F/CR/17/90

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

BEFORE: The Honourable Mr. Justice David M. Dickson

AT: Burton Courthouse, Burton, N. B.

ON: May 16 & 17, 1991

- TRANSCRIPT OF EVIDENCE AND PROCEEDINGS -

VOLUME XII

Court Reporter:

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COURT RESUMES MAY 16, 1991

COUNSEL PRESENT

ACCUSED PRESENT

THE COURT: Now, we are still in the voir dire of course. You are continuing, Mr. Walsh.

MR. WALSH: Yes, my lord, thank you.

DR. KENNETH K. KIDD, still under oath, continued to testify:

DIRECT EXAMINATION CONTINUED BY MR. WALSH:

Q. Dr. Kidd, I have a series of questions for you with respect to the areas that -- some of the areas that we covered yesterday, the latter areas yesterday. The first question, doctor, what is your opinion as to the general acceptance in the scientific community of the fixed bin method for the calculation of allele bin frequencies for forensic purposes?

A. Let me think just a moment, the method is recognized and as far as I know accepted by a large number of people as one of the possible methods of compensating for the problem of being unable to identify an allele specifically. There are some people who advocate and favour a floating bin approach as opposed to a fixed bin approach but I don't think anyone would argue that it is an inherently wrong approach, it is simply some people would prefer one approach to the other approach. Some people prefer the fixed bin approach. The different approaches have their relative strengths and weaknesses and I don't think there is complete unanimity on any

approach being absolutely superior in all possible cases. But it's a good approach. I think most people will say it has built in over compensation for the estimates of allele frequencies and as a pragmatic approach is perfectly acceptable.

Q. In your own opinion as to its reliability for forensic purposes?

A. I think it's highly reliable.

Q. Doctor, what, if any, opinion do you have about scientific acceptability of the Caucasian data base employed by the R.C.M.P. and the method of pattern frequency calculations made by the R.C.M.P. from that data base or DNA forensic purposes?

A. I think the data base is high quality and more than sufficient for this purpose. I think the method of calculation using the fixed bin approach, the assumption of Hardy-Weinberg, the product rule, the independence of loci are all quite acceptable procedures that will give a reliable result. The only difference I would have with the way in which they report the frequencies is that I would also advocate that one report confidence intervals in addition to the best estimate. I have no qualms about the estimate they report, I would add the additional information if I were doing it of including a confidence interval.

Q. And what will that enable -- when you add a confidence interval, what are you essentially telling or explaining with respect to the best estimate?

A. I think it gives an -- adding a confidence interval conveys also the degree of certainty one should associate with the estimate. So that if the confidence intervals are relatively narrow one knows that that is a relatively precise estimate. If the confidence intervals are very large, one knows that it is not, from a statistical sense, such a precise estimate. And one can therefore form an individual opinion of how much weight to give to the estimate itself. Certainly an estimate of one in a hundred thousand with confidence intervals that range from one in ten to one in a million is not a very precise estimate, because it could be as frequent as one in ten. Whereas an estimate of one in seventy with a confidence interval that ranges from one in fifty to one in ninety, one knows that it is bracketed and it is not any more frequent than one in seventy say.

Q. Doctor in your opinion to what extent do the frequencies generated from the data base, the R.C.M.P. data base, reflect the Canadian Causasian population as a whole and New Brunswick for VNTR purposes?

A. I think they are very representative, it would be hard for me to imagine creating a better, more representative sample than the one that has been assembled.

Q. Doctor, in your opinion, what, if any, bias would be found in the probability figures generated in a DNA forensic case by the R.C.M.P. lab?

A. There is a very built-in bias of always attempting to overestimate and that's the very nature of the binning process. So that I think it's a system that is designed to be conservative and give every possible doubt to the defendant in the case. There is not -- there is certainly not a bias against a defendant. The ability to detect an exclusion is very high and so the questions of the data base and the calculations only come up when there is no exclusion, in the case where there is a match. One clear non-match, and the question never arises, it is assumed that they are from different individuals. And the assumption of Hardy-Weinberg using 2PQ, et cetera is supported by analysis of the data base, the assumption of the product rule is supported by examination of the data base and the knowledge that any deviation that might exist cannot be very large and could go in either direction and would only exist under limited circumstances. So the assumption of the product rule is a reasonable one because on average it is still the assumption that gives the best estimate. After all, these are all estimates, they are not precise calculations, because the very nature of the problem is, we cannot know everything. We do not have perfect knowledge and therefore we have to estimate.

Q. Doctor, if you would -- do you have any opinion with respect to DNA typing and how -- the program, how the DNA typing is being developed and applied, how that compares to other forensic

evidence, for example, serology, do you have an opinion on that?

A. Yes, as a graduate student I did a lot of serology, not specifically of humans, the serology I did was of cattle. But now I do DNA of humans and the fundamental scientific questions and the forensic questions are essentially identical. There is no difference in the fundamental questions being asked. The very important difference is that the DNA methodology is extraordinarily more powerful for exclusions and it is by in large a more robust system, less prone to errors than many of the protein electrophoretic and classic serologic techniques. So that from all perspectives, DNA data, the DNA approach is better than classical serology which has now been used in legal system for decades. ABO was discovered in 1900, I'm not sure when it was first used in forensics. The RH system was discovered in 1949, and certainly has been used in forensics for a long time, and many of the others have a very long history. But the DNA is extremely powerful, in my opinion it's greatest value is its tremendous power to exclude potential suspects. And maybe this is hearsay, but certainly I have talked with lots of prosecutors who are always concerned about eye witness identification, in traumatic situations like a rape, and the DNA does in fact exclude suspects who have been identified by eye witnesses. So it's a very powerful technique favouring true justice.

Q. Doctor, I am going to show you VD-54, which has been identified as a report produced by Dr. John Bowen in relation to the case of The Queen v. Allan Joseph Legere, would you look at that for me, please and tell me whether you can identify it?

A. I have seen a photocopy of this.

Q. Doctor, have you had an opportunity to review the original autorads from which that report was generated?

A. Yes.

Q. Can you tell us, please, doctor, are you familiar with the conclusions that Dr. Bowen has drawn in relation to the case specific evidence here?

A. Yes, I am familiar with them.

Q. And would you tell us, please, doctor, what your opinion is with respect to Dr. Bowen's conclusions in relation to the calls that he's made, particularly, the matches, the so-called matches that he's made?

A. Short and succinct, I agree with all of them. To give a slightly more elaborate answer, I looked at all of the main autorads in this case that had -- the first set of autorads, looked at all of them and I called what I thought were matches on it without any prompting from Dr. Bowen and then compared what I saw with what he had called. And we agreed in all of the cases, including the cases that were sufficiently faint bands or fuzzy bands that he called them inconclusive. There was certainly in those cases no evidence of an exclusion. There were

no bands seen where they would have been different from a match, but the bands that I saw, definitely saw them, in my laboratory I probably would have called them because I work in research setting and bands of that sort are ninety to ninety five plus percent of the time correct but he quite appropriately chose to call them inconclusive. Because as I said, in a research setting they're ninety to ninety five percent of the time really correct but that's not appropriate in this forensic setting. And so he called them inconclusive and he did not use them in any of his calculations.

Q. And do you agree with his conclusions in that regard?

A. Yes, I think that was the appropriate call to make.

Q. Doctor, what -- so we clarify, in your research setting, some of those calls you indicate Dr. Bowen called inconclusive, what would you have called them?

A. I would have called them a match.

Q. In that particular report, doctor, have you had an opportunity to look at the statistical significance that Dr. Bowen associated with these calls of matches that he made, were you able to see those in the reports?

A. Yes, I was able to look at those.

Q. And what is your opinion with respect to those conclusions?

A. That is exactly the way one would calculate the

frequency. The only difference is the one I mentioned earlier were I doing the calculation, I would have gotten not only the number he got but I would have also added a confidence interval to it.

Q. Doctor, I am going to refer you -- what, if any comparison did you make other than in addition to the lane to lane comparison within the first blot, which is identified by this chart, VD-88, Blot 89 OL 1191-6, you're familiar with this characterization that's shown?

A. Right, I saw a typed version of that table and we compared that with what we called on the autorads and that's an appropriate summary of where matches were called.

Q. What, if any, comparison did you make, doctor, between the second blot which has been identified as two additional standards purportedly coming from Allan Joseph Legere, what, if any comparison did you make with the second blot to the blot 89 OL 1191-6?

A. I did visual comparisons of the probings on that blot with those of the standard and all of the matches on the first one and I called it a visual match. They were indistinguishable. I looked then at the printout that had been generated from the actual sizing of those bands and they were all within the match window that is used by the R.C.M.P. So there was no difference, they were indistinguishable quite clear results.

Q. With respect to the first and second blot, what, if any, band shifting did you observe, doctor?

A. I did not see any evidence of band shifting. The constant marker, D2S1 and the male specific marker which for this purpose is essentially a constant mark -- a constant band in the male samples all showed no evidence of band shifting.

Q. Doctor, did you have occasion to observe what has been called in this particular proceedings, a third blot, it was the comparison of a single root hair found -- from the evidence found on the top of the leg of Father James Smith. Do you remember reviewing that particular blot?

A. Yes, I did.

Q. And the evidence has been that that hair was excluded --

A. Yes.

Q. -- there was no matches called?

A. Yes, it had a different pattern.

Q. And you agree with that call of exclusion?

A. Yes, it was a very distinctly different pattern.

Q. Did you have an opportunity to review the -- what, if any, comparison did you make between that third blot, that particular blot, the known standard purporting to come from Allan Legere to the first blot, identified as VD-88?

A. The standard on the third blot was a visual match with the first standard and all of the other standards. It was clearly from looking at the autorad was in fact overloaded in terms of there being a bit too much DNA in the lane, and

it looked like it was running very slightly faster, when looked at the size measurements it very difficult to tell because on the first probing of that filter the size markers were actually also quite overexposed and so were very wide bands. So there was a great deal of imprecision in trying to align it to get sizing. And on the original sizing it was, I think, 3.5 percent different in the size estimates. I have also seen a second probing of that same filter, where the marker lanes were much more precise, narrow bands, and when the size estimates were done on that probing of the same filter, the bottom band was, I think, five percent off. So it was clearly at the -- at sort of the borderline at the statistical match window. But that was essentially what I would expect and I'm not bothered by that.

Q. That's leading to the next question, what, if any, concerns, would you have as a result of seeing those particular sizings on that third blot? What, if any, concerns would you have with respect to your opinion as to the reproducibility of the R.C.M.P. RFLP system?

A. I think it's highly reproducible. The match window is set at about ninety nine percent level the 5. percent, that is an empiric value based on their own results with known samples that were identical, ninety nine percent of the time they vary up to 5.2 percent. That also means one percent of the time they vary by slightly more than 5.2 percent. And in comparisons,

if one takes all of those other samples that did match and considers how many comparisons are being done across the filters for the multiple probings something in excess of seventy different comparisons were being done of what is possibly the same DNA sample, and one band in one of those comparisons on one of two probings was just outside the match window. That's essentially at the one percent level. So it's about what they have stated is their level of reproducibility.

Q. What, if anything, did notice about the «tightness» of the sizings in relation to the first blot comparisons lane to lane within that same blot?

A. They were very tight, they were much tighter in comparison between the first blot and the second blot, and that's exactly what one expects. The variation from lane to lane within a blot is almost always less than the variation sample to sample run in two separate gels, simply there is an additional level of independence. The fact that they represent two separate gels, two different electrophoretic runs in two different buffers, two different temperatures, two different levels of voltage, all of those of course one is trying to make identical run to run, and the R.C.M.P. lab is very highly standardized. But there is no such thing as absolute identity when you do the same thing twice. So one expects a slight amount of additional variation.

Q. Doctor, I am going to -- have you had occasion to read an affidavit by a Dr. William Shields filed in the case of the State v. Daniel Vandebogart in New Hampshire?

A. Yes.

Q. Have you had occasion to -- that affidavit was dated April 12th, 1991?

A. I was sent by your office a fax, this is the fax that you sent me which the cover page states that it is such an affidavit and it reads as though it is all part of a single document.

Q. And in that particular affidavit, doctor, were you able -- did you see anywhere in that particular affidavit reference to this particular case?

A. Yes.

Q. I refer you to page eight, page eight on the bottom of your sheet --

THE COURT: That affidavit is an exhibit?

MR. WALSH: No, my lord, that's the affidavit that we referred to, I believe when Dr. Carmody was testifying he provided opinions on that and I provided a copy to Mr. Furlotte.

A. I am sorry there are two numberings here because it's been faxed twice.

Q. At the bottom there are numbers.

A. Okay, yes.

Q. Doctor, you had occasion I believe you said to read through this particular affidavit?

A. Yes.

Q. In particular I would ask you to look at page eight.

A. Yes.

Q. Do you have any comments to make -- perhaps, I'll ask you this, have you had occasion to make any comments or to form an opinion with respect to any parts of that particular affidavit?

A. Yes, I have several comments that I marked when I was reading through it. I found several of the statements at various places to be statements that I strongly disagreed with.

Q. Would you, please, doctor, if you would, would you go through that and refer his lordship to the actual statement that you're referring and your comment in relation to it?

A. Okay, at the general level, he says, based on this, some information before and some published papers, «-- I reiterate my earlier conclusion that a large number of population geneticists, working from both theoretical and human prospectives all agree that substructure must be investigated in order to validate the current FBI protocol for determining match probabilities.» And my marginal comment was not possible. This is an argument that is being made, has been made in several cases in which I have testified, that one cannot assume there is no substructure, one must investigate it and demonstrate unequivocally that there is no substructure. And that is simply not possible in the human setting, homosophian is not like mouse or drosophila or

annual plants or snails around the periphery of Hawaii, populations that have been studied extensively. The amount of information one would need to meet this standard that is being put up is simply horrendous and I simply reject the need to meet that level -- that standard. I have looked at a lot of data, I have examined a lot of human populations. It is impossible to say there is no substructure. What one can say is that there is no evidence of relevant sub-structure to the VNTR's as used in forensic settings. And I think that has already been looked at a fair amount. It will continue to be examined, data are accumulating. But it strikes me as setting up a standard that has never been applied to other kinds of forensic data and that the only reason it's being raised now is something I don't quite fathom.

Q. For later reference, could you just refer to the bottom page number where that comment --

A. The comment occurs at the top of page seven.

Q. Thank you. Could you continue, doctor.

A. At the top of page eight, from the bottom of page seven on to the top of page eight, he talks about estimating match probabilities based on true racial database could alternately over and under-estimate the TRUE frequencies of a coincidental match for individuals. And my comment was that in fact one never knows what the true frequencies are, we are always dealing with estimates

On page ten, he does some calculations from this previous case using two different FBI databases.

Q. If I could, doctor, is that the paragraph in the middle of page ten?

A. That's correct.

Q. I'll read it to you and correct me if this is not the statement that you're referring to:

«That this is not simply a theoretical problem can be illustrated by recalculating the probahilities of «random» matches for particular cases using more than one database and comparing the results. I have done this for Mr. Vandebogart in this case. As the evidence already indicates the FBI reported that a random match to his genotype would occur with a chance of 1 in 51,744 using the C2(old) database. The new chance of a match is 1 in 102,934 using the FBI's C3 composite database and would be 1 in 200,107 using the RCMP database. I performed a similar calculation in the Canadian case as well.» My understanding that is reference to the Legere case?

A. That's my understanding as well.

Q. «Here the probability of a four locus match to the defendant's sample was estimated to be 1 in 5.2 million using the RCMP database and a much smaller 1 in 9.6 million using the FBI's C3 database.» Do you have a comment with respect to that?

A. I have several comments with respect to this paragraph. First of all, what the FBI reports and what the R.C.M.P. report is not the probability of a random match to this genotype but the probability of randomingly finding a pattern that would show the same binning pattern. Many of those that show the same binning pattern would be recognizably exclusions and not the same genotype. This is the overestimate that is built into the procedure.

The comment that I have then with respect to his calculations is that this is exactly the sort of variation I expect to find. It is part of the reason I like to see some sort of confidence intervals built into the reporting of these systems. None of those difference is significant and really meaningful in a forensic setting.

Q. That is the difference between 1 in 5.2 million and 1 in 9.6 million depending on which database you went to?

A. Absolutely, that is -- let's say, it's a factor of two, one in five and one in ten million. If there are ten million lottery tickets sold and you buy one, you've got a one in ten million chance of winning. If you buy two, you have twice as much, a one in five million chance of winning. But whichever it is, you've got very little chance of winning. And like I said yesterday, it's only very slightly greater than if you never buy a lottery ticket. And that's why I never buy a lottery ticket because I know probabilities

it's not worth the risk. I've got better places to put my one and two dollars a week. And similarly, the 1 in 52,000, 1 in 103,000, 1 in 200,000, the maximum difference there is one in four. But all of those numbers are -- I mean not one in four, it's a factor of four, but all of those numbers are very small. It's very different from saying, 50,000, 100,000, 200,000, yes, if that's the amount of money you pick, that's a reasonably big difference. But when you're taking your reciprocals, you're dealing all with very tiny numbers. And so at this level, it's not a meaningful difference. So long before you asked me about commenting on this, first passed through the following paragraph, he comments -- well, actually, I'm sorry, it's not the following paragraph but in the next two or three paragraphs, he comments that these are very large meaningful differences and I completely disagree. I think that -- oh yes, at one of those points, in the middle paragraph on page eleven, the last sentence in that paragraph: «I do know that if a physician were explaining the risk of a certain course of action to me (i.e., what my chances of dying were should I choose a particular treatment for a disease), I would certainly find the difference between 1 in 50,000 and 1 in 100,000 highly significant and of critical importance in making an informed and rational decision.»

And my marginal comment was nonsense. First of all, in medical risk estimates, they are even

more imprecise than these forensic estimates and there is no meaningful difference in medical risks. And I deal with those in the context of being a medical geneticist, no meaningful difference between one in fifty thousand and one in a hundred thousand.

Q. Doctor, there is one comment I would ask to draw your attention to at the bottom of page ten and I believe you have touched on it to some degree but I would like some clarification. There is stated there at the bottom of page ten: «If two populations differ in allele frequencies, then choosing the wrong sample for comparison is expected to produce a result biased against the defendant(i.e., the estimated probabilities are predicted to be incorrectly lower when an individual is tested against a subpopulation other than his own).

A. Yes, my marginal comment was in capital letters, NO with an exclamation point. That's an absolutely incorrect statement. It depends, given the premise, two populations differ in allele frequencies than choosing the wrong sample for comparison, will accept the premise, choosing the wrong sample for comparison is expected to produce a result biased against the defendant. A simple counter example, if the population the defendant comes from has a frequency of one percent of the band seen in the defendant, and the other sample has the frequency of ten percent of that band, and we choose the other sample, then we are biasing by a factor of

ten in favour of the defendant. So that it is equally likely that the defendant would come in these hypothetical situations from the population with the lower of the two frequencies, as that he would come from the population with the higher of the frequency. So that it is absolutely incorrect to say, it will always bias in favour of the defendant. The same thing applies with multilocus markers. Any bias that might be present as I have already said, I am convinced will be a very small magnitude. But one never reaches perfection, you can never know anything, so let's assume there may be some small deviations. The deviations have to sum to zero, for every deviation up for one allele there has to be a deviation amongst some other alleles in the other direction. So the deviations will as often favour the defendant as they will go against him, and once one then has a multilocus system, the probability that the deviations always go in the same direction across all systems becomes vanishingly small. For one system they may favour the defendant, for the next one they may slightly bias against him and the expectation is that they will average out. That's similarly by always taking a bin frequency that for each allele is larger than the true frequency and how much larger is something that's always debated, but whichever bin frequency one takes, it's almost always guaranteed to be larger, that is multiplying a factor of five or ten minimum for

every allele. So that by the time one gets to a multilocus match this is a probability of five or ten raised to the eighth to tenth power which is a very large number, bias in favour of the defendant. That's why the FBI results of presenting one in five million is really a very conservative estimate. This technology is approaching but isn't quite there, which is why we build in all these factors, it is rapidly approaching and probably within two or three years will reach the point of being able to uniquely specify the DNA pattern of every individual except identical twins. And in fact we all know, it is theoretically possible right now, the DNA of every individual is absolutely unique. It's just we have to look at enough markers in order to be able to see it, and we are getting very close to that right now.

