degradation. Typically degradation, partial degradation, for instance, will be generated from the highest molecular weight downward. But if it's consistently all at the bottom of a gel, that's a hallmark feature of degradation.

Q. What about your quality of DNA to start off with? If you have just a bare minimum amount, I understand it would probably show up with very light bands on your autorad? You're not going to get

good intensity bands, is that right?

A. Yes, 50 nanograms is sort of a threshold limit.

Q. And in such conditions is it, again, less likely that you're going to detect degradation?

A. No, if you've got 50 nanograms of DNA in your gel and you've got a band, that says almost the exact opposite. That says whatever you have on your gel isn't intact enough to not only bind, but give a signal out.

Q. That's obvious by seeing the band.

A. Correct.

Q. But if you've got a very light band, I'm just considering the analogy where you've got the nice heavy bands because you've got a lot of DNA to analyze and it shows degradation when you only have a very light band to begin with, you might not be able to observe the degradation?

A. I would think that the feature of degradation besides the ethidium bromide staining which I already told you about is that you get sort of a threshold background. It almost looks like you've coloured in the lane and then there's bands over it, and that's indicative of degradation. And if you haven't got a lot of DNA there, it's often difficult to see the background, if that's what you've saying. But if you actually have degradation, you won't see the band either.

Q. You see the band where you have lots of --

A. If you've got -- if you have a band with 50 nanograms of DNA; it has a band and you've looked at it on several different probes, then you know it's not degraded.

Q. If we get into the autorads, the originals or the slides, it was obvious that there was all kinds of degradation in these samples?

A. There's probably some degradation, yes.

Q. And it was nice heavy bands and then all coloured in between showing the degradation, and even degradation which, maybe, looked like bands. It almost looked like multiple bands in the lanes.

A. There's a lot of reasons for not--

Q. Dr. Bowen contributed that to degradation.

A. It could very well be. There are other reasons for multiple bands in lanes besides degradation.

Q. So maybe what's on the autorads is not degradation?

A. I'd have to look at the autorads.

Q. I thought you already looked at the autorads?

A. That's correct. I've looked at a lot between then and now.

Q. You mentioned if there was degradation on your high molecular weight DNA that it would affect the mobility and the migration rate. To what degree?

A. I think my words were it could affect, not that it would.

Q. How much could it affect them?

A. It's variable.

Q. How much is the highest it could affect?

A. I have no idea.

Q. Now, Doctor, the R. C. M. P. has the biggest match window of all forensic laboratories in North America. Is that correct?

A. Probably not.

Q. Probably not?

A. That's correct.

Q. Who has?

A. From what I understand, the Center of Forensic Science may have a larger window than us.

Q. Does that make any difference?

A. Not to them.

Q. That's up to them?

A. If they can validate their studies and back it up with evidential samples and all their controls, which I'm sure they have, then I don't think it's going to matter to them.

Q. How big a matching window would the general scientific community tolerate?

A. The general scientific community, so forensic scientists as well as others?

Q. Well, I understand there's what, at least in the United States and maybe Canada included, there might be about 3,500 people in your field who does these tests regularly?

A. I think there's about 12 or 14 labs representative in TWGDAM and there's --

Q. Okay, I'm not talking about forensics any more.

A. Okay.

Q. In the general scientific community, in your field of expertise, who runs these DNA samples there would be at least 3,500?

A. The RFLP typing technology, which is very similar in a clinical arena as it is in forensics, there's probably more than 3,500.

Q. Right, so the forensic community is very small compared to the general community? Is that a fair assessment?

A. That's probably true. The science community of

forensics is fairly specialized and the DNA typing procedures that we currently use and the labs that are implementing them have been careful to start their program off slowly. As a result, there are some labs that are into this procedure now, and there are some labs that are getting into it. So I think you'll see more and more. I think there's about 250 labs in the U. S., for instance, that practice forensic analysis just in general.

Q. Some members of the general scientific community are concerned about forensic laboratories having large matching windows. Are you aware of that?

A. You would be talking about some of the Yee report material, is that correct?

Q. Have you ever heard that criticism before?

MR. WALSH: Why doesn't he -- excuse me, I object, My Lord. Why doesn't Mr. Furlotte ask --

MR. FURLOTTE: He's asking me questions.