Q. Doctor, this affidavit, the affidavit that you read, what, if anything, in total, what, if any, concerns would you have about the opinions that you've given in relation to the validity of the R.C.M.P. DNA system and the validity of the test results in this particular case. What, if any, concerns has this affidavit raised in your mind?

A. This affidavit has raised no concerns that I have not long been aware of. These are the kinds of arguments that are being raised by the defence in many cases. I've thought a lot about them. I completely reject it and in fact I find some of these statements are clear misstatements of

fact or using wording that I think gives a very incorrect impression of what the method is really doing, and it raises no concerns in my mind about what the R.C.M.P. is doing. I think the approach they are taking is a very scientifically methodologically sound approach at the molecular level, and I think the method they are using to calculate frequency estimates for these binning patterns are conservative and appropriate as one of the ways of dealing with the inherent underlying uncertainty in the biology.

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

THE COURT: Thank you very much. Are you, Mr. Furlotte ready to --

MR. FURLOTTE: Do you want to start now or do you want to take your morning break.

THE COURT: Well, let's have a break then now and this will be the morning break.

COURT RECESSES FOR 15 MINUTES

COURT RESUMES

ALL COUNSEL PRESENT

ACCUSED PRESENT

THE COURT: Now, Mr. Furlotte.

DR. KENNETH KIDD, still under oath, continued to testify:

CROSS EXAMINATION BY MR. FURLOTTE:

Q. Dr. Kidd, being a scientist and being involved in a lot of your scientific research and work, I assume you put a lot of confidence in what you're attempting to achieve while you're attempting to achieve it and you basically work very hard to accomplish your goals?

A. I don't quite agree with the wording there, in fact I think as a scientist my main task is to always be skeptical of the results that are coming out in the laboratory. Certainly I work very hard to obtain the new knowledge that I want, but I never place great confidence in any single result. That's part of the scientific method to always be questioning, always be skeptical.

Q. Would you agree, doctor, that it's human nature to place a lot of value in our own opinions and basically for our opinions to be proved wrong, then you want somebody to prove your opinion wrong beyond a reasonable doubt?

THE COURT: He's not an expert in human nature.

Q. He should be an expert in his own feelings?

A. My own feelings are that certainly that I have opinions. I feel fairly confidently that it is human nature to have opinions. The idea that someone has no opinions on issues is not tenable. When it comes to scientific matters I try to make it very clear where my opinions are

based on a fair amount of experience and knowledge and where I really have no knowledge on which I form a strong opinion. So that a very common response that I give to various questions, if I don't have enough knowledge, I'll say, I don't know.

Q. But would you agree that somehow scientists, lawyers, judges, no matter what professional person it is, we tend to have a built-in biases, sometimes it's not easy to disprove or dislodge them?

A. Oh, I would say most people will have some biases.

Q. Doctor, would you agree to an extent that these tests in forensic purposes, not only the conduction of the test but the theories behind them and all the assumptions that are made in drawing conclusions from these tests, that the tests basically are highly technical and incapable of observation and requires the majority to either accept or reject the scientist's conclusions that it can be done, that it was done properly and that the results are reliable?

A. No, I wouldn't agree with that at all. In fact the autorad is a very clear demonstation of what was done. The autorad can be looked at, if one has enough background information, you can tell by simply looking at the autorad that virtually all of the procedures up to that point in fact worked properly. That's one of the nice natures about this test, that if something goes wrong, the usual consequence is no result or a

visible problem on the autora .

Q. The usual, in most of the tir ?

A. Yes, the overwhelming majorit of the time.

Q. You do admit, doctor, that mi takes are made where sometimes the picture c esn't give a perfect picture of what happ..ed?

A. That's true in every situation in life.

Q. When the probes are binding to DNA fragment lengths, they will bind the fragments that are carrying not necessarily all the base sequence but sometimes just part of the base sequence of which the probe is designed to attract, is that correct?

A. Yes, the level of stringency sed in hybridization and washes is designed to mal it such that the only probe that remains boun is that that has a very high degree of homolo , almost identical match with the fragments. Bu it does not have to be a hundred percent iden al match for binding to occur.

Q. How much would be necessary p rcentage wise for a probe to bind to a fragment?

A. I can't give you an answer to that in the general sense because it depends on the DNA base composition and it depends on the level of stringency, the temperatures cing used, the ionic strength. But we -- when we have a perfect match we can get good binding, a sequence of fifteen to twenty nucleotides if we use the appropriate conditions. We can set

the conditions to allow very imprecise matching and can probably go down in studies across species which we are doing in my lab to identify by hybridization sequences that are on the order of only ninety percent identical. But the normal Southern blotting procedures and stringencies used would certainly not distinguish between ninety eight to a hundred percent in that range, they would, I would imagine, be indistinguishable. I have to say that I have not done the studies I simply do not have that detailed sort of information. I doubt that many people do.

Q. Am I to understand, doctor, that in your lab you don't use these specific probes that the R.C.M.P. has used in this case?

A. We use some of them. We have used D2S44, we have used D17S79. We have in the lab but have not yet used D1S7, D4S139. I'm not sure whether we have D16S85 or D10S28. We have probes in my lab for over seven hundred different loci. I can't remember all of them. And we have used in our studies over two hundred in the last some years and I simply don't remember all of them.

Q. In the Wesley, when you testified, you testified that it was impossible to get a false match, did you not, do you recall?

A. That's my opinion.

Q. Now, in the Wesley case when you gave that opinion, was that opinion on a false match on one probe or was that a false match across the board?

A. As I would say it now, I quite honestly don't remember what it is in the transcript four years ago or the context, but by a false match I will make clear the distinction I made yesterday, that is two patterns that are really very different and would under normal circumstances be distinguishable, happening to be because of error indistinguishable. That is very different from a match caused by a coincidence, where the patterns are in fact quite similar, because that is not an impossibility, that is precisely what all the statistics are about.

Q. Let me put it this way, doctor, four years ago, did you think that a false match for a single probe, double banded probe, four years ago did you think that was impossible?

A. I quite frankly don't remember what I thought four years ago. I know, I certainly thought it was highly unlikely. I don't think that I thought it was impossible.

Q. Four years it wasn't thought that band shifting could cause one single probe to create a false match?

A. No, I think band shifting was recognized four years ago. We certainly dealt with the problem in the research laboratory, overloaded lanes migrated faster than underloaded lanes, but I would say over the last four years we certainly know more about the causes of band shifting than we knew four years ago.

Q. I believe also, Dr. Kidd, that you've in the past in your testifying, you testified when Lifecodes had conducted the forensic testing?

A. That's correct.

Q. And you also visited their -- you reviewed their protocols and you visited their laboratory?

A. That's correct.

Q. And you observed each step in the DNA fingerprinting process?

A. Yes.

Q. And you basically formed the opinion then that Lifecodes was the most detailed and specific laboratory protocols for the procedures involved that you ever seen?

A. That's correct that was my opinion at that time that's what is correct.

Q. Has it changed since that time on Lifecodes?

A. Yes, it has changed since that time.

Q. What has your opinion changed to?

A. Well, I have seen other protocols that I think are more detailed and more specific. Their written protocol in fact is still quite good and quite detailed and quite specific, far more detailed than one would normally expect to find in a research laboratory. But I've subsequently seen other protocols that -- and methods of operation that I think are better.

Q. Have you ever found any problems with Lifecodes to make you want to retract the good credentials tha you gave them at that time

A. I have seen two of their results that I think should probably not have been entered into the legal system. One of them I was shown by a district attorney who was wondering about using this evidence in a case. I advised him against using the evidence in the case and so he did not use it. And I -- though I was --

Q. Was that the McLeod case?

A. What?

Q. Was that the McLeod case or are you thinking of a different one?

A. I never knew the name of the case because DNA was never involved. I was sent the autorads, this was a case in Los Angeles. The other case that I know something about is the quite famous to infamous Castro case. I saw duplicate copies of the autorads and I thought they were of less than optimal quality. I thought they were not good enough to be used in a forensic legal application. Though they clearly did not disprove the point being made in the case but they were not of good quality. I have to add since you raised the question that I have also seen from Lifecodes some absolutely stellar and spectacular autorads of a type that I would be proud to have come from my laboratory. So this is not a universal condemnation of their procedures, it's just sometimes things have not gone well.

Q. I believe you testified in the Yee case also, did you?

A. That's correct.

Q. Dr. Gilliam testified in the Yee case?

A. I believe he did. I have not seen any of his testimony and I was certainly not there when he did if he did.

Q. Reading from the judge's decision on page 33 Dr. Gilliam considered the problem of developing a qualitative match criteria to be one that has not been dealt with by the medical genetics community, stating it's only come up in forensic laboratories. Would that be a fair assessment?

A. Yes, I think that's quite a fair assessment, it's basically not a problem in most medical applications. We are doing clinical medical applications in my laboratory in terms of prenatal diagnosis for an inherited form of cancer, and of necessity we are using probes close to that locus that we know very well, understand we are dealing with them in family situations, and visual matches are all that is required to be certain of what's happening in the family.

Q. Are you saying you don't ever have a match window in your lab?

A. No.

Q. Because your system is accurate enough or because --

A. Yes, because we are dealing with qualitive differences. I can tell the difference between

a 7KB band and 4KB band from ten feet away and there's no need to do measurement on that, it's either up here or it's down there.

Q. I believe you said you were using some of these probes in your lab, the D2S44, what do you do with these?

A. We're using in linkage studies where a number of alleles in a given family is a very limited subset of these alleles. And the situation is then reduced to one of qualitative differences. Within that family we can usually but not always quite clearly distinguish the alleles. If there is a problem we always rerun the questionable samples in adjacent lanes sometimes multiple copies and use visual matchings. We do not by in large resort to measurement in those situations because when one can do replicate testing and get a consistent pattern on replicates, one doesn't need the measurement probability. Again, we are not attempting there to estimate the precise size of those alleles. We are saying that this individual and that individual's first cousin do have the same size allele, whatever it's size might be.

Q. So the match window is only a problem for forensic scientists basically, is that what you're saying?

A. That is certainly the area that I think it is the largest problem. I certa ly will not say it's only there that it's a problem, there may be other applications I'm not aware of.

Q. So when Dr. Gilliam says that he considered the problems of developing a quantitative match criteria to be one that has not been dealt with by the medical genetics community, you would agree that probably those issues should be dealt with by the medical genetics community?

A. No, I said earlier that it does not come up within the medical genetics community. Now, the medical genetics community can certainly make its knowledge of the use of these things appropriate, make its knowledge available to the forensic community and deal with it in that sense. But it doesn't need -- there is relatively little need in the medical genetics community. There may well be some need and it's probably something that might be thought of but the technology is changing. Most of the medical genetics community is not going to be using this methodology in another year or two. It's rapidly changing to PCR based typing, CA dynucleutide repeat loci which are -- which have a completely different set of interpretation problems and completely different methodologies.

Q. It's quite possible in another year or two that even forensic labs will not be using this technology any more, that they will be using the PCR or going to discreet allele system?

A. It's entirely possible, there are many people working toward that with a variety of different techniques, simply to get around the problem presented by the absence of discrete alleles for these systems.

Q. So whether or not this technique is reliable it's going to basically have to be dealt with now before it becomes obsolete, would you agree with that, otherwise the interest will have dispersed?

A. By the medical genetics community you mean or by forensic scientists?

Q. By the medical genetics community?

A. I'm not sure I have an opinion on that.

Q. In the Yee case, Dr. Gilliam concluded at page 33 again, «--that the proponents of the forensic application of DNA technology are, in using a quasi-continuous allele system, taking DNA electrophoresis methods about as far as they can go, and stated that it was a 'very technically demanding problem'.» Would you agree with that, that it's much more technically demanding than in medicine in your lab?

A. Yes, by in large I think it's more technically demanding.

Q. There's more room for error?

A. I think I would have to say there is more room for problems to arise that will result in no interpretation being possible, whether that would be in the sense of carrying through the method an error it would not be an error in interpretation of the final result.

Q. Using the quasi-continuous allele systems, Dr. Gilliam concluded by asserting that he was sure that investigators could discover probes that identified discreet alleles and that a

forensically useful DNA identification technology could be developed based on a discrete allele system and this would put the forensic scientist laboratories back into the realistics of established technology and it would eliminate a lot of problems, matching rules and binning systems that we now have to deal with.
Would this eliminate the problems that we have with binning systems and calculations of their frequencies?

A. Yes. The problem with that at the moment we're dealing in the real world not what might be double in four or five years. These as basically continuous allele systems are really not very good for much of my research, because I wish to be able to identify discrete alleles, which is why much of my research does not use them. But they are very powerful per locus or per hybridization in excluding samples in definitely stating the two samples are not identical. If one resorts to two allele systems, then one has to get the same power for exclusion, one has to use many such two allele systems because each one has very little power, perfectly valid but very little power. And when DNA material is limited one cannot do that number of tests. But theoretically I could go through with fifty markers if I have an unlimited supply of DNA I can do fifty markers each of two alleles and I can come up with statistics that are of the same level as being obtained in this case.

Q. Well, when you agreed with Dr. Gilliam that it would eliminate a lot of the problems including match rules and binning systems and calculation frequencies and you must admit that there are problems with the binnings and the calculation frequencies, to eliminate problems there must be problems to begin with?

A. Well, we've been talking about for the last day the kinds of problems, the estimation problems the uncertainties in the way one deals with those so those are certainly the problems that I am aware of. It's an empiric pragmatic solution for the problems raised by having continuous allele systems, it is one of many and there is room for a lot of discussion which is absolutely the best way to do it, but they all, almost all of them, the floating bin approach, the fixed bin approach achieve the same general objective of giving a number that is a definite over-estimate of the frequency of that allele.

Q. Now, doctor, also in the Yee case you expressed your opinion that, you know, while you might obtain a false match over one probe across four or five it would be highly unlikely.

A. Correct.

Q. Did you draw that conclusion on the assumption that band shifting would occur, I suppose, uniformly with each band or is it on the assumption that band shifting or the degree of band shifting might differ depending on the size of the fragment, size of the DNA fragments?

A. Band shifting can show many different patterns but they are not random with respect to individual bands or to the position on the gel. If band shifting is a certain degree in a certain region of the gel, then it will very similar for any band in that region, it may be more or less in another region of the gel but within that other region of the gel, it will be in general correlated with the first and they will all be very similar. So if a lane tends to run faster than it should have, virtually every fragment will have migrated somewhat further, some parts they will have migrated, deviated a little more than in other parts but it won't be that it's slow at the top and fast a third of the way down, slow again at the middle and fast down near the bottom. It will be a much more uniform sort of shift. And therefore, it is essentially -- it is in my opinion virtually impossible for band shifting to cause a pattern that would be really different to be falsely matched over multiloci.

Q. Okay, as I've been understanding things so far and I could very well be wrong, I understood other experts to say and from reading case law that the degree of band shifting from your different size fragments they may vary because of the fragment length?

A. Yes.

Q. Maybe fragment lengths of three thousand base pairs may shift by a one percent and basic fragments of five thousand base pairs may shift by two percent, something in that vicinity,

is that a fair example?

A. As an example, I won't accept the actual numbers --

Q. Oh, no, I don't expect you t[illegible]

A. I don't know but -- excuse me yes, that's the sort of thing I was talking about. But they would tend to be extraordinarily rare for it to be in opposite directions, and certainly not if they're in the same region of the gel, and three thousand and five thousand are often in pretty much the same region in the gel.

Q. If the fragments, say, were quite a difference in size, it might be that if you are going to compare two individuals that they may legitimately without band shifting match in two probes, is that correct?

A. Oh, sure and that's what the probability --

Q. And depending on the sizes of those fragments if they match, there might not be much of a mobility shift but in the size of the fragments where they don't match maybe the band shifting or the mobility shifting might bring those into a line which again would give you a false match and make it look much more substantial than what it is?

A. No, I won't agree with the second part because you're implying a difference in probabilities. The probability really remains the same almost because you're still then talking about a very rare event, because the probability that hypothetical example, uniform band shift every allele is slightly misplaced and they're all

brought into alignment. You have a pattern of essentially the same order of magnitude of rarity of the known standard and you have the added factory of the unlikelihood of a band shift bringing it all into alignment. In your example you're talking about a pattern of non-uniform band shift, so that you have some bands matching exactly and some offset being brought into alignment. The probability there is a non-correct sample, the same rarity as the known standard and the additional unlikelihood of a non-uniform band shift. So any of these scenarios has the same level of being extremely rare on the order of something less than the frequency of just a flat out match in the population.

Q. Would you agree, doctor, that again it is possible for two individuals that their bands match in say, two, maybe even three probes and the fourth probe where they don't match the band shifting because of the fragment size could actually cause them to line up and that they would be indistinguishable, where if there was no band shifting, you would be able to see a distinguishing difference in the fourth probe?

A. That's the question that I just answered and a very succinct answer is, yes, that's possible but with a very low probability as I just went through. I was talking about the probabilities I never said it was an impossibility.

Q. But it's not that uncommon for individuals coming from the same community to have two and maybe three probes match?

A. Oh, no, there I would say it's very rare for individuals to have two or three probes match.

Q. But it does happen?

A. I'm sure it does happen. There's one -- at one of the loci in the evidence here a locus that's particularly informative the known sample and one of the victim's samples happen to match at both bands. Clearly it happens at one locus, and the probabilities that it happens at two are simply the products of the probabilities that it happens at each one, so, yes.

Q. Have you known the FBI to go to court with just a two probe match, four bands?

A. I believe I have heard that but I don't know for a fact that they did go to court. My comment would be you only need a one band match to go to court because one can estimate a probability of one band. If that's all the evidence there is and there's no exclusion, that's valid evidence. It may have a probability of one in three but it's a probability of one in three. That's the order of informativeness of classical markers, any of these -- one can go to court with one marker and I have seen cases where because the sample was limited or because something happened results were obtained for only one marker. And there're perfectly valid results, they just don't have these

astronomical probabilities but it would no different than an ABO match.

Q. Doctor, you say that equilibrium is a condition that exists when you find gene frequencies to be what you would expect by chance alone, if everything were independent and unrelated, is that a fair expression of what equilibrium is?

A. Let me think, I think that's probably about the simplest statement, it's just simple probabilities on the assumption of statistical independence of everything and chance operated.

Q. And that for the alleles to be random in the gene pools that two preconditions must exist first, the occurrence of alleles must not be caused by linkage disequilibrium on different chromosomes and second, that the relevant racial population as a whole must be in Hardy-Weinberg equilibrium, would that be fair?

A. One can expect equilibrium to result if those conditions are met, but they are not a prerequisite for finding the alleles to be distributed as though they were random. I mentioned yesterday that in fact one can do tests and if the alleles are distributed as though the conditions were met, then one can do the calculations without ever having demonstrated that the conditions are met. So that one looks at the end result and says, yes, it's in Hardy-Weinberg equilibrium, I don't need to worry about how it got there, I observed that it is. And one is forced in the circumstances to do that because

of the inherent unknowability of precise population structure, precise mating patterns, et cetera.

Q. So you're allowing the product to justify using the theory basically is that what you're doing?

A. No, I'm saying the product stands by itself and can be shown that genotype frequencies are the fit 2PQ and if they fit, then you can use 2PQ. The underlying theory of what would predict from a theoretical point of view 2PQ remains untested. One is simply empirically showing that in fact that is the way one does it.

Q. But if you can't show what empirically justifies 2PQ how can you use the calculations of it to justify that it does, it seems to me that's what you're doing? You're saying your mathematical formula is valid because such and such exists now when I conduct this mathematical formula on this criteria, look at the nice number I got therefore the cause must exist?

A. No, I'm not saying the cause exists. Now separately I can make a very strong argument for in fact the theoretical basis being very closely met. But I'm talking now empirically, all that is really necessary is to show that 2PQ works and that the data fit the application of that algebraic formula. I don't have to go through number theory to multiply two by two and get four if I simply know that two times two equals four and take that as a given I can then do that simple multiplication.

Q. How do you show --

A. It's not an absolutely perfect analogy, it's hard to -- I'm having trouble addressing your question.

Q. Maybe I'll make it easier for you, explain to me how 2PQ works. We know why it's supposed to work, now, explain to me how it works?

A. How it works, 2PQ is the way a population geneticist normally thinks of it because of a two allele system, where Q is one minus P, in fact in a multi-allelic system one has to think of 2P1 and P2 or PI PJ. But the simple thing the underlying statistical assumption is that the probability of taking two samples from this pool, one I and one J is simply the probability on the first draw of getting an I, and on the second draw of getting a J, plus the probability of on the first draw of getting a J and on the second draw getting an I. So that it's the probability that the father transmitted Band I and the mother transmitted Band J, plus the probability that the father transmitted J and the mother transmitted I. So it's the product of the two probabilities that's why there's a two there, two probability of 1, probability of J

Q. But that is only valid if everything is by chance alone, is that correct, the probability of picking out a P and the probability of picking out an I that has to be gover ed by per chance for that proposition to be valid, is that not right?

A. I am tempted to say, yes, but I think you mean by pure chance something that's different than what I mean, but for the moment I will say, yes.

Q. That's okay, doctor, we've been playing that game for two weeks.

A. So I will just say a simple yes, just chance, independent events that there is no correlation in the statistical sense, having drawn I the first time that does not alter the probability of drawing a J.

Q. That is the reason that you cannot use related individuals to form your data base, there's too strong a correlation between related individuals?

A. No, that's not true.

Q. What is?

A. One can include related individuals in a data base provided the individuals are selected without prior knowledge of the genotype. Gene frequency estimates are not biased by including related individuals, work done by Kotterman(phonetic) in the 40's and 50's showed that. The variance of the estimate is affected. You have a higher variance if some of the individuals are related than you have if all of the individuals are unrelated. So the best sample, the most information for indiviudals typed is obtained by using unrelated individuals, but it's not incorrect to include related individuals if your confidence intervals and your variances are calculated taking that into effect. It does not bias the estimate.

Q. What if you had a data base that fifty percent of the people were related, would you again be operating by pure chance?

A. Yes.

Q. It would be pure chance.

A. It would be the equivalent of a data base of unrelated individuals of roughly, well, let's assume they're first degree relatives, something on the order of fifty percent the size. So a sample of two hundred individuals where half of them were brothers and sisters, for example, would be, I think I said two hundred individuals, would be the equivalent of a data base of unrelated individuals closer in size to a hundred and twenty five not two hundred. But the frequencies estimates would not be as precise as a sample of two hundred unrelated, but they would not be biased, they would not necessarily for any one allele be higher in any systematic way or lower in any systematic way, and that's what a bias is. They would be less precise, that's what the variance measures.

Q. That's why you're saying if subpopulations exist then it's totally irrelevant?

A. No, that's a non-secular, we're talking about different things. I'm not sure what you mean but if you mean by subpopulations including related individuals, closely related individuals certainly they are then related. If you are talking about large populations of each subgroup still of largely unrelated individuals, which is

bascially we're all Homo sapiens, we're all related. We all have -- there's more similarity between my DNA and your DNA than there is between my DNA and a chimpanzee or yours and a chimpanzee. The level of relationship basically depends on how far back in human evolution you want to go. But that's -- I mean I'm impressed by the findings we just published in the February proceedings of the National Academy of Science. We looked at racial groups from around the world at one hundred different DNA markers that are polymorphic in Caucasians, that's why they were chosen and in all ethnic groups we find almost all of the alleles are still present. Now, these were not VNTR's but basically means that all human populations showed this variation, that the variation predates the modern diversification and subdivision of the species. And so I find many of the questions of subdivision to be relatively minor levels of variation compared -- and they only deal in frequencies, not presence or absence of whole classes of alleles. For the VNTR's, some of the VNTR system definitely show different distributions in the major ethnic groups, which is why it's very important to subdivide them, the Chinese and the Blacks look different than the Caucasians.

Q. Isn't that proof that they are not selected or determined just by chance?

A. If one -- that statement would only be valid if one were trying to mix a data base of Caucasians

and Chinese or of Caucasians and Africans. But within Caucasians which is the relevant point here I know of no evidence that there is really significant meaningful substructure with respect to these systems.

Q. Is it really necessary to find what you consider meaningful differences, isn't all that's necessary is that you can prove that VNTR's are not selected or produced in individuals just by chance, because in order to use the 2PQ things have to happen just by chance?

A. You're confusing and confounding issues and I'm not sure how strictly to answer that. You better ask it again.

Q. If I'm confusing and confounding this, doctor, it's only because I am confused. I would like to be straightened out, please help me.

A. One of the issues is a meaningful difference. I have already said that something that differs by a factor of two once one gets to these levels, I do not consider a meaningful difference. That has to be distinguished from statistical difference. There are clearly statistically significant differences that exist within human populations, but a difference of five percent for one bin in Italians versus eight percent for that bin in Scandinavians, to take a hypothetical example, is not a really meaningful difference given that the bin frequency is already just an estimate, that is designed to be a several fold overestimate.

Q. What is the meaningful difference, doctor?

A. A difference between one in ten and one in a thousand in a final result is a meaningful difference. I would say --

Q. Let's get back to bin frequencies, what would be a meaningful difference in your opinion?

A. In the, let me talk about a specific example, in which I believe these were calculations I did in a trial on Cellmark data in Van Nuys, California, I don't remember the case name. When I increased the size of the floating bin and then took three standard deviations, I ended up with a difference for one band of an estimate going from three percent up to, I think the largest difference got up to almost twenty percent. Now, for that one band I thought that was quite a meaningful difference. By the time I had factored in these corrections to really overestimate and get a frequency I was confident that the true frequency was less than. I was not confident that the true frequency was less than three percent, I was absolutely confident the true frequency was less than twenty percent. At that level that was a meaningful difference. By the time I went through all of the loci, instead of a value that they got of one in eight hundred million, I calculated a value of one in, I think, two million. And I did not consider that a meaningful difference. So that all of these individual differences at the individual locus level, if indeed that were the

only band in evidence, that would have made a big difference. Three percent, I would consider chance is unlikely. Twenty percent chance is very likely, but that's where in a trial jurors have to make their own decisions of what is meaningful. But by the time it was factored in, it turned out in my opinion to be not a meaningful difference.

Q. So as I understand, doctor, you in the case for Cellmark that you don't recall the name, you found maybe a difference between one in eight hundred million and one in two million but no significant difference?

A. Correct, I'm sorry, no meaningful difference in a forensic application.

Q. In a forensic application. As long as the one in two million would be sufficient to have meaning?

A. Correct, if the difference had been one in eight hundred million to one in ten, I would certainly say that was significant but one in two million is still a very rare event.

Q. Is that what you call using the product rule, the outcome, the product to justify the use of Hardy-Weinberg formula and the product rule?

A. No, that's something very different. The justification for using it is the demonstration looking in the data bases, that -- or at least part of the justification for using it is looking in the data base and finding that among individuals there is no correlation of alleles, and finding to the degree that it can be tested

that there is no correlation of alleles across loci. And I have looked at some of these data bases, breaking them down by bin frequencies at one locus and then looking at the distribution of bin frequencies for another locus, for individuals who fall into each of those loci, and there's no evidence of any correlation. So that would justify the use of the product rule across loci. But I've gone, in that particular calculation I went really a step further because I was taking in all of the situations, applying the product rule, I was taking the upper ninety five percent confidence limits, whereas in fact true variation would say that for some of the loci that the true frequency is much less than the estimated frequency, given all the rules of sampling error and the best estimate would have been far lower than the one I calculated, and even the statistically correct upper confidence limit would have been a number far lower.

Q. Let's go along this basis, doctor, I think maybe some other scientists are following this line of reasoning, if --we've had evidence that the Caucasian data base, it doesn't matter if you use it in Ottawa, or New York or anywhere in the States, the bin for RFLP's or VNTR's are not going to change across political borders, they're going to be pretty well consistent?

A. They are in my opinion pretty well consistent, yes.

Q. What I am concerned about if general population data base which the FBI is using which they consider to be good enough for all the United States, is that right, all Caucasians in the U.S.?

A. That's my understanding.

Q. There's a population of two hundred million, we'll use for rough estimates two hundred million is that close enough?

A. The Caucasian population is probably around that, I think total population is closer to two fifty.

Q. Take, Mr. Legere's case, here and what Dr. Shields has done, general population of the United States two hundred million, frequencies come out to one in nine million, Canada's general population, Caucasian, is roughly twenty million, frequencies come out to one in five million, okay. We keep dropping down to smaller population areas, where these -- you're going to form your data bases, once you get down to a small population and restricted population, i.e., subpopulation, where there is only five thousand people, your one from one in ten million down to one in five million might just drop down to one in five hundred, the analogy is there, is it not?

A. You can always draw a straight line between two points and extrapolate it into nonsense and you have taken two values and attempted to draw a correlation. It would have been entirely possible that the number calculated for the Canadian data base would have been a smaller number than for the FBI data base.

Q. That's possible but probably irrelevant.

A. In which case -- well, I'm simply stating that your argument is equally irrelevant, because there's no way of knowing that there is a true correlation there, it's just two numbers pulled out of a hat and two pairs of numbers if you will and one can always make a correlation with two points and extrapolate, it has necessarily no meaning and I would argue there is no association. When one gets to a population of five thousand, my experience would say that there are far more than five thousand possible genotypes that will be present in that population, the numbers that will be calculated will most likely be far smaller than one in five thousand. And one then gets into the philosophical argument of how can the probability be one in two million, when there are only five thousand people there. And that's simply an artifact of the mathematics.

Q. Because the 2PQ and the product rule operates in the abstract?

A. That's correct.

Q. They don't operate in the real world, you're using formulas that apply to an abstract world and you're applying them to a real world, is that correct, they're only valid in the abstract world because there's nothing in this world by chance?

A. Oh, nonsense, most things that happen in this world are by chance. What sperm fertilizes,

fertilizes a given egg at the time of conception is an extraordinarily chancy event. There are millions of sperm present usually hundreds of thousands reach the egg and which one gets in is entirely chance. And that's a fundamental rule of genetics. We are dealing with chance and probabilities all the time in genetics. They are the fundamental way, genetics and inheritance works.

Q. And that applies to your lottery draws?

A. Yes.

Q. It appears to be just by chance?

A. That's correct.

Q. And even if it's not by one hundred percent chance, there may be some little thing ruling why certain numbers come out and still, it's still greatly by chance so therefore it's okay to use the product rule. But when you're dealing with populations and small populations and inbreed populations, a lot of figures are simply not by chance and your binning procedure --

MR. WALSH: My lord, objection, is this a question?

Q. -- or does your relation, the relationship you have with your parents have something to do with it?

A. Chance is still the primary factory in these situations. Chance can produce a variety of different outcomes. But I have seen chance produce in one of the smallest, most isolated populations I know out of this Amazon Basin Indian population, I have seen chance produce everybody having a unique genotype. I have

studied a hundred plus DNA markers on a small tribe from the highlands of a small island off the Coast of New Guinea where there are twenty seven mutually unintelligible languages spoken on that island and very tight inbreeding for generations, and there's tremendous amounts of genetic variation. Some frequency differences of course but chance is still the major factor and there is still tremendous variation. So that knowing that I am willing to say that the deviations that may occur I can never rule out the occurrence of something I have not studied and looked at, of course not. But I am willing to say based on all of this experience that those deviations are going to be numerically small and I am perfectly happy to not worry about them. The product rule is still the best way of estimating the overall probability because deviations that might occur will occur in different directions for different alleles. And so the product rule averages in a vague sense across those.

Q. And that's why you're saying that the difference between one in eight hundred million and one in two million is a small deviation for forensic purposes?

A. Yes.

Q. But doesn't that deviation -- doesn't that tell you that to use the product rule to begin with is improper and invalid?

A. No, not at all, it's irrelevant.

Q. So if the one in eight hundred million dropped down to one in eight hundred and you still figure that the chance of one in eight hundred being a very rare event, then again that would be a small deviation?

A. We're getting into very judgmental areas at this point. I would have to say that if and we're not really talking about the product rule here, we are talking about factoring in other kinds of safeguards and overestimates, and then using those with the product rule. We are not talking about modifying the product rule per se. But if I did my calculations and went from one in eight hundred million to one in eight hundred, I would say, gee, there's a lot of uncertainty here and by the time we're getting to one in eight hundred, that's a very important level of uncertainty, it's still not a common event but I would be much happier if the jury were presented with that variation of numbers. Let them make their own choice. Decisions have been made on -- it's only one factor in the evidence and it certainly is still admissible. My apologies I'm not a lawyer or a jurist but it is still scientifically valid and in my opinion, admissible to be considered.

Q. How many times have you testified on behalf of the FBI, I suppose when their lab was used for gathering evidence?

A. Two cases, three times, the two federal cases Jabobetz and Yee, I testified in the pre-trial hearing and during the trial in Jabobetz and I testified only in the pre-trial hearing in the Yee case.

Q. Have you in those cases also formed the opinion and brought to the Court's attention that you thought it would be proper to use the ninety percent upper confidence interval?

A. I don't honestly remember whether the issue came up. Sorry, I don't remember. Had I been asked I would have said, it's relevant.

Q. But it wasn't necessary then, was it because at that time you weren't aware of these great deviations or small deviations, I'm sorry, in your words?

A. I have of course been aware of these sorts of things for twenty five years, since I first started doing --

Q. Of this magnitude?

A. Not the VNTR's --

Q. One in eight hundred million to one in two million, have you been aware of that magnitude for that length of time?

A. No, but of the types of variation that led up to it, it's something that people who have done gene frequency studies would find nothing unusual about.

Q. Were you aware of the Pennell case?

A. The name is not familiar, I may have heard about it but I don't recall hearing anything under that name.

Q. I believe you said you testified in the Jabobetz?

A. Yes.

Q. And Dr. Lewontin was a witness for the defence in the Jabobetz case?

A. I believe so, if you say so, I won't challenge it, I did not see him and I did not read the testimony in that case.

Q. In that case the trial judge found at page 26 that, Dr. Lewontin claimed that because no studies have examined generic substructures for VNTRs, in Caucasians, it is necessary to assume that substructures exist because analogous studies involving blood type (non-VNTR) genes show there is substantial substructure within European Caucasians. Therefore, it was inappropriate to use one date base for all Caucasians --

THE COURT: I don't think the trial judge found that, Mr. Furlotte. He merely repeated.

MR. FURLOTTE: He repeated what Dr. -- I didn't say the trial judge found that --

THE COURT: Oh, I misunderstood.

MR. FURLOTTE: I'm sorry, maybe I didn't express myself well.

Q. Basically that was the evidence given by Dr. Lewontin. Are you saying that -- did I understand you to say that substructures are a red herring?

A. I believe I used that word yesterday. I mentioned yesterday clearly substructuring does exist, defined in a variety of different ways,

clearly allele frequencies at classical markers vary across European populations. It is undoubtedly going to be true that for some allele frequencies, even some bin there will be statistically significant difference between the bin frequency in Italians, say and Swedes. What I -- the reason I used the term red herring is because I have seen enough data to convince me that those differences will be numerically rather small and will be insignificant in the final conclusion that is reached from a multi-locus forensic application. These are not like conventional two allele systems that human population geneticists have dealt with for decades. All alleles are rare. It is not a situation where a frequency of an allele may go from five percent in one population to ninety percent in another. It may go from five percent to eight percent but not to ninety percent. And the situations that give rise to multilocus disequilibrium require that there be large differences. So I don't -- I disagree with Dr. Lewontin's conclusion about the necessity of doing a lot more than what has already been done with these VNTR system. I don't disagree at all with the premise that substructuring has been demonstrated with other genetic loci. That's clearly true.

Q. You disagree with Dr. Lewontin and I believe Dr. Budowle also disagreed with Dr. Lewontin in the Jabobetz case?

A. I don't know what Dr. Budowle said, it's in the transcript.

Q. And Dr. Nadeau and Dr. Mueller agreed with Dr. Lewontin?

A. Yes, if you say so.

Q. The point is, Dr. Kidd, is that there's a good many scientists out there in the general community who will agree with Dr. Lewontin, is there not?

A. Certainly there have been quite a few people who have testified in court cases to very similar opinions and have advanced them in other settings.

Q. As Dr. Lewontin? As Lewontin's opinion or as your own?

A. As Dr. Lewontin's opinion, that's correct. Not all of those people are, in my opinion, very well qualified to deal with these issues. Dr. Lewontin is eminently qualified in this area I am not going to in any way challenge him. I have reached a different conclusion.

Q. Your opinion is not generally accepted -- how should I put that?

MR. WALSH: Carefully.

Q. We've been playing with words here for a couple of weeks now, a slight of tongue can cause a lot of damage. Your opinion, doctor, would be hardly accepted by a majority of the scientists who would be qualified to give an opinion?

A. I have no good way of answering that. I can give a counter response, I don't know who would

be qualified, I know many colleagues that I consider well qualified will agree with me. I know there are others who will not. There is room for scientific disagreement. In one court case I was presented with two lists by a defence attorney, people who had testified in much the same way I had and a list considerably longer about four times as many names who had testified against the admission of DNA and said, doesn't this prove that most scientists disagree with you? And I simply refused to accept that numbers game because a sizable percentage of that longer list I would not personally considered qualified. Many of them were people who had never done the molecular technology in their own laboratories. Whereas as I said, I have done hundreds of thousands of DNA typings in my laboratory. Many of them had never worked with humans, the problems of human population genetics are different from those of drosophila population in genetics. It doesn't mean that people can't learn, that these people are inherently not intelligent, it simply means, I don't think they have as much specific knowledge and are qualified to talk in this area.

Q. Doctor, you would have to admit there is at least ample evidence to show that your opinion may be wrong?

A. No, there is not evidence -- I will not admit that there is ample evidence to show that my opinion may be wrong. There are people who will

disagree with my opinion but that doesn't convince me that my opinion is wrong. And they have to be very careful about what opinion and what aspect of this -- there are certainly many things I have said, that virtually everyone will have to agree with. The fact, take a point earlier this morning, that about related people in a data base. There is clear, published information, anybody who knows about calculating allele frequencies will have to admit that including related individuals in an estimate of allele frequencies does not bias it, if they're selected prior to being typed.

Q. Doctor, answer me this, I believe you admitted you have testified in quite a few criminal trials and come to -- and expressed your opinion?

A. Correct.

Q. Have you ever subjected your opinion for peer review?

A. There is no avenue for such a mechanism.

THE COURT: I was going to say that judges do it but really that isn't peer review, is it?

WITNESS: No, it is not strictly peer review unless the judge has a title.

MR. FURLOTTE: I think we'll break for lunch --

THE COURT: I think we'll stop there and recess for lunch. It appears there might be some likelihood that you would perhaps finish with this witness this afternoon, Mr. Furlotte?

MR. FURLOTTE: I'll know better at four or four thirty, usually the initial part is always slow anyway.

THE COURT: Pardon:

MR. FURLOTTE: Usually the initial part is always slow.

THE COURT: Well, I thought we might perhaps give some indication whether you might get away.

WITNESS: Even if I might be able to know whether I could make travel arrangements to get out tomorrow morning.

THE COURT: Oh yes.

MR. FURLOTTE: Maybe tomorrow afternoon, depending on the time in the morning. At four thirty, if I can cut tomorrow short, I wouldn't mind going a couple of hours tonight, I'll do whatever I can to accommodate Dr. Kidd.

THE COURT: Well, suppose you hadn't finished by this afternoon. You may finish by this afternoon, I take it. I'm not asking you to commit yourself?

MR. FURLOTTE: No, I can't finish by this afternoon

THE COURT: Well, if you didn't finish this afternoon.

MR. FURLOTTE: I wouldn't count on my finishing this afternoon.

THE COURT: If you didn't finish this afternoon, would the likelihood be one in eight hundred million that you would finish this evening, if we devoted two hours, say, after supper?