MR. WALSH: Why doesn't Mr. Furlotte simply, as opposed to playing a game here where I got the information from, why doesn't Mr. Furlotte simply refer to the statement, where he got it, ask him the question, whether he agrees or disagrees, or explain it. But Mr. Furlotte's playing a game here, I give you a statement, you tell me where it came from, and I think that that is improper and we're wasting time.

MR. FURLOTTE: I think it's obvious, My Lord, who is playing the game here.

MR. WALSH: Mr. Furlotte, in the Crown's humble opinion, is wasting time. Refer the witness to the statement and he can deal with it.

COURT: That's what Mr. Furlotte is going to do. Are you going to refer the witness, Mr. Furlotte?

MR. FURLOTTE: I'm going to have to go back and fumble through every -- I'm trying to save time by just asking the general questions rather than go through all my notes again like before in order to save time. But if Mr. Walsh wants me to go to specific reports, and specific case law or whatever --

COURT: Well, what was your question again, Mr. Furlotte? The witness, I think, was merely trying to narrow down the question and see precisely what it was you wanted to inquire about.

MR. FURLOTTE: I just asked, Doctor, do you know whether or not some scientists out there in the general community are concerned that forensic labs have two big of matching windows in declaring matches?

A. Some labs have a concern. I would assume that that's possible, yes. The forensic community that is actually practising DNA typing have pretty well established that, in fact, the five percent, 5.2 in our case, is actually well within the accepted precision measurement accuracy of the system itself. There are limitations in our system in terms of accuracy and precision, but if you canvass those labs that are actually doing DNA typing, I think you'd be very surprised. In Australia they use five percent, New Zealand, I believe one of the labs is in that vicinity. The British system they use a slightly different approach. They use up to, I believe, three percent or 2.8, but then they use another procedure on top of that which is a probability calculation procedure.

Q. Correction factor?

A. Pardon me?

Q. A correction factor?

A. Well, I don't know if they'd like you to call it that, but they have other means of determining the match beyond the 2.8 percent window. We prefer, once it reaches the 5.2, to consider it inconclusive, for instance.

Q. Would you agree that a matching window could exceed the limits of acceptability?

A. Yes, that's possible.

Q. And what degree would that be?

A. You'd have to define that based on your actual empirical results. In other words, a similar type of experiment that we've run in our own lab where you would start off, probably, with precision studies with possibly a monomorph, and then you would actually look in your forensic samples or even mock forensic samples, for that matter. You could sort of test your system to see how many calls are within your 5.2 percent and how many are excluded with known standards that you know are, indeed, a match, for instance. It's certainly something that you could establish empirically in the lab.

Q. How would you describe your measuring window, or your matching window, as measuring what?

A. It's the difference between, say, one band compared to the other band, the percentage difference in base pairs.

Q. Does it have anything to do with measuring the accuracy of your system?

A. Yes, I think it would.

Q. So in some sense, you might be able to say, "Well, that makes room for five percent error?"

A. I would certainly be concerned, for instance, if we ran a group of samples that we knew were the same and we consistently got eight and ten percent. I would start looking for problems.

Q. Are you aware whether or not some scientists in the general community believe that in the initial conducting of each probe that there should be 95 percent upper limit of reliability?

A. You mean confidence limit?

Q. Confidence limit?

A. Yes, I believe Eric Lander has written a number of articles along those lines.

Q. You probably base then if you're going to leave room for five percent error, then it should have a 95 percent upper confidence limit?

A. I think the confidence limit is actually placed on the frequency of the result.

Q. Yes, but it takes -- it wants to take everything into consideration along with the possibility that the operator might make an error?

A. I think actually you've touched upon the major point of any concern in a forensic lab, is the chance that someone has actually made a mistake, or put the wrong sample in, for example.

Q. Some of the forensic laboratories in the States have, I understand, very small matching windows compared to the R. C. M. P.?

A. I think everyone that's a member of TWGDAM has adopted five percent window. There's some that are -- I think there's one lab that's 5.4, actually.

Q. There are some with a window of about one percent?

A. Which lab would that be?

Q. I'm supposed to ask the questions, Doctor. Okay?

MR. WALSH: Well --

COURT: Mr. Furlotte, it's fair enough for the witness to ask some elaboration on that question. What he's, in effect, saying is he doesn't know and if you want a better answer, you've got to name the lab or suggest what lab it might be.