MR. FURLOTTE: With those kinds of odds if I finish this evening, I think the Crown might as well withdraw the charges.

THE COURT: What I was trying to get at was, what I'm indicating is that I would be prepared to sit this evening, I don't like sitting in the evening not on my own account but on any reporter here and others, I don't like sitting in the evenings.

MR. FURLOTTE: I expect things to pick up this afternoon and move a little swifter but we never know.

THE COURT: Well, let's see, it looks, well, I don't know, you'll have to take a chance on your morning flight out of town. If, I throw that open that if it could be finished up, say, after supper tonight, I'd be prepared to sit in the interest of getting it concluded, so the witness could get away tomorrow morning if necessary. I don't know when the next flight is, next week sometime?

You're here in the middle of fiddlehead season, you know, do you eat fiddleheads?

WITNESS: I have never had them fresh, I am told that they are going to try to see that there are some fresh ones for dinner tonight.

THE COURT: Buy them right up the road here at the Indian stand this side of the highway, I seen them there this morning.

Well, we'll adjourn now, can we say two o'clock?

MR. FURLOTTE: That's fine, my lord.

COURT RECESSES FOR LUNCH AT 12:30 P.M.

COURT RESUMES AT 2:00 P.M.

ALL COUNSEL PRESENT

ACCUSED PRESENT

THE COURT: Okay, Mr. Furlotte.

DR. KENNETH K. KIDD, still under oath, continued to testify:

CROSS EXAMINATION CONTINUED BY MR. FURLOTTE:

Q. Dr. Kidd, back to your testimony in the Yee case, you did admit in the Yee case that you conceded that substructure did exist but that was insubstantial, is that correct, as far as you recall?

A. I do not recall specifically admitting that substructure did exist. I certainly have said here and have always acknowledged substructuring defined in some ways definitely exist.

Q. Do you recall whether or not you stated in the Yee case that if you saw a difference between one in eight hundred million and one in two million that that would be insubstantial?

A. I doubt that I said that in the Yee case but I honestly don't remember what I specifically said.

Q. If I was accused of a crime in, say, New York City, and they run my profile through the Caucasian data base, the FBI run my profile through their Caucasian data base and the

probability factor come up that it would be one in a million and then they run my profile through the Black data base for Blacks and it come up as one in five hundred thousand, would that be of any statistical significance?

A. I have absolutely no idea because it would depend on the sample sizes in the data base whether or not that level of difference reached statistical significance, and I simply couldn't do that when I don't know the sizes of their data bases at the moment and it's a complicated --

Q. Okay, for argument. sake, we'll say they are substantial --

THE COURT: Just a minute, give the witness a chance to finish his answer.

A. It's a rather complicated calculation to say whether or not those differences are statistically significant.

Q. Okay, let's say the Caucasian data base of the FBI has five thousand people in it, let's say that the Black data base of the FBI has five thousand people in it. Now, under those assumptions, run my profile through the Caucasian data base and it come up one in a million, and run it through the Black data base and it come one in five hundred thousand, would it make a significant difference?

A. You've used slightly different wording.

Q. Would it make a statistically significant, I'll get my tongue around it after awhile?

A. It probably would be but there are many variables that would go into calculating the significance, the number of loci that were used, the actual allele frequencies and standard errors for each of the component alleles that went into that calculation. So that it is not a simple calculation and I simply -- I cannot do it but I will concede that if the data base is approximately five thousand, it probably would be statistically significant.

Q. Would there be any difference if those differences arose within the Caucasian data base, as you gave an example awhile ago, you know, there was no significant difference, I believe, between one in eight hundred million and one in two million, that would have been within the same race, data base of the same race of people?

A. That is not what I said.

Q. Okay, what did you say?

A. I said that those are -- that one can make estimates, one in eight hundred million was a best estimate for a frequency, the one in two million was a deliberate attempt at over-estimation in all situations, a type of upper confidence limit and that for the purpose of making a decision of likely or very unlikely for this to be a coincidence, I saw no meaningful difference between them. Statistical significance doesn't apply there, because one is clearly a biased estimate.

Q. Okay, as I understand now that's when you were using the ninety nine percent upper confidence interval?

A. Correct.

Q. The difference between one in eight hundred thousand or one in eight hundred million or one in two million.

A. That's correct, the upper confidence limit was one in two million, more or less, yes.

Q. In Dr. Shields' calculation, when he run Mr. Legere's profile between the FBI data base and the R.C.M.P. data base, he was not using any ninety nine percent upper confidence level, he was just using only straight procedure that the FBI has been running to court with and which, I don't know, but I'm assuming the R.C.M.P. never used the ninety nine percent upper confidence interval in court before, and that this -- maybe this is the first case they're going to concede that point. Do you know whether or not that's a fact?

THE COURT: Which fact, now, I think in fairness to the witness, you've got me confused, probably you had me confused before you had the witness confused.

Q. Do you know whether the R.C.M.P. ever went to court and conceded that a ninety nine percent upper interval limit would be acceptable or --

A. I have no idea, I doubt it since it's my understanding that the R.C.M.P. has not used DNA evidence in many cases yet. But that's the only basis for -- so that I douht they have used it, I don't know that they've ever been asked to present such confidence intervals or not.

Q. But I understand from your testimony yesterday and today that you are promoting the idea of using that ninety nine percent confidence interval?

A. I am promoting the idea of presenting it as well as the initial estimates, because --

Q. Have you ever done that in court before --

A. Yes, I have I stated --

Q. -- for a fixed bin -- for a fixed bin approach?

A. For a fixed bin, I do not believe I -- I know I did some of the calculations along those lines in the Jabobetz case for my own purposes to convince myself before I would testify that these were reasonably robust numbers. I honestly don't remember whether I ever presented those calculations in testimony in the court.

Q. Did you see a need for having different data bases for the different races and ethnic groups?

A. For the major races and ethnic groups, yes, I do.

Q. Why would that be necessary?

A. Because we know and have known for decades that the difference in gene frequencies between the major ethnic groups is far larger than the differences within the ethnic groups. The difference between any Caucasian and any African is greater than the differences found among Caucasians. And consequently, it is quite reasonable then to take account of this higher level of variation.

Q. Now, what degree of variation would it be necessary to see between races or ethnic groups to be certain that it's necessary to have different data bases for each?

A. That is a judgment, it's an interaction between pragmatism, funding available, time available and degree of precision that one wants, and I can't make any specific judgment. There are situations where I know it is of virtually no importance and situations where I know it is likely to be quite important.

Q. So there is some mathematical formula which you can calculate --

A. No --

Q. -- as to what degree is necessary before you need the different data bases?

A. It depends on what your purpose is and how much accuracy you want, it's a continual. If you want absolute precision you have to type every human being on the earth. And then you are left even there with the philosophical or logical question about what ethnic group does someone belong into. My ancestory is Scotch, Irish, English, Dutch and French and Norwegian, well, it's all European. But there are lots of people that aren't even pure European, where do they fit in, how do you define those ethnic groups.

Q. Okay, let's just go for forensic purposes and with generally the sizes of data bases that the different forensic laboratories have constructed and apparently some of those laboratories and

law enforcements have found it necessary to construct different data bases for the Blacks and the Whites, they must have found it necessary to find that they needed some degree of statistical difference between them to justify them or justify the necessity of different data bases. Now, do you know what that degree of differences is?

A. It is my understanding that it was not a degree of statistical difference, it was a legal matter that it was legally important that there be different data bases. This was not a decision based on prior knowledge because the markers had not been typed and the frequency distribution were by in large not known when the decision was made. For some of the systems, they are reasonably similar in Caucasians and Africans, for other systems, they are very different, even those that are very different have some bins that are very similar, other bins that are fairly different.

Q. If you could show the same degree of difference in the bins, say, that are the bin sizings that are between different ethnic groups and say, the Whites and the Blacks, if you could show that same degree of difference within a race, would that be sufficient to, I suppose, invalidate the the use of one population base for the general public?

A. No, because it's going to depend upon what race and how one defines it. African as a race show

far more difference among the different groups than in all of Caucasians. So one might very well find that the Masai in Kenya have very different frequencies from the San in the Kalahari, from the Bygmies in the Ituri Forest, from Bantu speaking Nigerians on the West Coast. Those might all show more differences between them than we find in any Caucasian. So that would argue that in Africa, I'm talking my expectation, this has not been done, but it's based on some of my other typings of some of those populations.

If one were going to apply this forensic approach in Africa, it would be preferable to have those separate populations tested and separate data bases made. That's quite different from the American Black, for example, which is an amalgamate, a very hybrid population, so that one does not have the level of substructure in the U.S. Black population that one has in native African, tribal and ethnic groups. But whatever we found in Africa would not in any way relate to -- would bear no relationship to the validity or invalidity of using one data base for Caucasians, that must be based on what we know about the extent of Caucasian variation and its relevance.

Q. Now, in your study of populations and for purposes, I suppose, of genetic studies, how are races defined?

A. They are defined by the decision of the person who is defining them. It is a highly subjective, highly contraversial, there have been dozens, if not hundreds, of different racial and ethnic classification schemes, some of them are based on linguistics, some of them are based on geography, some of them are based on presumptive genetic evidence. But there are always fuzzy boundaries. We know there are dark-haired Irishmen because the remnants of the Spanish Armada washed up ashore on Western Ireland after the defeat of the main Armada. We know that there are blue-eyed Sicilians because Vikings landed on Sicily and left their genes behind. The ancient, not too ancient but certainly an ethnic slur was scratch a Hungarian and you find a Tartar, because of the invasions out of the Asian steps that came all the way as far as Central Europe. So where one draws the line has always been a question and there are no absolute boundaries any place.

Q. So are you saying you couldn't say that the Germans are a different race than, say, the Russians or the Frenchmen or the Englishmen?

A. There are -- at what level of difference do you wish to call them different. They have, if you pool everybody who speaks German and you pool everybody who speaks Russian and do gene frequencies on them or look at average hair colour or look at average height, you will find average differences between those two groups.

But there are more similar to one another than either is to a Nigerian.

Q. Okay, for the -- let's say for the purpose of forensics and the profile and collecting data bases for VNTRs, what would distinguish race in this instance, how would you distinguish that one person falls in one race and not the other?

A. By in large I would be often very hesitant, there would be large numbers of situations where one cannot state specifically what race an individual belongs to. And take, for example, most people at least in the United States except for the southwest who call themselves American Indian or native American, the majority of them have more Caucasian ancestory than they have Amerindican ancestory, and it is highly mixed up. there has been segregation. So at one locus there may have an allele that had its ancestory derived from Europe and at another locus they may have an allele that had its ancestory derived from crossing the Bering Land Ridge out of Asia, what definition would you call these people, there's a clear social definition. In the U.S., the FBI has a Hispanic data base. From a genetic point of view that's nonsense because Hispanics range all the way from, for example, one of my graduate students who is Puerto Rican, who has entirely Spanish ancestory to people who are Mexican in origin who have entirely Amerindian ancestory.

THE COURT: Haven't we, Mr. Furlotte, explored this matter of racial data bases almost sufficiently in depth now?

MR. FURLOTTE: Not quite, my lord.

THE COURT: Soon, I hope.

Q. Would you use the same data base for your American Indians, Amerindians?

A. No, I would not. I would prefer to use a different data base but in --

Q. How do you go about using -- establishing data bases for your Amerindians?

A. I know there's a lot of genetic variation among Amerindians. I would want a very wide sampling. I would probably want to look very carefully at the known degree of Caucasian admixture. It's an extremely complicated project to determine how one would go about doing that. Probably the way I would go about doing it is trying to get several different reasonably pure Amerindian data bases with little Caucasian admixture, and then do multiple comparisons so that I would say for a given case in a forensic situation, I'm not sure which is the appropriate comparison population. I will make my calculations against all of these, so that if the criminal were a Navaho, this would be the probably of chance, if he were an Inuit, this would be the probability if he were a Seminole, this would be the probability.

Q. If an Amerindian was charged with a criminal offence and they run a DNA profile on him, how

would you calculate the frequencies?

A. In the way I just said, I would not calculate a frequency, I would be tempted to calculate several different ones because of a lack of knowledge of which would be the most appropriate. There are actually two questions that are being confused at this point, and that is there are at least two different reasons for calculating a probability. One does not necessarily know the ethnic type of the criminal, the individual who left the forensic sample. Sometimes in a rape and the victim is alive there is an identification that it was a white man or a black man. But if the victim did not see the attacker or the victim can't testify, one doesn't know. There is then the suspect who is a different individual and there the ethnic identity is known. In one case one can calculate the probability of pattern observed which will only come up if there is a match, the probability of the pattern observed occurring by chance in the general population, if we don't know what the appropriate ethnic group of the criminal is, how common a pattern is this, the other is the probability of someone else in the ethnic group of the defendant, how likely is it that another person of the defendant's ethnic group has the same probability. And one does those calculations against different data bases ideally. So I know in some of the cases where the results are being report, where the ethnic identity of the criminal is not known, rather

than use only the ethnic identity of the defendant the calculations are reported if the criminal is Hispanic, if it's Black, if it's Caucasians, these are three probabilities that would be relevant. And then it's up to ultimately a jury to decide how to interpret those numbers.

Q. I understand you did your own studies of the Amerindians?

A. Yes.

Q. Similar to which Dr. Carmody is doing in Canada, is that correct?

A. I am not familiar with all of the details of what Dr. Carmody is doing in Canada, so I can't say how similar it is.

Q. And what were you basic findings in your study about the Amerindians?

A. We found looking at approximately thirty loci in two Amazon Indian populations and in a population of mines in the Center of the Yucatan Peninsula that over all the amount of genetic varability was reduced by no more than twenty seven percent. Almost all of the alleles, over ninety percent of the polymorphisms that we had known before in Caucasians were also present in the new world. And we have a paper in press that argues that this is reasonably strong argument against a very restricted narrow bottleneck in the settling of the new world. Some of the data that I've seen on those look reasonably similar to data I've seen on much larger Chinese data bases for some -- at least for some of the VNTR loci. But these

are individual villages and small tribes. So that we are not calculating VNTR allele or bin frequencies because we are taking a defined known limited sample, but from what can be done the distributions look very like those for Chinese.

Q. Now, doctor, I remember you mentioning that if you're comparing bin frequencies and you found a difference from five percent to eight percent that would have no statistical significance but if it went from five percent to fifty percent or eighty percent then it would?

A. No, that's not what I said.

Q. That's not what you said?

A. I said whether or not five percent to eight percent was statistically significant would depend upon the sample size. If the sample size were large enough that difference would meet the statistical criteria of being significant meaning that it's likely to be real in that sense but I --

Q. Let's say a sample of two hundred?

A. No, it's relevant to talk about sample sizes because what I did say is that I would find that difference not meaningful in a forensic application, irrespective of its statistical significance. The distinction here that I can -- if I do a large enough sample size I can show statistical significance between a frequency of 5.1 and 5.2 percent but at the level that we are trying to make evaluations here, that is not a meaningful difference in the forensic applications. And I would say even a difference of five percent

to eight percent, they are both small numbers and when looked at in the context of multiple allele systems and multiple loci that difference does not matter.

Q. Now, doctor, you're an expert in population genetics, are you also an expert in statistics?

A. I have given many lectures in statistics classes, I have taken courses in statistics, population genetics is very much application in data analysis statistical procedures, by many people I am considered an expert in statistics. Statistics as a broad field is very large, there's a lot of room for many different levels of expertise and there are certain aspects of statistics that I am certainly not an expert in. But I --

Q. How would you -- do you know Seymour Gissier?

A. No, I do not know him.

Q. Have you heard of him?

A. I have heard the name, I am not familiar with his particular area of expertise and his work.

Q. Do you know Dr. Caskey?

A. I know him quite well.

Q. He has testified for the prosecution in the States in different cases along with yourself?

A. That's correct, there have been I think at least two cases where we have both testified, though not necessarily at the same time.

Q. Do you know whether or not he shares the same opinion as you, as that it's not necessary, definitely not necessary to have smaller data bases within the large population?

A. He would not call himself an expert in population genetics, but he has told me that he feels the data bases, at least for Caucasians, are adequate and quite sufficient for this case. We have not discussed his opinion on Hispanics. My sense would be that he might not hold the same opinion for Hispanics. I don't hold the same opinion either for Hispanics.

Q. Do you know of any scientists who supported your opinions on the reliability of the RFLP, VNTR technique and the reliability of the calculations who have supported those opinions along with yourself in the past and who have now become opponents of it?

A. No, I'm not aware of anyone who supported it in the past and now is an opponent of it. I am aware of a lot of people very like myself who have testified and supported it in the past and are now simply refusing to testify any more because it is too great an imposition.

Q. Refusing to testify because they now have their reservations about the reliability?

A. No, because they have already said several times what they feel and find they are growing quite unhappy with the legal system that is requiring them to continually state this over and over again in every new jurisdiction. I must qualify this with respect to my view in Canada, this is the first time I have testified and I'm not aware, I'm not applying that generalization to the Canadian system.

THE COURT: I hope we are not enlarging the imposition, we probably are.

Q. What about Dr. Weir, I understand he was on the statistical committee for the FBI along with yourself?

A. Yes.

Q. And does he still hold that the Hardy-Weinberg formula is applicable or can be used?

A. To the best of my knowledge he does, we did as part of that works, he did some analysis of the Caucasian data base and concluded that it -- that there was no problem in the Caucasian data base. He, I believe, found some evidence from suggesting that that could not be made as a blanket statement about the Hispanic. I don't remember what his conclusion was with respect to the black data base.

Q. Is Dr. Kidd(sic) still a member of the committee -- are you still a member of the committee --

THE COURT: Dr. Weir.

Q. -- for the FBI statistical committee?

A. It was an ad hoc committee and as far as I know a final report was written and the committee ceased to exist.

Q. It has ceased to exist now.
Did you testify at the Yee case that it can happen that deviations at one locus of two alleles could disfavour the defendant but the probability that deviations across loci would have that effect is very slight?

A. If that's in the transcript I said it, that's what I feel, I will say that now I don't simply remember using those words in that case.

Q. Is it what you meant by that at that time that what bin frequency might --

THE COURT: Well, let's establish whether it was said or not. The doctor says he doesn't remember whether he said. Are you quoting from -- what are you quoting from a judgment?

MR. FURLOTTE: I am quoting from the judgment.

THE COURT: Perhaps, you could read the words and--

MR. FURLOTTE: That's what I did I read the words.

THE COURT: Did you get them sufficiently?

WITNESS: That is certainly the sense of my testimony, if the judge summarized it in those words, I will accept that, that's the sense of my --

Q. Okay, that's -- now, I assume, doctor, what you meant from that if for one probe or loci an accused was disfavoured that he probably would gain his favour in another one and at the end, it would balance out?

A. Something to that sense, yes, because this is a situation where chance is operating. There is no way to -- there is no such thing in these situations as a uniform bias against the defendant. So on -- of course there could be a slight bias at one locus but the probability that there would by chance be a uniform bias, I think is vanishingly small.

Q. In the Legere case here, where Dr. Shields went across all the five loci in the FBI data base and the R.C.M.P. data base and at the end it definitely didn't balance out, because --

A. No, you're talking about two different things.

Q. When you go from one in nine million to one in five million, that's not balancing out, is it?

A. No, but you're talking about two different things. Both of those are estimates, I don't know that one is, that there is any bias pro or con, there are using slightly different numbers and of course, come, slightly different numbers going into a calculation will result in different numbers coming out. They differ by a factor of two, that's a very tiny amount of difference. So I would say that's a completely different situation.

Q. Have you ever published some of your works which were later shown to be wrong?

A. Oh yes.

Q. Many?

A. I think there are only two, two studies, they were not -- they were never shown to be wrong in the sense that anything was done erroneously, but they were shown to have been by chance statistical flukes, where we thought we had a significant finding that additional subsequent data showed was almost certainly just something that arose by chance. That's happened to me twice out of two hundred and fifty major publications, not counting the abstracts and such

which is another two hundred and fifty or so. But that's the very nature of science, that's why repeatability is desired.

Q. And the error went just the opposite way, rather than highly unlikely for one, it just went highly unlikely for the other, something to that effect?

A. No, that's not the nature of the studies.

Q. What was the nature of the study, doctor?

A. One of them was finding an association between a particular genetic marker and a possible mechanism for the causation of Downe's syndrome. Where we followed up own study, we pursued it and we showed ourselves that our initial finding that looked very promising as a possible explanation for Downe's syndrome was in fact a statistical fluke.

The other study was evidence for linkage and hence, a genetic causation for maniac depressive illness where we had what we thought and I might add, what the entire scientific community thought was very meaningful and significant evidence for a particular gene predisposing to maniac depressive illness. It was published in Nature, in fact both of those papers were published in Nature, an extremely rigorous prestigous journal. They were both wrong but we they were wrong conclusions, we had not found a gene, subsequent data that we helped developed, we meaning me and my collaborators, almost no research is done any longer by a single

individual, designed the studies to pursue this to determine whether we could replicate our own findings and new data were obtained that were not available at the initial publication, and we had to conclude and publish that we re-evaluated our original conclusions on the basis of new data. That's the way science operates.

I have had lots of other publications where the findings have been overwhelmingly supported by other scientists in subsequent studies.

Q. Have you any publications or conducted experiments in the forensic field that we are dealing with here today?

A. It depends on how you define forensic field. If one --

Q. This type of evidence that we're dealing with?

A. Well, let's take DNA typing down there, I have done hundreds of thousands of those typings in my laboratory. Let's take the question of matching bands across different autorads to see whether or not they match, that is something that is done on a daily basis in the course of interpreting our data that we're generating in the laboratory. The question of identity, is this sample of DNA identical to that sample has come up several times because somebody screws up in the laboratory and mislabels a tube, and we suddenly have a tube of DNA thought was something that it is really different, and we have to go through tests and try to figure out what it is. Does it match this? Is it really from that other individual?

Q. What about the use of the quasi continuous allele system and the use of contaminated?

A. We get contaminated samples, we try to keep that to a minimum but we have certainly had contaminated samples. It created a major problem for one of my graduates students who brought back baboon samples from Africa and was unable to have purified distilled water, so the samples came back contaminated with an unknown plasmid that cross reacted with PBR322, the plasmid used in most of our probe. We had to figure what was going wrong. We had samples mixed up, DNA from two individuals in the same two -- in the same lane, we have to figure out what went wrong. So we do an awful lot of troubleshooting on a day to day basis, and we deal some with VNTRs, they are not the major type of work, so that though my laboratory is not a forensic laboratory and does not generate data for forensic purposes we do every type of study that is involved in forensic study. And we do it on a fairly large scale.

Q. Doctor, do you have a protocol at your lab?

A. Yes.

Q. And have you set matching standards for your students?

A. No. I testified earlier this morning that by in large those sorts of matching standards that are required in forensics are not required because we can repeat the tests, and we can apply what defacto is a far more rigorous test of

repeatability and other types of analysis that simply aren't possible in a forensic setting, where the sample material is limited. That doesn't mean I have no standards, to say I don't have those matching standards I would say, we have a higher level of standard that's just not possible in most forensic application.

Might I interject an addition to one of my earlier answers. When you were asking about anything of mine being proven wrong. I know from previous trial situations and have been told by my colleagues that certain defence attorneys have asked them about that in an attempt to discredit me because something I did was shown wrong. And in fact I feel very proud of having done the studies that showed my initial work was not correct. And in fact most people in the scientific community have said that the way in which we as a collaborating group systematically pursue validation and when we could not validate published that fact is something that is very laudable. Sitting here thinking about it, I felt I would like to say that.

Q. Doctor, what's the degree of probability that two siblings profiles might match?

A. Twenty five percent per locus.

Q. Per locus, and how would that compare to somebody who wasn't related? We can't give a distinct figure but roughly?

A. It depends on the system and the degree of discrimination but certainly most of these loci the numbers that were calculated that I saw per loci were on the order of one in fifty, one in seventy as opposed to one in four. So the probability of two unrelated people matching at a single locus is much lower than two full siblings.

Q. If you were to assess, say, a group of samples who come from different people, maybe you would run an autorad of ten different people and you were to see these ten people sharing a lot of common bands, maybe the average of twenty five percent, would you assume -- and using these probes, and using those probes, would you assume that maybe these people are related or would that be pure chance?

A. It certainly could happen by chance alone, if you've got a limited sample of ten people. Depending upon how many bands were shared, how few bands were represented, I would be -- the more bands shared among the people the more likely I would be to say, yes, it's more likely they're related, but it's a continuum of probabilites and any pattern is possible by chance alone, that's the nature of chance, any single pattern is extremely unlikely by chance alone.

Q. If you were to find a community who happened to show a lot of common bands, say, on the twenty five percent level, would it be fair to assess somebody in that community with a general

population data base, that maybe the FBI or the R.C.M.P. has?

A. It depends on the question you're asking because if you have no prior basis for saying the criminal comes from that small community, then it's by definition a small community, a very small part of the total population. So all of them are fairly rare. If you now want to say, here is an individual from that community, what's the probability that someone else in the community has the same band? Then you probably want the frequencies of that band in that very specific community, if you can show that they're different from the population at large.

Q. So it might be that that community ought to have their own population data base?

A. It might be, depending upon what it was.

Q. Do you believe in running open and blind proficiency tests in laboratories as a measure of quality control?

A. Open and blind?

Q. Yes.

A. Those are by in large as I understand them two different kinds of proficiency tests, an open proficiency test and a blind proficiency test, and I think they're quite appropriate, one is always interested in measurement of quality assurance in a forensic setting, I think that's important. We don't routinely do it in a research setting but there are often the equivalents so that we can test how well a given technician or post doctorate or graduate student

has done their work and interpreted their work by having somebody else repeat it, especially if questions arise.

Q. Do you have any opinion as to how often those proficiency tests should be conducted, say, in a forensic setting?

A. No, I have no opinion, it depends on what you wish to demonstrate by those proficiency tests.

Q. I understand that a lot of labs in collecting their specimens for analysis that they would like to have dried stains right away, have them air-dried and freeze them right away, is that your understanding or do you know anything about this?

A. I know that that is a very good way to store DNA, and it is far better than storing it liquid, depending upon the liquid solution it's in. We don't do that, we don't follow those procedures because most of our sample, DNA samples come from cell lines, where we actually grow the cells in the laboratory, but we do in some of our diagnostic tests get blood samples sent to us where we get the DNA from the blood. We sometimes get tissue samples of tumors sent to us. We always do the analysis fairly quickly, so we don't have to worry about it. But if it were a problem of transportation or long term storage before we could get to the analysis, then I would say, dried and frozen blood samples or purified white cells, dried and frozen would be an optimal way of storing the DNA.

Q. Why would that be, what's the purpose of it?

A. Keep the DNA from degrading, to maintain samples so that there is something later to analyze. Bacteria if they are growing will slowly chew up the human DNA. Other sorts of chemical reactions can occur if the DNA is in a liquid solution unprotected. A variety of things can happen. And if it's dried and frozen, there will be no bacterial activity and very little chemical activity.

Q. Have you read Dr. Lander's Branbury Report for the Office of Technology Assessment?

A. There is a Branbury Report article from a meeting, a Branbury Conference that is as far as I know very different from what the Office of Technology Assessment has published. I know of Lander's article in the Branbury Report. I was present when he gave the talk that resulted in that article.

Q. I believe he suggested for the use of the ninety nine percent upper limit confidence as you're suggesting today, is that right?

A. He talked about many things. I have not read the article in two years. I think I read it when it first was published. I would expect that he would agree with me that that's a good thing to do. So if you say it's written there, I would agree with it.

Q. Were you in agreement with him at that time or did you oppose the idea at that time?

A. I certainly did not oppose the idea at that time. I don't know that I voiced in any way agreement but I certainly was in general agreement with that.

Q. Do you know whether or not band shifting was initially denied by some of the experts and the opponents of this method?

A. I don't know for a fact that anyone denied its existence, someone may have.

Q. Could you describe, I suppose, the phenomenon stated as star activity, you've heard that expression before, I assume?

A. Certainly, there are some restriction enzymes that when placed under non-optimal conditions or when allowed to be incubated for too long or at too high a concentration will cleave DNA at secondary sites that do not have precisely the sequence of the primary recognition site. And so one gets fragments cut into additional smaller pieces when that occurs and it can occur partially, in fact it often does in our experience and we had it happen with certain batches of some enzymes, it's never a complete phenomenon but it gives rise to shadow bands that are smaller.

Q. That would show up something like, what, partial degradation?

A. Not like partial digestion which gives bands of larger size because the DNA has not been cleaved but additional bands often fainter of smaller size because of additional cleavage at other sites. It's not a very common phenomenon and

in most real situations because the buffers and protocol for digestion are designed to avoid star activity. And it's not present for all enzymes but only for some. It's a fairly well understood phenomenon.

Q. How could you distinguish between star activity and degradation?

A. A star activity will tend to give you discrete bands, degradation will tend to give you a blur because degradation is random cleavage at additional sites. Whereas star activity is occasional cleavage at specific additional sites. So one has no sequence specificity and the other has sequence specificity.

Q. How would you interpret an autorad that had star activity?

A. One would see additional bands that were not present which might indicate a mixture of DNA samples or star activity. One would want to know about the enzyme that was being used whether it was an enzyme known to have star activity. And then one would look at what one saw. I can't say how I would interpret because there are many possibilities. I would -- from my experience it would usually be recognizable that something was not quite right and if it could be explained by star activity, often for the systems we use we know exactly what to expect. We sometimes see a very specific additional band and we simply disregard it, because we know that's what its cause is.

Q. Would you attempt to interpet a lane that had star activity or to declare a match that had star activity in it?

A. It depends on what the lane looks like and whether I thought it was likely to have star activity. Most likely I would say that it was an equivocal lane and not tried to give a hard interpretation. But it depends on a variety of other circumstances.

Q. Do you know whether or not there's any evidence of star activity with Hae III restriction enzyme?

A. I do not know for certain. I have not made a point of looking at it. I know if it might occur under some circumstances it does not occur commonly because it is a very robust enzyme that's used, and I've seen lots of autorads using it in my lab and elsewhere, where it is clear there was no star activity, whether it may ever have had -- I'm sure the FBI and the R.C.M.P. have looked into the issue. I do not know what they found.

Q. Are you aware of an article entitled, The Meaning of a Match, Sources of Ambiguity and the Interpretation of DNA Prints by William C. Thompson and Simon Ford?

A. I believe I saw that a year or two ago, something by them. I don't remember if that was the title. Where was it published?

MR. WALSH: I think to assist, Mr. Furlotte, that's a chapter of a book of Forensic Technology, I'm not quite sure of the title, that's my understanding, it ended up in print as a chapter in a book entitled, Forensic Technology, I don't know the full meaning and I can't remember the publisher.

WITNESS: So it's not a peer reviewed article. I may have seen a draft of it. I certainly have not seen it as a printed chapter.

MR. FURLOTTE: My lord, maybe it might be an appropriate time for a break.

THE COURT: Okay, we will take fifteen minutes here.

COURT RECESSES FOR 15 MINUTES AT 3:30 P.M.

COURT RESUMES AT 3:50 P.M.

ALL COUNSEL PRESENT

ACCUSED PRESENT

THE COURT: Okay, Mr. Furlotte.

DR. KENNETH KIDD, still under oath, continued to testify:

CROSS EXAMINATION CONTINUED BY MR. FURLOTTE:

Q. Doctor, before I go on with something else, I am just going to ask you a question in relation, you mentioned that anything you want to check for DNA it should be -- say, like stains, it should be dried, air dried and frozen immediately to preserve it, to stop it from degrading?

A. I didn't say it should be, I said that was an excellent way of preserving it, as long as it has not degraded it can be analyzed however it's stored.

Q. It would degrade quicker if it wasn't?

A. Quicker but DNA is remarkably stable. They are in fact able to study DNA now from frozen specimens in glaziers of extinct animals, from Egyptian mummies.

Q. What about stains from DNA stains, whatever, subjected to high heat, how long could they withstand high heat?

A. I have no idea whatsoever.

Q. Would heat affect the integrity of it, DNA, say, temperatures 100, 150, 200 degrees?

A. If the DNA is dry it will have much less affect on it than if it's wet. One increases molecular motion when one increases heat. So I assume it would have some effect on increasing the rate of degradation, but I do not know that, I have not studied that.

Q. So it would have a greater effect -- would heat have a greater effect on dry stains or on liquid?

A. On liquid.

Q. Dry stains would last longer then, would be less effective?

A. Yes.

Q. Would the DNA maintain its integrity if it was cooked?

A. To some degree, yes, it depends on the temperature, the pressure and the environment in which it exists. But yes, it would not be completely degraded by that treatment.

Q. Now, doctor, you mentioned that for case

specific that probe D16S85 was ruled inconclusive because of faint bands?

A. That's correct.

Q. I take it that you would agree to a degree with that chapter in the book by Thompson and Ford which was referred to earlier about the interpretation of faint bands, that if they're too faint, then they should not attempt to interpret any results out of them?

MR. WALSH: Objection, my lord, I would file an objection. The doctor has pointed out that he hasn't read that or at least he's not aware of that particular authority. He has heard the name. He wasn't even -- when I pointed out that it was in a textbook, he pointed out that it wasn't in a peer reviewed journal. He has not -- Mr. Furlotte has not established that this is in fact an authority from which he should be actually reading excerpts to the doctor to ask him to comment on.

THE COURT: If you have proposition, Mr. Furlotte, you want to put up and ask the witness's comment on that, that's okay.

Q. Doctor, would you say that faint bands are quite difficult to distinguish from phenomenon, such as smudges on the film and artifacts produced in the electrophoresis and Southern transfer?

A. The fainter the band the more difficult it is, yes, that's a --

Q. To distinguish it from an artifact?

A. That's correct. In fact when I looked at those

I was convinced that they were not artifacts, but I felt that correct sizing in interpretation was sufficiently questionable, that it was best to leave them out. They do in fact--the sizing of them was perfect. They are a match. They can be seen sufficiently to be sized and the sizes match.

Q. Yes, they fall within the 5.- percent window?

A. Yes.

Q. Yes.

A. And that is not what one would expect of an artifact.

Q. When you're -- someone is going to attempt to interpret faint smudges or something on artifacts or just marks on the x-ray film, would one be more apt to deciare something like that a band if that mark was where you would expect to see a band?

A. Many factors go into deciding whether or not you want to call it a band. One of those factors that may affect that would be the sort of subjective bias that you were talking about, that is clearly a possibility if the band is sufficiently faint.

Q. Given the fact that you might want to interpret a faint mark on an autorad, that you might want to determine it as being a band because maybe by checking it with a cross lane, you know, that's where you might expect to see a band. Would it not be better to interpret as to whether or not bands exist in a lane without looking at any other lanes?

A. That is in fact what the computer software generated by the FBI does when it does a size estimate. It looks for whether or not it finds sufficiency density of pixels that it is willing to call a band and then it gives an estimate of it, and it does that irrespective of where it occurs in the lane.

Q. How does the R.C.M.P. operate?

A. They use that software.

Q. They use that software?

A. Yes.

Q. Does the operator tell the computer as to how many bands he sees in the lane?

A. The version of the program that I saw at the FBI allows the operator to override and force the computer to focus on certain bands, but the version I saw the program would find more than two if there was a sufficient density difference. But you could tell it as an option to find only two. I don't know what the version of the software in the R.C.M.P. lab actually does.

Q. When you reviewed the autorads did you also use the computer to see how many bands the computer would detect yourself?

A. No, I did not but I saw no evidence of any other bands. The autorads were really quite free of extraneous artifacts of things, blotches, smears, whatever, general background noise that might be confused with bands. And certainly, I would have been confident in a research setting where I can

always go back and repeat things and reevaluate if it turns out to be critical, I would have been quite confident in calling those bands and saying there were only two and that's where they were, irrespective of what elsewas on the autorad.

Q. When was the -- are you finished?

A. Yes.

Q. When was the first time you saw the autorads?

A. A year ago I saw several of the autorads, those that had been done up to that time at the R.C.M.P. lab in Ottawa when I visited there. I may, I don't remember, I think not, I may have looked at them again when I was there in October but I think not. And the first time I saw the originals of the more recent probings was last night when I reviewed the data after I had gotten here, since they could not send me the originals through the mail. I had received copies but the copies are not of a sufficient quality.

Q. But it would be about a year ago that you, I believe you said you were contacted about a year and a half ago to assist in this case?

A. Something like that, yes.

Q. So you would have seen -- when you first viewed the autorads you would have seen the autorads for D2S44, D1S7, D4S139, D17S79 and D16S85?

A. I'm sorry, I cannot remember which ones had been done, I believe I saw the original probings of all of those, if I remember correctly, D10S28 was done later. I did not see all of the reprobings,

some of the autorads are reprobings done subsequently to that date but of the same probe on the same filter and I saw those last night.

Q. At that instance when you observed, when you reviewed these probes somewhere about a year ago, you said, did you make any notes at the time as to what you observed?

A. Yes, I did make notes. I made notes on many aspects of the laboratory procedures, just to refresh my mind. I did not make specific notes on the particular lanes and the particular probes that were used but some general notes on the autorads.

Q. Did you make notes as to what your interpretation was?

A. I did not write down in my notes my specific interpretation because it was so simple that wherever the bands occurred it was a clear match and there were no bands that were non matches. And I did not write that down.

Q. Were you informed as to why they ceased testing at the D16S85 and waited approximately a year to continue?

A. Yes, the laboratory was closed down completely for renovations, so all testing work in the laboratory ceased sometime a little over a year ago, and the laboratory had just been -- the renovations had just been completed when I was there and they were just starting to get the laboratory functioning but then were doing

instruction in the laboratory for several months and no actual casework through most of last summer.

Q. So when you did your review, they were in the new laboratory?

A. They had just moved into the new laboratory but had not started using it for casework and the autorads that I saw had been done prior to the laboratory being closed down. And I knew at that time, was told that there were plans to do additional tests but they could not do them until they finished the teaching and started the lab up for forensic studies again.

Q. Had you been to the R.C.M.P. lab before that?

A. No, I had not.

Q. So you don't know what the conditions that the R.C.M.P. were in whenever the majority of these tests were conducted?

A. It depends on what you mean by the majority of them.

Q. Well, up to the D16, when the first four probes -- the first five polymorphic probes were run, you don't know the lab conditions?

A. When they were run on the first probing but the second probing of several of those were done afterwards in the lab that I saw. So it depends on how you want to say the majority. Some of them had been done prior to the renovations in the laboratory, and it is true I did not see that laboratory, because that laboratory no longer existed it had been renovated.

Q. But wh: 's most important, doctor, I would assume and you may correct if I'm wrong in this, the co: itions under which the first gel and the second el and the third gel were run to get the Southe transfer on to your membrane, after that you can run the probings in anybody's lab, would that be correct?

A. I'm sorry, I lost a word some place, your statement is not a question, I'm not sure what you were asking.

Q. When is the most important a: ect of, I suppose, reliability and quality of a work, when is that crucial point, is it when you first run your gel or is it in the running of s: sequent probings?

A. They are all crucial. It is clearly important that you do the initial running of the gel correctly and do the initial digestions of the DNA correctly. It is equally important that you don't screw up the probes and use the wrong probes or mix probes, do the hybridizations wrong. So they're both important.

Q. But once you run your gel, the fragments are fixed to a membrane in the Southern transfer procedure?

A. That's correct.

Q. And you have your permanent record, is that correct?

A. Reasonably permanent record.

Q. And then after that step is completely, then you begin to run your different probes to see where these fragments are attached to the membrane?

A. That's correct to illuminate, identify, in the jargon, to light up the individual bands.

Q. And that step had already been done before you ever visited the R.C.M.P. lab?

A. That step had been done --

Q. In the old lab?

A. -- in the old lab, I was told that the same procedurial manual was being used. I reviewed that manual. I was told that much of the equipment was in fact the same. It was simply that additional lab benches had been set in. It was perfectly standard equipment. So it's -- I don't see that there is any serious problem but technically you're correct.