Q. Do you know what the matching window of Lifecode is?

A. No, I don't.

Q. Do you know what the matching window of Cellmark?

A. Not off-hand. They use a sliding bin approach as well. It's slightly different approach.

Q. They use a different binning system?

A. That's correct.

Q. The binning system really has nothing to do with the measurement of, I suppose, the accuracy of your system which is what the matching window is?

A. Well, you want to make sure you're matching window is well within your bin size.

Q. Oh, definitely. They would have to have a different binning system. It would be much more --

A. No, no, I'm talking about our fixed bin. That's a major criteria. If you read the Budowle article, for instance, it's outlined very clearly there.

Q. The fact that Lifecode or -- would have a smaller matching window than you has nothing to do with the binning system?

A. I don't know.

Q. It's a measurement of system imprecision, isn't it?

A. Well, I think what they're doing is actually -- they don't have a fixed bin. They will move their bin according to the number of bands they see in that frequency and they adopt it as such.

Q. That would still have nothing to do with their window size?

A. They probably have done the same studies we have with respect to, you know, numerous repetitions, for instance, and defined their match criteria or match window, for instance, based on their system. Now, my understanding of Lifecode's protocols is that they're much longer gels, for instance, so there may be some variation in that respect.

Q. Let me put it this way, Doctor, is it true that the smaller the window size, the probability of greater exclusions and inconclusive results?

A. If you limit your window, you will get more exclusions.

Q. Right, and you will also get more inconclusive results?

A. That's probably true, yes.

Q. So the larger your window, the more inclusions you can get?

A. The window itself is used as a safeguard with respect to what your initial match was made, so once again, the actual match is made visually with the expertise of the analyst and you may, in fact, exclude something that's within the match window for reasons, so you could have the exact opposite effect, too.

Q. Well, you're aware, Doctor, in, as you reviewed the case, aware that in some of the matching samples from Mr. Legere that they were pretty close to the matching window?

A. Yes, I think you're correct.

Q. Some 5.2 percent?

A. I'd have to review the actual case notes, but --

Q. Did any exceed the matching window?

A. I think there was one, actually, that exceeded the match window.

Q. One actually at 5.5 percent?

A. It was just over 5.2 percent. I can't recall the exact amount.

Q. So is it possible in another laboratory if they run those tests that, rather than the R. C. M. P., that there would have been a lot more inconclusive or exclusions?

A. I seriously doubt it.

Q. Is it possible?

A. Sure, anything is possible.

Q. And there's no material left for Mr. Legere and myself have an independent laboratory run an independent test on his behalf?

A. You'd have to actually ask Dr. Bowen. I don't know that.

Q. Didn't you read the reports, his test results? You must have known whether there was sufficient material left?

A. I think there is some that had sufficient material and some that didn't. There's some samples that there was enough material left and there's some that weren't.

It depends which samples you're referring to I would think.

Q. I'm speaking about the evidentiary samples?

A. Yes, I think they're --

Q. Not -- I know there are probably lots of known samples left. The evidentiary samples, there would be none left for Mr. Legere to run his own tests?

A. I believe most of the sample was consumed, yes.

Q. Now, you mentioned about Major Weeden and Desert Storm using DNA to identify different bodies, is that right?

A. They used several procedures, one of which was DNA typing.

Q. To try and put the pieces all in one box?

A. Yes.

Q. So they could send the remains home? But, of course, there's no way of you knowing what kind of accuracy there was? That's the best technique they use?

A. Actually, I think Dr. Weeden had a confirmation on every single body with respect to actual DNA analysis.

Q. You're going basically right on opinion evidence? You never did any research into it yourself?

A. No, there are certain things, like, there'd be three people in a particular vehicle and three dog tags, and they could -- for some reason, I certainly recall the fact that there was a tatoo, for instance, and it happened to be the social insurance number of the individual on the shoulder, and they independently matched up the body fragments with that individual and then confirmed it by the actual tatoo.

They also used a second test on every single case that they ran.

Q. They used a second test on every single case?

A. Yes.

Q. To verify?

A. Basically what they're trying to do is develop a system that will be potentially useful in the field, and what they're looking for is an actual, fast procedure for identification and the major difference between what they do and what we do is that they're going to establish a known data base.