Q. Do you know whether or not some scientists in the general community or even the forensic community believe that there ought to be a certain degree of intensity before you can interpret whether a band is present or not?

A. I certainly believe that there has to be a certain level of intensity. It has to be detectable and clearly greater than the background variation. In fact I will say I will not make a call at a level that modern computer enhancement procedures such as used in the Space program would find quite acceptable for pulling out and saying definitely there is a concentration of silver grains in that strip that is non random. I think everybody would agree there has to be a certain intensity, I'm not sure

that anyone has said what that has to be in terms of optical density, and relative optical density of the particular area compared to the background and variation in the background.

Q. Now, doctor, for two people in the same community or whatever to share a couple of probes while not common, it's really not -- in some cases it wouldn't be all that rare?

A. That's correct, it might be one in a hundred, one in a hundred and fifty for a single locus or a pair of loci, it could be.

Q. And whether or not a match was called on the third probe and maybe even a fourth probe, it would be crucial to the outcome as to whether or not the person would be convicted?

MR. WALSH: Objection, my lord. I don't know what relevance this particular question has to what we're doing here.

MR. FURLOTTE: Maybe if you'll hold your horses we'll find out.

A. I'm sorry, I'm not able to answer the question because I don't know what you mean by that. I have given the probabilities, if there are matches at additional probes, those probabilities are multiplicative and the probabilities come out whatever they come out in the situation.

Q. Let me put it this way, doctor, it's probably not all that highly unlikely that two probes in your profile might match two probes on, say, mine?

A. If we are using binning and --

Q. If we are using binning, yes.

A. -- and we are taking two of these, possibly a probability for two loci might be one in a thousand, that's not extraordinarily rare, it's small but I certainly wouldn't be surprised by it And certainly I would not be surprised at all it's going to be on the order of one in a hundred at one locus.

Q. Now, if, take for third locus, if the bands were light so to speak, interpretation may become a problem, and the operator interpreted some artifact as being a band, it would be highly prejudicial to yourself, if you were an accused person, for that operator to interpret it as a band when maybe it isn't, would you agree with that?

THE COURT: Well, let's not put it in the terms of an accused person, let's put it in the terms of the difficulty in making a proper comparison, drawing a proper conclusion?

A. If the bands are quite faint, then it is appropriate that a call not be made and simply because eventhough I would say I am perfectly convinced that there is a far greater than ninety percent probability for matches at D16S85 in at least two of the situations, I don't remember which two but I remember the autorad, ninety five percent certain is good enough for me to make a call in the laboratory and wait for that to be shown by subsequent work to be correct or incorrect, it is not good enough in a forensic setting. And so while I was quite convinced that

those were matches, that I could see real bands, I completely agree with Dr. Bowen in his call that they were sufficiently faint that the proper use of them was to say, inconclusive and not include them in the statistic is just a safeguard against the very slight possibility that there was an error.

Q. If you were charged with a criminal offence and you were innocent --

MR. WALSH: Objection, Mr. Furlotte is starting to go into the probabilities of guilt, not the probabilities of two samples matching.

MR. FURLOTTE: I'm not going into probabilities of guilt.

THE COURT: Well, you're talking about what is reasonable doubt or something, I'm not sure what.

MR. FURLOTTE: I am not going to ask about reasonable doubt is. I'm not going into the areas of probabilities.

THE COURT: Let's not get into the philosophical matter of guilt and innocence. We are talking about comparisons and priority of comparisons.

MR. FURLOTTE: I want to talk about reliability here.

THE COURT: Well, talk about it in general terms not in terms of what would constitute reasonable doubt which is what you're talking about. Go ahead, Mr. Furlotte, but avoid this talking about guilt or innocence, we are not concerned with that here.

MR. FURLOTTE: I'm not going to talk about guilt or innocence, I do have to, I have to establish that basis.

Q. I was just saying, doctor, if you were charged with a criminal offence and you were innocent would you subject yourself to DNA testing and allow somebody else to interpret the results?

A. Absolutely, I think it is the most certain way going to prove my innocence.

Q. But would you want to conduct the test first yourself?

A. I'm a scientist, I'm curious if it deals with me, I would like to look at it, I'd certainly, if it in the very unlikely chance it failed to show my innocence I would certainly scrutinize it carefully and I think that's what the defence has a right to do and what I've done when I've consulted with the defence on other cases. But any of the laboratories that I've had experience with, FBI, R.C.M.P., Cellmark and Lifecodes I would be quite happy to have them do the test because with almost certainty they would demonstrate unequivocally I was not the guilty party.

Q. I understand Dr. Ray White helped the FBI set up their laboratory?

A. He consulted with them, yes, that's -- he has told me that and they have told me that, I've never been there at the same time with him.

Q. Do you know whether or not he agreed to take the test like you just agreed, under the same circumstances?

A. I have no idea whether he's ever been asked that hypothetical question, I'm pretty certain he's never been accused in a real situation.

Q. I'm not suggesting that.

A. I do know for a fact that other people, such as, Dr. Haig Kazazion(phonetic) who is a noted human molecular geneticist has explicitly said that the very first thing he would want is to have his DNA tested if he were accused of a crime and were innocent.

THE COURT: Well, now, this is, Mr. Furlotte, just another example, you're devoting your energies to the other side, is it?

MR. FURLOTTE: Yes, I'm full of those tricks, my lord. My lord, when you have a witness like Dr. Kidd who is so sure of anything, you have nothing to lose.

THE COURT: That is not what most counsel would say, most counsel would sit down and call their own witness.

MR. FURLOTTE: I am not most counsel.

Q. Doctor, are you aware whether or not some scientists out there are concerned about smaller inbreed populations?

A. I know tht some people have testified that they are very concerned about that. I must say that I have personally studied several small inbreed populations and what I have found has led me to conclude that it is not a major concern.

Q. Are you aware of the words of by Ronald T. Acton and his paper entitled Comparison of VNTR Allele requencies in White and Black Population

A. Yes, I don't remember all the specifics of the article but I have read it.

Q. Did he express legitimate cause for concern about one population data base being sufficient for the blacks or the whites?

A. I'm sorry, I don't remember enough of the details to comment on it. It's been sometime since I read it. I would hazard a guess that since you're raising it, he probably did.

Q. How would Mr. Acton rate as a population geneticist?

A. He is not recognized as one of the leading human population geneticists in the country. He is a competent geneticist. I have no criticism of him as in anyway unqualified. But I would say he is not among the leaders in the field.

Q. I understand the FBI took part in that study also?

A. My understanding is that there was a comparison of samples typed of the same samples being typed at the FBI and in his laboratory. At one point I don't know if that's in the particular paper you're talking about. But there was one study that the FBI was involved in that was a, if you will, a cross laboratory reliability study.

Q. And Bruce Budowle was one of the authors of that paper?

A. As I said I don't remember the details of the specific paper. If you have it there and he is

listed as an author, then, yes, he was. I don't remember the specific paper you're referring to. Bruce Budowle in the comparative study I was talking about, Bruce Budowle was the person, primary person at the FBI working on that study.

Q. Do you recall whether or not they found that there was statistical significant difference within the black population?

A. I believe that different black samples collected in different parts of the United States showed some differences. I know there has been a lot of controversy over how significant those differences were. And I don't remember what the level of statistical significance was.

Q. Two to four times greater for bin frequencies?

A. It's entirely possible if that's what they say for some bins.

Q. Doctor, do you think other people's works are important?

A. Of course.

Q. And to assist you in you performing proper conclusions?

A. Of course I rely quite a bit on data collected by other people in almost all of my science and conclusions.

Q. Did you read the expert report by Eric Lander in the Castro case?

A. I believe I did read it, if it's what I remember reading it was, I thought, stated a little bit with a little bit too much hyperbole, and certainly his unrefereed commentary in Nature, I thought was taken with a little bit too much hyperbole and not enough rigorous logic.

Q. How is Dr. Lander rated in your field of expertise?

A. He's rated very highly. I know him, respect him, I disagree in this case with the emotional level to which he took the issues in his commentary.

Q. Do you agree, doctor, that reproducibility is the most fundamental test which a method must satisfy before it is generally accepted in the scientific community?

A. Yes.

Q. And that first the same observer must routinely be able to obtain the same results when the procedure is repeated ultimate times, do you agree with that?

A. Yes.

Q. And would you agree that different skilled observers must be able to obtain the same result with the procedure is repeated multiple times?

A. Yes.

Q. Would you agree that until a procedure satisfied the test of reproducibility the procedure cannot even approach being generally accepted in the scientific community?

A. I would generally agree with that but I would also note that with the extremely rapid advance of technology that's happening right now that newly reported techniques that are logic, reasonable and reported by reputable scientists are

almost instantly accepted as being true. Almost everyone will say, yes, I'd really like to see confirmation of that but this is so plausible and it comes from such good people who do good work that I'm not going to waste my time trying to reproduce it. I am just going to build upon it and if I can't build upon that result, it will be self evident. So that modern science thought it adheres to that abstract idea, in fact does not go through rigorous repetitions of precisely the same experiments in order to show reproducibility but rather infers the reproducibility by trying to build and do new things which would only be possible given the truth of the original result and so in that way demonstrate the reliability of the findings.

Q. Doctor, since you've testified in a lot of these cases, even the cases that you don't testify do you concern yourself enough to obtain the expert reports of the opponents to the admissibility of this evidence or the reliability of this evidence?

A. In fact it has been a tactic of some prosecutors in order to get me to testify either in the trial or as a rebuttal witness in pre-trial hearings to send me the testimony of some of the witnesses for the defence who are arguing against DNA because in some cases I have quite outraged at the misstatements they have made, and that's been the motivation in order that there be some truth and reasonableness present for me to testify.

So, yes, I have read some. I do not make it a point after the fact to go back and get all of them, this is not my profession, this is not what I intend to make a career of.

Q. Would you call it a form of peer review?

A. What a form?

Q. The fact that witnesses for the defence go to court, provide expert reports as opponents to the reliability of RFLP --

A. In fact I think it's a complete breakdown of rational and proper presentation of evidence into the court system, because virtually all of the people I know that I consider highly qualified experts are refusing to testify because it's too great an imposition. And some of the people who are regularly testifying have no credentials that I think are acceptable at all, and not all of them certainly but some. And I think it is far easier for the defence to get witnesses than it is for the prosecution. I should qualify --

Q. Doctor, some of the witnesses for the defence have contributed their time voluntarily --

MR. WALSH: Objection.

THE COURT: You didn't finish your answer, doctor. Let the doctor, the witness finish his answer.

A. I was going to say that I -- that my statement might seem prejudicial against the defence. I was thinking of the majority of context that I've been involved in. I should have more properly said, pro DNA is harder to find witnesses to testify than anti DNA.

Q. And in that respect it makes it easier for defence lawyers to get expert witnesses, that's the context you meant it in?

A. That's correct.

Q. You testified in the Yee case, you've already stated, doctor?

A. That's correct.

Q. And Dr. Caskey who has testified in behalf of the FBI on different occasions?

A. Yes.

Q. Do you know whether or not Dr. Caskey testified at the Yee case stating that two standard deviations is the generally accepted standard in the scientific community?

A. I don't know that he said that, I have not read nor was I present for his testimony. I will accept and state that I agree with that statement, that in most statistical applications in science one presents the data as the estimate, plus or minus two standard deviations.

Q. And what is -- how would you calculate the R.C.M.P.'s standard deviations in comparison to what is standard, bigger -- how much greater?

A. Well, the R.C.M.P. has not specifically calculated standard errors or standard deviations. I understand that Dr. Carmody did, I don't know what particular method he used. But I have been advocating three standard deviations as opposed to two, simply to give an extra level of benefit to the defendant. The beauty from my perspective of the DNA data is that it is so

powerful one can bend over backwards and throw out data that are perfectly interpretable but maybe a little bit faint and one can use three standard deviations instead of two, always bending over backwards not to underestimate the probability and still get numbers that are in a forensic settings very meaningful.

Q. How would you rate Dr. Hartl in his field?

A. He is someone I consider a personal friend. He and I were graduate students together. I have known him for many years. He has written excellent textbooks that I have used in teaching my courses.

Q. Do you know whether or not his opinion is that matching criteria employed by the FBI would not be considered as generally accepted and reliable in the scientific community?

A. I think based on personal conversation with him at a scientific meeting after the testimony in the Yee case, that he and I have very similar opinions.

Q. Except for it being reliable?

A. No, no, I think we have very similar opinions about the reliability and the way the data should be used. He --

Q. Did you read Dr. Hartl's report from the Yee case?

A. The one that he submitted in writing, --

Q. Yes.

A. -- I read, I thought he was foolhardy in submitting that in writing because it contained many factual errors which were brought out in the cross

examination. And it greatly distorted some of the relevant facts in the case, and I think he was very upset that he gotten drawn into that case and I believe as a result of that is now refusing to testify again. He found it a very unpleasant experience. That's one of the reasons we talked afterwards when we met at a scientific meeting. And he was very concerned about some of the issues about of precision. He had been given data by the defence attorney out of context and relied upon that. He was very unhappy about that. And I think he feels that if one takes a conservative approach, he is -- that certainly the basic molecular methodology is quite sound, statistical questions involved really are very difficult to deal with, with precision, and in my opinion it's impossible to be precise, which is why I am willing to accept a pragmatic empiric approach of deliberate biases that will more than overcompensate for whatever small amounts of imprecision are there. And I think he would feel that that is reasonable acceptable way of proceeding. I believe he is -- would like to see more statistical precision. I would like to see it as well, we don't have it at the moment but that doesn't mean we can't proceed with what we do have.

Q. So are you saying, doctor, that Dr. Hartl in his reasssessment of the FBI data base was -- he was totally wrong in his conclusions, did he admit that?

A. I did not say he was totally wrong. Some of the statements he made in his report were completely wrong. His statements about the MNS blood group system and so on and I think he would agree with me that that is not really an appropriate analogy to use. It is not proof of substructure because there is a serologic explanation for the finding and a two locus system is not an appropriate model for these multi-locus system.

Q. When he come to the conclusion that the FBI could only identify their own agents sixteen percent of the time, he never changed his opinion on that, did he?

A. We did not discuss that but I presented a different approach to analyzing the data and I think that that is a statement, whether he would agree with it today or not, that I think is a very mis -- is a misrepresentation of what the data actually were in the two different data bases by the FBI, the test and retest data base. They were not a true test, retest data base, the methodology changed a variety of things, changed, they were not designed to say whether you could identify your own agent. And in fact I personally would disagree with his evaluation and his statement. But I don't know whether he changed his opinion.

Q. I understand that the FBI has rebinned and redone their whole data base all over again and was Dr. Hartl's assessment of that a factor in playing that role for the FBI to do it a third time?

A. I honestly have no idea. The FBI is continually improving and refining its methodology and doing reevaluations. I don't know what particularly led them to the third data base.

THE COURT: Well, now, the Crown wants you to go with this cross examination, Mr. Furlotte, but the only question is whether you should do it now or in the morning? What do you think about -- have you got very much to go?

MR. FURLOTTE: I spent all last night going through the first two volumes, the first one I went through and this one here, and I just folded the pages just to specific questions I wanted to ask Dr. Kidd and I'm through but second one now but I have not had time to go through the third volume as such and that would take --

THE COURT: Is that the last volume?

MR. FURLOTTE: This would be the last volume, yes.

THE COURT: Well, why -- do you want to finish up with that book there, have you got very much?

MR. FURLOTTE: I just have a few more pages in this book, maybe about four pages.

THE COURT: Well, why don't we finish that perhaps this afternoon.

Q. Dr. Kidd, you were at the April 17th, 1990, meeting of the National Academy of Science and National Research Council Committee on DNA Technology and Forensic Science?

A. I was there one day, I don't that it was April 17th, but --

Q. Well, what day it was -- I understand Dr. Bruce

Weir, you stated was a member of the FBI Statistical Standards Committee?

A. Yes.

Q. And is it true that you and Dr. Bruce Weir took strongly opposing positions on the appropriateness of the FBI using the Hardy-Weinberg equation to calculate genotype frequencies at the single locus?

A. I would not say that it was true that we took strongly opposed views. We have different opinions. He is attempting to find a statistically correct way of estimating frequencies in the absence of assuming Hardy-Weinberg, and I am quite satisfied with assuming Hardy-Weinberg based upon the evidence that I have seen, and the other ways of building in for the inherent imprecision.

Q. And did Dr. Weir propose an alternative to the current FBI approach?

A. Yes, he did, I believe.

Q. And what was that alternative?

A. I don't remember the exact mathematical formula. It was not an alternative to the binning approach but to whether the calculation at each locus, and I don't remember the formula he proposed.

Q. It would have been more conservative, I assume.

A. It would have been more conservative, yes than the actual estimate. In most cases it would not have been more conservative than taking three standard errors, but there is no way of demonstrating algebraically and in the abstract which method is always the most conservative.

Q. At the meeting of the National Scientific Council, I believe Dr. Lawrence Meuller was there?

A. Yes.

Q. And was Dr. Charles Taylor?

A. Yes.

Q. Daniel Hartl?

A. Yes.

Q. And yourself and Bruce Budowle?

A. Yes.

Q. And of course Dr. Weir?

A. Yes.

Q. And basically there was only yourself and Bruce Budowle who agreed on the ability of the FBI to use the Hardy-Weinberg equation?

A. I honestly don't remember. There was a lot of discussion about whether or not one could come up with an alternative to the Hardy-Weinberg that would always be conservative and it could be shown analytically mathematically to always be a conservative estimate, even in the presence of deviation from Hardy-Weinberg. And most people were looking for some such alternative. And Bruce Weir presented one.

Q. Aside from yourself and Dr. Budowle, would you say that there seemed to be agreement amongst all the other scientists that the assumption of the Hardy-Weinberg equilibrium which underlies the FBI computation of genotype frequency is inappropriate for the probes used by the FBI given our current state of knowledge?

A. I certainly know that some of the people at that time at that meeting felt that to be the case. I know there are other scientists and there are other data subsequently available, such as the Devlin Paper in Science that shows that the majority of the data agree quite closely with the predicted values assuming Hardy Weinberg, and for those data sets it is a quite valid assumption.

Q. And also amongst the other scientists besides yourself and Dr. Budowle, there seemed to be agreement that the assumption of linkage equilibrium which underlies the FBI's use of the product rule to compute frequencies of multi-locus genotypes, DNA prints has not been verified for the probes used by the FBI? Was there also that general agreement besides yourself and Dr. Budowle?

A. I certainly can't say that there was general agreement, I think it is quite true that the existence of linkage equilibrium among these loci has not been demonstrated. One can never demonstrate the nul hypothesis. One -- there have to be deviations. The question is can one detect the deviations in any reasonable sample size or with any statistic, and there have been analysis done that show with the -- by the method being used one cannot find disequilibrium, they're not powerful methods. But one can never ever demonstrate that disequilibrium multilocus does not exist, it has to be disequilibrium, at

what level can be shown not to be present. So I would agree that it hasn't been demonstrated not to exist. I am convinced it does not exist to any significant level, any meaningful level.

Q. But, doctor, at least there was great disagreement between yourselves and Dr. Budowle and in numbers, not just on matters on quality but in number and quality of professional people who attended the National Science that it is improper and unreliable for the FBI to use the Hardy-Weinberg equation and the product rule in estimating its frequencies?

A. I do not know that to be true. With those words that you used, I do not know that everybody else held that opinion. I know there was a lot of discussion about it. But I have seen no published summary and in fact, there was no official vote taken on what that general opinion would be, do I don't know --

Q. It was the general -- yes --

A. -- I don't know what is the basis for your statement.

Q. The basis for my statement is an affidavit by Lawrence Meuller?

A. I am sorry I will not accept an affidavit by him because I simply do not accept his credentials as an expert in this area. He has said many things under oath that I would very strongly object to.

MR. FURLOTTE: I believe it would be -- I'm finished this volume, my lord, and it would be an appropriate time, I guess for --

THE COURT: Well, you're not going to get away in the morning.

WITNESS: Might I ask if it's possible to leave soon after lunch which would allow me to get home by tomorrow night?

MR. FURLOTTE: I think there's a good chance I'll be finished by lunch time.

THE COURT: You may your reservations for after lunch, can we say that?

MR. FURLOTTE: Yes.

THE COURT: You want to start at nine o'clock.

MR. FURLOTTE: That mightn't be a bad idea.

THE COURT: Not to give you longer but to give you more time to have your lunch.

MR. FURLOTTE: Well, I can get home a half an hour quicker, too.

THE COURT: All right, we'll start at nine o'clock in the morning.

COURT ADJOURNS MAY 16, 1991 AT 5:10 P.M.

COURT RESUMES MAY 17, 1991 AT 9:10 A.M.

ALL COUNSEL PRESENT

ACCUSED PRESENT

THE COURT: Now, Mr. Furlotte.

DR. KENNETH K. KIDD, still under oath, continued to testify:

CROSS EXAMINATION CONTINUED BY MR. FURLOTTE:

Q. Doctor, as I recall yesterday you mentioned that some defence lawyer put a list of scientists who were coming to court as opponents to the reliability of this procedure and you said that half of them were nobodies and half of them weren't? So maybe if I could ask you how you would rate Ronald T. Acton?

THE COURT: I'm not sure about the half nobody quotation, did you use those words?

A. I did not use those words and I was about to say --

Q. Something to that effect?

A. -- that I considered many of them not qualified --

Q. Not qualified?

A. -- in this area.

Q. Would Ronald T. Acton be qualified in this area?

A. I commented on him yesterday, I don't know all of his areas of expertise but he has not been one of the primary researchers in human molecular genetics or in human population genetics. So I would not consider him one of the best qualified people in this area. But I don't know all of his research.

Q. Would you say that he was incompetent?

A. Did you use the word incompetent?

Q. Yes.

A. No, I would certainly not say that. I am not saying of these people I consider not qualified

or not well qualified. To be incompetent, there are certainly many areas in which I am not qualified or not well qualified to address and that doesn't mean I am not competent in other areas where I do have knowledge.

Q. And I believe you already gave your opinion on Dr. Eric Lander?

A. Yes, I did.

Q. And what about Lorraine Flaherty?

A. I do not know that person.

Q. You don't know that person.

A. I have not heard the name before.

Q. Do you know Joseph Nadeau?

A. Yes, I do.

Q. And how would you rate him?

A. He is a very well respected mouse geneticist. He has not worked in human genetics to any appreciable degree that I'm aware of.

Q. What about Paul Hagerman?

A. He is a molecular geneticist. I have read some of his testimony. He certainly has some qualifications but I had differences of opinion with some of what he said in at least one case.

Q. Well, that's okay, you have differences of opinion with Dr. Lewontin and Dr. Lander, so that doesn't make them unqualified?

A. No, but I think -- well, he has no experience in human population genetics at the molecular level. He is a molecular geneticist, not a population geneticist.

Q. Peter D'Eustachio?

A. He has some molecular experience, I don't think he has any significant training in population genetics.

Q. But in this field we deal more than with population genetics?

A. Yes, of course, this area is the interface of several different previously somewhat separated academic domains.

Q. Daniel Hartl?

A. I think very highly of him, I said that yesterday.

Q. And Richard Lewontin?

A, Very well qualified population geneticist and molecular researcher, not merely a molecular geneticist but uses molecular technique. He has not studied a large number of -- not done a great deal of work on human populations but he's very knowledgeable in the area.

Q. Lawrence Mueller.

MR. WALSH: We plowed this ground yesterday, my lord. He's going over some of the same things again.

THE COURT: Yes, I think a lot of these opinions have been canvassed already.

MR. FURLOTTE: By some of the other experts I did.

THE COURT: I have some misgivings actually about the witness being put on the spot here and asked to give ratings on all people connected with the genetic industry.

WITNESS: Many of them are my colleagues and it is not necessarily --

MR. FURLOTTE: I believe he opened the door, my lord, when he made the statement that half of them were not qualified.

THE COURT: Well, I think some question I forget what it you put to him either invited, you know, an opinion as to whether some of the people were qualified on either side, the prosecution or --

MR. FURLOTTE: I didn't put the question of qualification --

THE COURT: Well, what else do you want to ask?

MR. FURLOTTE: I put the question of numbers and he come up with the numbers that the defence had called about four times as many independent scientists to testify as has the Crown and half of them weren't really qualified.

MR. WALSH: My objection, my lord, was on the basis that Mr. Furlotte had replowed the same ground with respect to who certain people were and what Dr. Kidd thought of them. Dr. Kidd made it very clear yesterday what he thought of Lawrence Mueller when Mr. Furlotte was delving into and asking him questions from an affidavit. Now, Mr. Furlotte is going over the same thing this morning.

THE COURT: Mueller has been canvassed totally, who else do you have -- what others do you have on your list? Call your list off and we'll see.

MR. FURLOTTE: I have Bruce Weir.

THE COURT: You covered Weir I think yesterday.

Q. Charles Taylor?

A. I know the name but I don't know anything really about him.

Q. He was at the National Academy of Science?

A. He may have been, I do not know him well personally. I don't know what his research is or if I have known I cannot think of it at the moment.

Q. Marie Claire King?

A. I think very highly of her. She is a good scientist.

Q. Conrad Gilliam?

A. He's a very good molecular geneticist, I collaborated with him in the past.

Q. Joel Cohen?

A. He is a very eminent statistician but he has written an article that was published that I found quite misleading in implications of the statistics and found not really acceptable as a scientific article.

Q. To your standards but in the scientific community he's well accepted as --

A. As a statistician he has no real experience in human genetics or molecular biology, and the statistic relevant to human population genetics are not ordinary statistics.

Q. Would you admit, doctor, that statistics and a statistician that it would be necessary to have experts from those fields to validate the use of the Hardy-Weinberg and product rule?

A. No, I would not say that that's required.

Q. Dr. Ronald Libby?

A. I do not have a very high opinion of his qualifications at all. He has some molecular biology. He testifies a great deal. I strongly objected to some of his testimony in one case and I have never seen his C.V. I have no idea what his publication record is, I think it's very slight and he does not to my knowledge have a faculty rank he is simply a very junior investigator.

Q. Simon Ford?

A. I know of him certainly. I have found some of the things that have been written by Ford to be quite misleading and to contain what I would consider to be factual and scientific errors.

Q. Dr. Phillip Green?

A. At St. Louis?

Q. I believe it, yes.

A. He --

Q. I believe he was a witness in the Castro case.

A. Yes, I believe so. To my knowledge he has had very little involvement in many of these areas. He is a very good mathematical geneticist, specializing in human linkage mappings, studies in computer methodology and alka ryhthms(phonetic) for doing Yak Contigues(phonetics), a lot of what he is -- he is clearly experienced in analyzing RFLP for linkage analysis, I don't know what his expertise is in terms of population genetics.

Q. Rollin Richmond?

A. I don't know the name.

Q. He's a population geneticist and I believe he testified in the Schwartz case, you don't recall? Doctor, I am led to believe that Dr. Eric Lander has a new publication out to follow up from the Branbury report in which discusses the topic of the validity of the matches being made by R.C.M.P. and under these methods that the R.C.M.P. and the FBI use?

A. I don't know, I have not seen it.

Q. You have not seen it?

A. No.

Q. Doctor, many of these -- at least a few number of these scientists that I have mentioned have publications out for peer review criticizing this method and the reliability method, would that be correct?

A. The only one I'm aware of is the one by Joel Cohen and it did not, certainly did not criticize many of the specifics of this, it made primarily one statistical point.

Q. Well, I think that Eric Lander had, at least in the Branbury report, he criticized the reliability in this?

A. No, as I remember his article, it was mostly an article in which he discussed theoretical issues that needed to be considered, most of which I have considered and drawn an opinion that we have adequate data. That was almost nearly three years when that was written and there are

considerable additional data available today from what was available then.

Q. Have you ever written any articles in support of this method and put them up for publication to find out if your opinions would be accepted in the general scientific community?

A. No, I have not, if you are talking about the more forensic applications and some of the interpretations of the statistic, this is not something in which I am trying to build a professional reputation. It would be as far as I'm concerned a waste of tiem.

Q. When you appeared in court in other cases have you prepared and presented the court written expert reports as other --

A. No, I have never been asked to.

Q. Do you have any affiliations with Lifecodes?

A. No.

Q. Have you co-authored a paper with any of the people from Lifecodes?

A. Yes, Ivan Balazs.

Q. And what is your connection with him?

A. A scientific colleague with wh m I did one collaborative research study.

Q. In the Yee case did you testify that the differences in Lifecodes dat between Caucasians and Blacks was not very substantial?

A. I don't remember what I specifically testified in the Yee case with respect to that. You show it to me in the transcript I will say, yes, I did, I may have, I do not at this point several months

later remember what the specific frequencies are in those two data bases. When I testified in the Yee case I had the data available.

Q. Following the Yee case did you later make the comment at any time that and reflecting upon the same data between Caucasians and the Blacks in Lifecode's data was that it reflected dramatic differences?

A. No, I did not make that comment subsequently. You are referring to the --

Q. Branbury Report --

A. -- the cross examination during the Yee case by defence attorney in which he found a quote of mind in the original Albert testimony in which I had said at that time that there were some dramatic differences between the data bases and I subsequently said that they were not so great. There was in part over a two year period a change in my opinion. There was in part a change in the nature of the data, so the data bases changed during that period of time. And in part the differences are different for different loci. So that some loci show what are appreciable, if you will, even dramatic differences, that is not a term related to forensic significance or meaning, it's just quite visible differences. My interest as a population geneticist I find where my primary research focus is on looking at small differences between populations wherever they might, whatever they might be. I find those differences dramatic.

When I think about this in the context of a forensic application, most of those differences are on the order of some bins or areas. Lifecodes does not present their data with the FBI bins but more as floating bins. There are some parts of the distribution, size distribution where the frequencies may differ by a factor of two, four percent to eight percent, three percent to even ten percent, I don't remember the exact numbers. But at no point is it a difference that would be so large that I become terribly concerned about it in terms of the reliability of using this in a forensic setting. I have said before that I think it's reasonable to present the statistics, this is what it would be if you considered the criminal unknown to be Caucasian, this is what it would be if you considered the criminal to be Black, those are likely to be different numbers. It's reasonable to present them as well as the data for the ethnic group of the suspect. So, yes, my words from some cases have been thrown back at me, but I am quite content with my statements.

Q. Do you recall whether or not you gave conflicting testimony in the Jabobetz case and in the Yee case when you were discussing the hundred RFLPs that were involved in the Amerindian data?

A. I can't imagine that I gave conflicting testimony, my opinion largely there has not changed.

Q. In Jabobetz did you say that there was very little difference between the five populations that you had studied?

A. I doubt that I said that.

Q. Did the defence have to get a court order to make you provide the Amerindian data to the Court and to the defence in the Yee case?

A. No, I voluntarily presented it that under the condition that since it was unpublished research data, it not be distributed beyond the defence lawyers.

Q. I understand you have a chapter in Brambury report?

A. Yes, I do.

Q. And you had a table in that chapter which disclosed the data, some of it?

A. I had a table in that chapter which presented one way of summarizing some of the data from Lifecodes as it was being represented at that time in our computer data base.

Q. And did you find the frequencies for DS62 was significant, the differences?

A. D6S2 showed really quite remarkable differences among the five populations that we were studying at that time, African Bygmies, two different groups from a thousand kilometers apart, Chinese, Caucasians and Melanesians from the Island of Bougainville.

Q. And what was the -- how much of a difference was it, do you recall?

A. There were at least five different alleles and it's a very complicated process to describe the differences. I presented them as the actual

frequencies represented by a hystogram, it's a very dramatic, visual difference. I was highlighting one of the loci that happened to show remarkable differences. If you looked at our February, 1991 proceedings of the National Academy of Sciences Paper you will see that of the hundred loci we studied there were some loci that showed unusual levels of homogeneity across all of the populations. Others that showed the expected distribution by chance and some loci that showed more deviation among populations than we would expect to find by chance alone. And in that paper we discussed this distribution, D6S2 is one of those loci that shows a lot of variation.

Q. Did Dr. Hartl do any experiments with that data to see what kind of differences in frequencies he might get between one village and another?

A. What data?

Q. The Amerindian data that you had collected?

A. It is my understanding that the data I made available under court seal in the Yee case was shown to Dr. Hartl as a consultant for the defence and that he did some analysis of it. I was never sent those analysis. I have no idea what he did.

Q. Do you recall anybody telling you that if you had a combined probability pattern across three loci, the MS estimate is -- this is for Village A, without naming it, the estimate is one in three hundred and seventy thousand and if one

relies on Village B data base with the same pattern the combined probability is one in five hundred and seventy, could it vary that much, doctor?

A. Sure, I have never been told that, I don't know the basis for thatcalculation but of course, the villages were different, they are small basically individual families.

Q. And the two probabilities differ by a factor of six hundred and fifty within the same race, would that be a fair assessment?

A. Between those two particular samples in the Amazon, yes. I mean I am accepting the numbers I have not seen anything underlying it, but I am not surprised by it.

Q. Now, did I understand you to say that you were good friends with Dr. Hartl, you went to school together?

A. Yes.

Q. And after the Yee case you sat down and you discussed the evidence that he gave?

A. No, we did not sit down and discuss it, we met at a scientific meeting and discussed it walking from one auditorium to another.

Q. And you mean to tell me that he never presented you with his findings and you weren't curious enough to ask?

A. It was months later that I found out that he had done something and I don't particularly care what he did, one day I may find out, he certainly did not send them to me nor did the defence lawyer. I must say one of the reasons I am

stopping testifying is the fact that these sorts of things are being circulated among lawyers without my knowledge and that I find that not a very proper approach. And I am not terribly pleased with the way the legal profession is handling this.

Q. Now, doctor, before the Castro case I understand that you testified in court in support of the methodology and the data base compiled by Lifecodes?

A. That's correct.

Q. And you went to court and gave the opinion that Lifecodes data base was proper, valid and reliable, is that correct?

A. That's correct.

Q. And after the criticisms of the Lifecodes data base in Castro, Lifecodes voluntarily changed their data base, is that correct?

A. I don't know that.

Q. You don't know that Lifecodes decided that their data base also was unreliable and they constructed a new data base?

A. No, I do not know that to be the case. I know that Lifecodes has enlarged its data base, most of the data bases around have been continually enlarged and improved over the last few years, that doesn't mean that the version that existed before was unreliable or in any way bad, just that the new one is better.

Q. But at the time that you assessed Lifecodes' data base and promoted its validity in court,

Lifecodes had been using a smaller window to smaller window to calculate the probabilities than it did to declare matches, isn't that right?

A. I did not testify in that case.

Q. No, you didn't testify in the Castro case but before the Castro.

A. Wait, in the original testimony I did not testify as to the method that Lifecodes was using in a match, they were no data available, I did have numbers of match windows or the criteria for declaring matches readily ava lable to me. The issue did not come up. I was talking about the data base and the general way in which they were declaring matches. I agree that I subsequently learned about this numeric problem and they then went on to declare matches using different windows, they changed some of their procedures and improved them. But those were not issues that I directly addressed in my original testimony.

Q. Did you suggest in the Yee case that there was half a chance that a defendant would be hurt by substructure at one allele?

A. I'm sorry, I do not remember specifically what I said in that previous testimony. If you can give me a quote from transcript and a context.

Q. Is there half a chance that substructure at one allele?

THE COURT: Hasn't this been canvassed already? We spent a great deal of time yesterday on substructuring, surely every aspect of it was covered, it must have been. I mean merely

because you thumb through your pages there, Mr. Furlotte, and find yellow written on some new page or whatever the colour is, doesn't mean that you can open it up again. You've covered substructuring, you've cross examined this witness on that subject. Why do you keep coming back to it? I find it difficult to understand what you're trying to accomplish in some of this cross examination. Do you get my point?

MR. FURLOTTE: Oh, I've gotten your point long ago, my lord.

THE COURT: I don't seem to be getting it across, that's the unfortunate part. Haven't you really though covered restructuring totally, if you haven't why don't you finish off with restructuring in a few succinct questions and then put an end to that.

MR. FURLOTTE: My lord, if I was given time to prepare for this case I would have been able to have but I haven't been given the time so therefore I have to fumble my way through it.

THE COURT: Well, you're succeeding.

MR. FURLOTTE: If you don't want me to fumble my way through it, then cut me off and let's forget the whole matter.

THE COURT: You're succeeding in the fumbling and you've been given five months to prepare for this. I realize some of your problems, I realize it's a highly technical thing. I made the point earlier -- well, I'm not going to

review what I had to say earlier when you were cross examining one of the other experts. But surely you're relying, you're going to rely primarily on your own witness or whatever witnesses you call in this field.

MR. FURLOTTE: That's right, my lord, and all I can say, my lord, is if it looks as if I'm fumbling and struggling and incompetent, it's because I'm not prepared and when I'm not prepared I do not operate well under pressure and when I'm not prepared I'm under pressure to the prejudice of my client.

THE COURT: You see, Dr. Kidd, the judiciary suffers some of the frustrations that you do under in these matters.

Q. I believe Dr. Connelly testified for the defence-- for the prosecution in the Yee case?

A. That's correct.

Q. And Dr. Connelly regarded Eric Lander, the greatest genius in the profession in the last twenty years?

A. I did not read the transcript of his testimony. I can't comment on that.

Q. Dr. Kidd, are you aware of the works of Gilbert, Leaman, O'Brian and Wayne entitled, Genetic Fingerprinting Measures Population Differentation in the Channel Island Fox printed in the Nature magazine?

A. I think I've heard of the paper, I have not read it.

Q. Do you know whether or not they found that foxes on one of the islands had all the same DNA?

A. I have no idea and would consider it absolutely irrelevant in any case to the question of frequencies in human populations. Island populations of foxes bears no relationship to the human populations.

Q. Neither would the frequencies of VNTRs in the comparison to humans?

A. The population structures are totally different.

Q. Have you yourself ever made any attempt to validate the statistical independence on which the product rule depends in these cases?

A. I did for the Lifecodes data base some years ago, I know my colleages, Devlin, Risch and Roeder at Yale are looking at some of these issues from an even more rigorous statistical approach than I used some years ago. I have done visual examinations of some of the data base and it is clear that any deviation must be small and I am satisfied that none has been demonstrated. I also know that Dr. Carmody did an analysis of the R.C.M.P. data base to look at that and found no evidence in his analysis.

Q. Would you agree, doctor, that if one used a ninety five percent upper confidence interval that in some cases the degree of probability could change from one in six million to one in one thousand?

A. I suppose it's possible, anything is possible, depending upon the particular data and that data

base and the population frequencies, I -- of course, it's possible.

Q. Do you know of any other scientific research in which scientists rely on the product rule and the assumption of Hardy-Weinberg equilibrium to determine the frequency of genotypes?

A. It is done all the time in population genetics of all sorts of organisms. All Hardy-Weinberg is the product rule applied to a single locus and in that sense it is simple probability theory which is applied in hundreds of different scientific fields on a completely routine basis.

Q. Has any of them ever attempted to have it validated?

A. You don't validate theoretic mathematical truth and this is by definition, this is the rule that is used under certain axioms or assumptions, this is what it is and every elementary course in probability goes through dozens of examples of its application appropriately in real world situations. I suppose one could say the lotteries around the world are daily validations of these principles of probability.

Q. Would you agree, doctor, that clinical laboratories must meet higher standards to be allowed to diagnose strip throat than forensic labs must meet to put the defendant on the death row?

THE COURT: Don't bother to answer, please.

Q. Would you agree, doctor, that standards in the forensic community, DNA analysis is not as high as they are in the medical field?

A. No, I would not agree to that statement. There is variation among laboratories in the medical field and there is variation among laboratories in the forensic analysis, I would not say in any absolute way the standards of one are higher or lower than of the other.

Q. Would you admit, doctor, that there is a general disagreement as to -- in the scientific community as to the reliability of these standards and results of these tests and the conclusions to be based upon the results? Will you admit that there is general disagreement in the scientific community over the reasonable reliability?