Q. There was no second test done in this case, was there?

A. In this particular case?

Q. In this particular case.

A. No.

Q. I understand you have done research, or at least the R. C. M. P. lab and maybe yourself personally, research in the Canadian Indian?

A. Yes, that's correct.

Q. And you established two different population data bases for Canadian Indians?

A. Yes.

Q. One in B. C. and one in northern Ontario?

A. Correct.

Q. Do you have the figures on those as to how statistically different they were?

A. Actually, they haven't been done yet. Dr. Carmody hasn't done his test on the Native Indian populations. Visually they are apparently different and if it pleases the Court, I brought some slides. I can certainly show them to you.

MR. FURLOTTE: Yes, I would.

WITNESS: Right now?

MR. FURLOTTE: Depends how late you want to go, My Lord.

COURT: I think we had better stop there. You've got --

MR. WALSH: Dr. Waye will be next, My Lord.

COURT: Yes, he will be available tomorrow?

MR. WALSH: He's flying in tomorrow morning at 11:30, 11:00, 11:30. I was gauging that perhaps Mr. Furlotte -- I was thinking perhaps you'd be done by noon time tomorrow, but anyway, Dr. Waye is set up for that, tomorrow afternoon.

MR. FURLOTTE: There's a possibility I'll be finished by noon.

MR. WALSH: So Dr. Waye is coming in 11:00, 11:30 tomorrow morning, so he'll be ready for 1:30.

COURT: That would probably serve to balance the week out fairly well. Perhaps you will finish by tomorrow, Mr. Furlotte, but I'm not putting any limit on you tomorrow.

MR. WALSH: Dr. Fourney could set up the slides in the morning and have it ready for Mr. Furlotte.

COURT: You're going to read a report, Mr. Furlotte? You're going to read a report tomorrow?

MR. FURLOTTE: Yes, I'll read the report tonight and then I'll be able to --

COURT: It might be well, perhaps, if the witness could reread the report tonight then he'd be in a better position to speed up the answers a little.

(Accused escorted from courtroom.)

(Court recessed at 4:50 p.m. to 9:30 a.m. on Tuesday, May 14, 1991.)

IN THE COURT OF QUEEN'S BENCH OF NEW BRUNSWICK

TRIAL DIVISION

JUDICIAL DISTRICT OF FREDERICTON

B E T W E E N:

HER MAJESTY THE QUEEN

- and -

ALLAN JOSEPH LEGERE

AFFIDAVIT

I, Bonita DesRoches, of the City of Fredericton, County of York, and Province of New Brunswick, MAKE OATH AND SAY AS FOLLOWS:

1. THAT I am a stenographer duly appointed under the Recording of Evidence by Sound Recording Machine Act.

2. THAT this transcript is a true and correct transcription of the record of these proceedings made under Section 2 and certified pursuant to Section 3 of the Act, to the best of my ability.

3. THAT a true copy of the certificate made pursuant to Section 3(1) of the Act and accompanying the record at the time of its transcription is appended hereto as Schedule "A" to this affidavit.

SWORN TO at the City of Fredericton)
in the Province of New Brunswick)
this 24th day of May, A. D. 1991)
BEFORE ME:)
)
Verna Peterson) Bonita DesRoches
(Verna Peterson)) (Bonita DesRoches
A COMMISSIONER OF OATHS)

MY COMMISSION EXPIRES
DECEMBER 31, 1994

SCHEDULE A

RECORDING OF EVIDENCE BY SOUND RECORDING MACHINE ACT

CERTIFICATE

I, Bonita DesRoches, of the City of Fredericton, County of York, and Province of New Brunswick, certify that the sound recording tapes labelled R v Legere initialled by me and enclosed in this envelope are the record of the evidence recorded on a sound recording machine pursuant to Section 2 of the Recording of Evidence by Sound Recording Machine Act at the Voir Dire Proceedings held in the above matter on May 10 and May 13, A. D. 1991, at the Burton Courthouse, Burton, New Brunswick, and that I was the person in charge of the sound recording machine at the time the evidence and proceedings were recorded.

Dated at Fredericton, New Brunswick, this 13th day of May, A. D. 1991.

Bonita DesRoches