A. The way you have phrased the question I will not admit that.

Q. Would you admit, doctor, that the product rule cannot be applied to identifying characteristics unless a valid foundation is first laid for the probability assigned to each of the characteristics and unless mutual independence of each of the characteristics is established?

A. That sounds very good and I would generally agree to that except that I think what you are going to mean by some of the words in that statement will be different from what I would mean by them. So I will --

Q. Do you want me to read it again for you?

A. No, I will refer to all of the caveats and statements that I have made in my testimony for the last day and a half giving the way I would interpret that statement.

Q. Do you know of any papers -- which papers do you know of which supports the novel approach by the FBI and R.C.M.P., maybe besides the Budowle and fixed bin paper, do you know of any others?

A. I don't know specifically what you mean by quote «the novel approach of the FBI and the R.C.M.P.» end quote, I know of many published papers that I would consider in support of various aspects of what they are doing as a package. For application in forensics there are relatively few papers I am aware of because it is primarily not a scientific issue, it is an applied issue in a specific setting. The forensic literature may have data, I do not read that aspect of the forensic.

Q. When I say, novel approach I mean specifically the fixed bin approach, the use of the Hardy-Weinberg formula and the product rule?

A. Well, there are thousands of papers supporting the use of Hardy-Weinberg and the product rule in human genetics.

Q. In this, what I'm talking for identification purposes here in forensic evidence?

A. As a total package all together I don't think because most scientists wouldn't bother to write such a paper.

Q. Would you agree, doctor, that without the knowledge of frequencies of certain alleles as represented by DNA fragment sizes in a population it is impossible to calculate the likelihood that a match could arise simply by chance?

A. You can't calculate a probability without an estimate of the frequencies that go into the calculation.

Q. Are you aware of the report of New York State Forensic DNA Analysis Panel?

A. No, I am not.

Q. Doctor, I have an affidavit here which is purported to be yourself in support of the People v. Leonard McSherry case, do you recall that?

A. Yes.

Q. Do you want to have a look at that and see if that's an adequate reproduction?

A. Yes, I believe that's an adequate production.

MR. FURLOTTE: I move to enter this as an exhibit, my lord.

THE COURT: Have you shown this to Crown counsel?

MR. WALSH: I haven't seen it, my lord.

WITNESS: Might I comment?

THE COURT: Yes, if you want to enlarge on your last answer.

WITNESS: No, but with respect to that affidavit.

MR. WALSH: Well, my lord, before Dr. Kidd does if I had a moment I might ask Dr. Kidd a question to save him --

THE COURT: All right.

MR. WALSH: Does this affidavit deal with RFLP typing?

WITNESS: No, it does not.

MR. WALSH: I object on the grounds of relevance, my lord.

MR. FURLOTTE: The topics in it are relevant, whether it's to do with forensic testing, whether it's RFLP or PCR.

THE COURT: You don't object vigorously to it going into the evidence, well, I mean if it's irrelevant it's of no value.

MR. WALSH: And that's the very reason I object to the fact, I don't see why we should be wasting time cross examining or delving into areas of no value.

THE COURT: Well, I don't want to -- let's mark it here for the purpose of the voir dire as an exhibit in the voir dire, VD-115, if it doesn't have any relevance, Mr. Furlotte, don't bother examining on it. Do you want to ask questions on it --

MR. WALSH: I just -- if I could while he's questioning him on it --

THE COURT: -- as to the circumstances.

MR. WALSH: I would like to get a copy of that, if I could, just so I could follow along when he's questioning him, I haven't seen that document. It will just take a second.

THE COURT: Mr. Sears, could you make a copy, there, please, how many pages are there?

We'll just hold up for a minute here until we get them, perhaps you'd better make a couple of copies and the witness could use one. Well, give them both to Mr. Walsh, I thought he might want the witness to have one. You have a copy, Mr. Furlotte?

MR. FURLOTTE: Yes.

MR. WALSH: My lord, just as a point, I was hoping that we'd be able to forego with the Court's permission our morning break as a result of late yesterday, as a result of the representations were made, Dr. Kidd has booked a flight that leaves Fredericton at 12:40 at noon-time, so if we could forego our morning break, so we assure that he can make that particular flight I would appreciate it.

THE COURT: Well, you're not going to be more than an hour and a half, surely, Mr. Furlotte?

MR. FURLOTTE: I don't expect to be much longer.

THE COURT: Well, shall we go without the break, Mr. Furlotte, is that agreeable with you?

MR. FURLOTTE: That's fine with me.

THE COURT: Let's aim it, 12:40, you say?

MR. WALSH: The flight actually leaves Fredericton at 12:40.

THE COURT: At 12:40, which means you've got to leave here sort of 11:30, which is an hour and ten minutes, perhaps, we can sort of set that as an objective.

MR. FURLOTTE: I should be done within that time.

THE COURT: Do you have to pick up things at hotels or are you all set?

WITNESS: I am all set.

THE COURT: Fiddleheads packed? You're taking them back, surely, aren't you? Have you tried them yet?

WITNESS: Yes, under Court order I was served them last night.

THE COURT: I suppose your attitude was the same as what Walter Winchill said about English beer, as far as I'm concerned they can put it right back in the horse.

WITNESS: No, I actually enjoyed them.

Q. Dr. Kidd, on page two of that affidavit around the middle of the top paragraph, it's marked «Third, it is possible that different DNA sequences have different stabilities and that allele 1.2 degrades more rapidly than allele 4.» Would that have any implications on band shifting creating false matches?

A. Absolutely irrelevant.

Q. Irrelevant, is it because it's a different technique or is it because --

A. It's a different technique, they are different loci, the nature of the DNA sequence in the region is quite different.

Q. But it is the allele that is subject to degradation, is it?

A. Yes, but the nature -- that was a hypothetical example with respect to this particular locus and this particular circumstance as determined

by this particular technique and it has no relevance to RFLP analysis by Southern blotting technique of these VNTR loci.

Q. Now, I understand, in this particular case it was the defendant that was trying to introduce the technique to exclude himself?

A. That's correct.

Q. And you testified for the prosecution basically stating that this technique has not been proven yet and hasn't been proven to be reliable, is that a fair assumption?

A. That I did not feel the particular results in this case were reliable.

Q. And also that the technique itself was not proven to be reliable?

A. No, I do not believe I said that. I said this particular result, this is also a year and a half ago, no, over two years ago, almost two years ago and I have since modified my opinion somewhat with respect to this particular technique based on the information I now have. I still feel that these particular results in this particular case were unreliable because of a phenomenon known as allele dropout which was well documented by the FBI just subsequent to my doing this affidavit. Again, that was relevant to this technique and this locus and this particular result, not any result with this technique and is, in my opinion, absolutely irrelevant to the methodology in the loci and the analysis and data interpretation related to this case.

Q. But the techniques used here, PCR prior to this case, had been used by prosecution to gain convictions, had it not?

A. I do not know.

Q. You don't know. Okay, in the middle of paragraph two on page one, you state: «Thus, it is my opinion that forensic applications of PCR technology must proceed with great caution. Undoubtedly, the methods and natures of possible artifacts will become well understood in the next few years and problems currently present will undoubtedly be resolved.» And you state: «I am not aware of any literature at present that addresses these problems in a forensic context.» Did you feel that that was relevant that there was no literature at the present to address the problems in the forensic context? Would that also apply for RFLP?

A. No, that was simply a statement of fact that I was not able in this affidavit to point to any literature that was specifically relevant in this case. The point is irrelevant to this case.

Q. Doctor, I'll show you Exhibit VD-103 that is titled, Fix Bin Analysis for Statistical Evaluation of Continuous Distributions of Allele Data from VNTR Loci For Use in Forensic Comparisons, authored by Bruce Budowle as one head of the FBI and John Waye and Mr. Fourney who were and still are, Mr. Fourney is still

associated with the R.C.M.P. On page twenty nine of that draft report --

MR. WALSH: Which draft is this, we've got a number of them?

MR. FURLOTTE: This is the November '90.

THE COURT: That was the very original, I believe, the very first.

MR. WALSH: There's three in evidence, my lord.

THE COURT: They go in inverse order, I think.

MR. FURLOTTE: There's 49, 49A and this is 49B.

MR. WALSH: That's November '90, January 3rd, '91 and then the actual published publication.

Q. I draw your attention to page 29, doctor.

A. Yes.

Q. At the top of this page, it says,

«Ultimately, it would be desirable to define alleles discretely, to be correctly genotyping (not just phenotyping) VNTR profiles, and to reduce measurement imprecision. Then, it would be legitimate to apply the Hardy-Weinberg equilibrium.»

In the final draft, doctor, that paragraph was removed, did you have anything to do with that?

A. No, I did not.

Q. Do you know of any reason why maybe it was removed?

A. No, I do not.

MR. FURLOTTE: My lord, maybe if we could have ten minute recess, so I could discuss things with co-counsel and my client.

THE COURT: All right, if we s rt of bear in mind--

MR. FURLOTTE: I would not expect regardless of what our discussion is, that it wi l take any more than fifteen minutes thereafter.

THE COURT: All right, let's h ve our recess then.

COURT RECESS FOR 15 MINUTES

COURT RESUMES

ALL COUNSEL PRESENT

ACCUSED PRESENT

THE COURT: Now, Mr. Furlotte.

MR. FURLOTTE: I have no further questions, my lord.

THE COURT: No further questions.

Now, re-examination, Mr. Walsh.

MR. WALSH: Yes, my lord, briefly.

DR. KENNETH K. KIDD, still under oath, continued to testify:

RE-EXAMINATION BY MR. WALSH:

Q. This morning, Dr. Kidd, Mr. Furlotte referred you to questions regard Amerindians, I take it that's reference to American Indians?

A. That's correct.

Q. And there was mention this morning in relation to those questions on the American Indians to the National Academy of Science, I take it, that's a paper?

A. No, there is a publication in the proceedings of the National Academy of Science an eminent scientific journal that my wife and I wrote in collaboration with Cavalli Sforza and some of the people in his lab. Dr. Anne Bowcock is the first author. That paper deals with the analysis of data on one hundred different DNA

polymorphisms in five populations from around the world. It does not include data on any population from the new world, Amerindians. Separately, my wife and I and three other collaborators have done analyses on three Amerindian populations, two from the Amazon Basin, and the Mines from the Yucatan Peninsula, and that paper is -- it was the data from that paper that were presented under seal in Yee, and the manuscript is now accepted for publication and will appear shortly in the Journal, Human Biology. And it dealt with approximately thirty loci in just those three Amerindian population.

Q. Have you -- yesterday Mr. Furlotte put some questions to you with respect to American Indians, native North American Indians in the United States, have you seen data with respect to native American Indians?

A. Yes, I have seen some data that the R.C.M.P. is starting to collect and I have seen data from other researchers. There are relatively few studies and none that I'm aware of published on DNA polymorphims of North American Indians.

Q. You say you are aware of Canadians and Canadian work?

A. Yes.

Q. Would they take the form of hystcrgrams and pi charts?

A. Yes.

Q. I refer you to what's been marked on this hearing as VD-106 through to and inclusive 113, would you just look at that for me, please, and tell me whether you can identify?

A. Yes, these are the data I was shown.

Q. Doctor, with respect to the Amerindians and the native Indian populations that you have been seeing and the data you have been shown, is that -- what, if any, opinion do you have in respect to the effect of that particular data with respect to what you've seen with respect to Amerindians and native Indian populations in Canada, what effect does that have on your opinions with respect to North American Caucasian population, Canadian Caucasian populations and the data base in this particular case? Does that in any way, what effect does that have on your opinions that you've previously given?

A. The main effect it has on my opinion is that I note the very strong contrast in the nature of the population structures. The Amerindian populations are very subdivided, many different languages and not until fairly recently that much admixture, so that there is a fair degree of differentiation, allele frequency variation among the different subgroups, the different tribes. Whereas in Europe the degree of variation acrossed all of Europe is much smaller and the North American Caucasian population are a very much admixed selection from Europe where we're starting with a fairly comparative more

homogeneous population to start with.

Q. The particular exhibits that you reviewed, does that -- do these exhibits in your opinion, doctor, in any way, affect the validity of the opinions that you've given with respect to the North American Caucasian population, the Canadian Caucasian populations in relation to substructure, Hardy-Weinberg equilibrium and linkage equilibrium?

A. No, they do not alter these opinions.

MR. WALSH: *I have no further questions, my lord.*

THE COURT: Well, that would seem to complete your evidence.

EXAMINATION BY THE COURT:

Q. Dr. Kidd, I want to put two questions to you myself, neither are related totally to this case. But shortly after the second war I found myself a student at London University and a very eminent British journalist told a small group of students which included myself that an announcement was imminent of a new step in the treatment of cancer, which would have world shattering effect, and it never did materialize, this was told to us in some confidentiality. Although I saw this same friend on various occasions in later years, both in London and in Canada, it never did occur to me to ask what he had been referring to. Do you know what he would have been referring to? It seems to me it had something to do with

tumorous growths on trees and I always assumed it had some genetic connection?

A. No, I have no idea.

Q. There was no announcement, I gather?

A. No, there are always imminent break throughs in treatment of cancer, many of which never materialize.

Q. Well, that's the first question and my curiosity goes unresolved.

A. I'm afraid so.

Q. The second matter was this, what year was it that the Wright brothers flew their first airplane at Kitty Hawk, 1909, 1908, somewhere or 1903, perhaps but in the next dozen or so years leading into the use of aircraft and the first world war, the aircraft industry or the aircraft certainly underwent tremendous technological development. And so I likened the development, as a layman, the development of DNA technology to the development of the aircraft. And I suppose it's moving just about as quickly. What do you see happening, the state of the DNA craft in ten years from now? Can you make a forecast?

A. I would imagine that ten years from now virtually all of the testing will be based much more on the PCR reaction, polymerase chain reaction and that completely different loci will be used, that the technology will in fact be able to reach the level of refinement of essentially definite unambiguous identification

of each individual. So that there will be little question of statistics at that time in the majority of cases we are definitely not at that point now.

Q. What about time required in comparison and of specimens and formulation for conclusions?

A. I would expect to be much faster because at the moment now with the PCR technology that's available, a paper that we have just had published on a new method of DNA sequencing allows us to go from a blood sample or a small amount of DNA and know the sequence of a defined region for a few hundred base pairs within twenty four to thirty six hours. And if those -- the sections that are studied are select such as HLADQ alpha locus where there is a large amount of sequence variation, a few studies could be done simultaneously on a very small amount of DNA and it would be a very short period of time from having the sample to having a very powerful specific, largely, unambiguous DNA profile on that sample.

THE COURT: Any questions Mr. Furlotte or Mr. Walsh?

MR. FURLOTTE: No, my lord.

MR. WALSH: No, my lord.

THE COURT: Thank you very much then.

Mr. Walsh, you will ensure presumably that Dr. Kidd be provided with a copy of the transcript of his evidence, so that he'll have a record of it when his ideas are challenged in future cases that he may appear in.

MR. WALSH: Yes, my lord.

THE COURT: And perhaps also a copy of the transcript of any subsequence evidence that's given on DNA in this voir dire.

MR. WALSH: Yes, my lord.

THE COURT: Thank you very much.

Yes, you may be excused if you like, bon voyage.

You have no further witness, Mr. Walsh?

MR. WALSH: No, my lord.

THE COURT: That's the conclusion of the Crown's case on the voir dire?

MR. WALSH: That's correct, my lord.

THE COURT: And then we had scheduled for your first witness or your witness, your principal witness, I gather, Dr. Shields comes on Monday morning, May 26th, is it?

MR. FURLOTTE: 27th.

THE COURT: Monday, yes, that's Monday, at 9:30?

MR. FURLOTTE: Yes.

THE COURT: I think our earlier tentative scheduling is that his examination would perhaps take one day or two and then we'd have a break for a day or so and then we would argue the DNA aspect or I'd hear the representations of counsel on the DNA aspect of the voir dire on say, Thursday and Friday of that week.

MR. FURLOTTE: The only thing, my lord, because of the length of the voir dire and all the transcripts involved, it might be feasible to take more than a one or two day break, to give

us time to, I suppose, support our arguments with excerpts from the transcripts.

THE COURT: I don't want to give you too much chance to do that.

MR. FURLOTTE: I don't have much time left, so I don't want to waste any time that's for sure. I think in order to present fair argument even by the crown prosecutor that we probably will have to resort to excerpts from the transcripts because I know my notes wasn't able to cover long enough and especially on cross examination because I don't have any notes of what I asked -- what I found important on cross examination.

THE COURT: Well, I don't have a great problem myself with having a little longer recess. Although I must say that I would like to hear argument and I think there'd be a great advantage, even as far as counsel are concerned to doing it while it's fresh in mind and certainly counsel aren't going to want to go through the stack, I don't know what the stack is, seven inches of transcript, we've got, mind you some of that covers the body substance aspect of the voir dire and so on, which has been argued. But counsel, I wouldn't think, would want to go through all this evidence in on the DNA aspect before -- to read the whole thing through make take days and days to do.

What about the following week, does counsel for the crown have any problems with that?

MR. WALSH: No, I have no problem whatsoever. I can understand Mr. Furlotte's wish to have a little bit more time.

THE COURT: One of the problems or a minor difficulty actually is I told the Provincial court people that we'd be through with this courtroom here and I think they've gone and -- I don't know what they've done about the scheduling, but we have priority, of course, or at least we will take priority. But we don't inconvenience them any more than we have to. Could we settle tentatively now on -- what about June 6th and 7th, say, that's Thursday and Friday. June 6th and 7th, would that be good?

MR. FURLOTTE: That would be fine.

THE COURT: How does that work out? You people -- you have other duties, I'm sure, in which you may have contracted for or committed yourself to, does that interfere with you people?

MR. WALSH: Mr. Allman and I have discussed it, we can accommodate that particular request, my lord. We had some days scheduled for interviewing witnesses, however, we can make accommodations and I think that would be an appropriate time the 6th and the 7th.

THE COURT: Well, June 6th is the anniversay of D Day, so we won't forget that.

Are you -- without committing yourself, Mr. Furlotte, do you see, what, a day or two days, perhaps two days, I think we talked about two days?

MR. FURLOTTE: I have two days set aside for Dr. Shields, I know in the Bourguignon case, I asked him how long it took him, he recalls it just being one day himself, half a day on direct and half a day on cross examination. But I thought maybe -- but I set two days aside for him because I think there's more issues involved here than in the Bourguignon case.

THE COURT: Well, we'll think in terms of two days, if it takes longer, okay, but that would be -- we'll say the 27th and 28th then for that and then argument on the 6th and 7th.

As far as argument goes, oral argument should suffice. If counsel wish to prepare a very short brief sort of highlighting their principal arguments, just sort of the structure of their argument more than anything, then, perhaps any cases you do want to cite put it in there. I don't have it any mind any long brief. Counsel even may feel they don't want to do that, but it's up to them.

Do you see any advantage, Mr. Walsh?

MR. WALSH: I think perhaps an advantage would be gained by, as you've indicated, an outline of the argument in terms of just in general categories.

THE COURT: Very much as you did in the voir dire on the body substance, I think you had an outline, perhaps not given as detailed as that.

MR. WALSH: Yes, the bodily st stances paper I had dr fted there was qu te e tensive.

THE COURT: Well, I don't envisage anything quite as extensive as that.

MR. WALSH: No, I was thinking in terms of just a gene l outline in terms of the topic and where we were going through, so you could at least follow where our arguments were going while 're making them, I think would be reason le in this case.

THE COURT: Well, I'll leave it up to you gentle n, whatever you want to do in that regard.

That is all then for today and we'll adjourn until Monday, the 27th at 9:30.

COURT ADJOURNS FRIDAY, MAY 17TH, 1991.

DATED THIS 24th day of May, A.D. 1991.

DATED THIS 24TH DAY OF MAY, A.D. 1991

I, Nilah M. Amos, hereby certify this to be a correct transcription of my shorthand notes of these proceedings to the best of my skill and ability.

Nilah M. Amos

Court Reporter