

1 STATE OF MINNESOTA DISTRICT COURT
2 COUNTY OF WASHINGTON TENTH JUDICIAL DISTRICT
3 _____

4 State of Minnesota,

5 Plaintiff,

6 vs.

7 Tony Allen Roman Nose,

8 Defendant.

TRANSCRIPT OF PROCEEDINGS

File No. K3-00-4298

(Frye Hearing - Vol. 5)

9 _____

10 The above-entitled matter came on for hearing
11 before the Honorable Stephen L. Muehlberg, judge of the
12 above-named court, on the 1st day of November, 2002,
13 commencing at the hour of 11:10 a.m., in the Government
14 Center in the City of Stillwater, County of Washington,
15 State of Minnesota.

16

17 APPEARANCES:

18

19 John W. Fristik, Assistant County Attorney,
20 appearing as counsel for and on behalf of the State.

21 Christine Funk, Jeffrey Olson, and Megan Hunt,
22 Attorneys at Law, appearing as counsel for and on behalf
23 of the Defendant.

24 Tony Allen Roman Nose, the Defendant, appearing
25 personally.

I N D E X

WITNESSES

	Direct	Cross	Redir	Recross
DAN E. KRANE	579	639	686	694
LAURENCE D. MUELLER	698	733	751	754

EXHIBITS

#	Description	Identified	Received
24	curriculum vitae - Dr. Krane	579	579
25	overheads - Dr. Krane	610	612
26	compilation of 310 three-way mixtures	630	630
27	curriculum vitae - Dr. Mueller	698	699

1 WHEREUPON,

2 the following proceedings were had:

3 MR. OLSON: Your Honor, I have some questions
4 for the Court.

5 THE COURT: Sure.

6 MR. OLSON: As we discussed off the record,
7 both Ms. Hunt and I are sort of popping in and out as
8 other demands take us away.

9 THE COURT: That's not a problem.

10 MR. OLSON: One of my demands is playing taxi
11 driver. I was not present yesterday when the Court made
12 the ruling on the sequestration of witnesses. I guess I
13 just want some clarity. Half the time I'm the first one
14 they see, so I don't want to be doing anything, since I
15 wasn't present. If the Court would just --

16 THE COURT: My ruling was that someone who's --
17 let me put it this way: Someone who's going to testify
18 in the afternoon or later in the day, later in the
19 morning, cannot sit through the testimony of the earlier
20 witness.

21 MR. OLSON: Okay is that the extent of the
22 Court's ruling?

23 THE COURT: That's it.

24 MR. OLSON: There's no problem if I'm having a
25 casual conversation with a witness about what has

1 already transpired?

2 THE COURT: No problem.

3 MR. OLSON: It's just sitting through the
4 testimony.

5 THE COURT: Yes.

6 MR. OLSON: Thank you, Your Honor.

7 THE COURT: You're welcome.

8 I think it might be a good idea to state for
9 the record, two days ago when I became aware that two
10 witnesses were going to be here today despite my earlier
11 statement that I was going to do other work before we
12 started today, I did make arrangements for a bailiff, so
13 we have made arrangements for a bailiff to be here if we
14 run past 4:30 this afternoon.

15 I also made arrangements at that time to have a
16 clerk or judicial aid or judicial assistant be here
17 until we conclude today. I want to give notice that I
18 was able to do that and people are able to arrange their
19 schedules.

20 As to other issues, I think it's my
21 understanding, Ms. Funk, you correct me if I'm wrong,
22 but I believe I signed all the orders that you have
23 requested in connection with preparation of your case,
24 is that correct?

25 MS. FUNK: Yes, Your Honor. Well, as to

DAN E. KRANE

1 funding.

2 THE COURT: Right. And I cut some but that was
3 with your consent and then I've made some adjustments on
4 those as you have requested additional changes.

5 MS. FUNK: That is correct, Your Honor.

6 THE COURT: Including increasing some, is that
7 correct?

8 MS. FUNK: Yes.

9 THE COURT: Okay. Then unless there's
10 something else -- well, what I thought was we'd work
11 about an hour this morning, until 12:00 or 12:15. We'll
12 break, and we can talk about how long that should be for
13 lunch. We'll start again about 1:00, 1:15 or any other
14 time that we agree to, go until about the middle of the
15 afternoon, take a break until 4:00, 4:30, see where we
16 are at that time, but I would appreciate an update as we
17 go along so that I can advise people who are affected
18 concerning scheduling. Okay.

19 All right, Ms. Funk, you may proceed.

20 MS. FUNK: We'd call Dr. Dan Krane, Your Honor.

21

22 DAN E. KRANE,
23 being first duly sworn on oath, was examined and
24 testified as follows:

25

DAN E. KRANE

1 THE CLERK: Please state your full name,
2 spelling your last for the record.

3 THE WITNESS: My name is Dan E. Krane. Last
4 name is spelled K-r-a-n-e.

5 THE COURT: Ms. Funk, please.

6 BY MS. FUNK:

7 Q Dr. Krane would you tell us where you're currently
8 employed?

9 A I am an associate professor of biological sciences at
10 Wright State University in Dayton, Ohio.

11 MS. FUNK: If I may approach the witness, Your
12 Honor?

13 THE COURT: Yes.

14 THE CLERK: Exhibit Number 24 marked.

15 BY MS. FUNK:

16 Q Dr. Krane, showing you Exhibit Number 24, do you
17 recognize this?

18 A Yes, this is a copy of my curriculum vitae.

19 MS. FUNK: Okay. I'd offer that be entered,
20 Your Honor.

21 MR. FRISTIK: Can I see it?

22 MS. FUNK: Yah.

23 MR. FRISTIK: No objection, Your Honor.

24 THE COURT: 24 is received.

25 BY MS. FUNK:

DAN E. KRANE

580

1 Q I'll leave that up there for you Dr. Krane, in case

2 you'd like to look at it for reference.

3 Could you tell us about your a educational
4 background?

5 A Yes. I obtained a Bachelor of Science degree with a
6 double major in biology and chemistry from John Carroll
7 University in University Heights Ohio. From there I
8 went on to pursue a Ph.D. in the biochemistry program of
9 the cell and molecular biology department at Penn State
10 University. After completing that work I went on to do
11 some postdoctoral studies, first at Washington
12 University in St. Louis in the genetics department of
13 the medical school there, and then after that at Harvard
14 University in Cambridge, Massachusetts in the department
15 of organismic and evolutionary biology.

16 Q And after you completed that -- that was postdoctoral
17 work?

18 A That's correct.

19 Q Where did you go from there?

20 A Upon completing that type of work and study I accepted
21 my first faculty appointment, which was as an assistant
22 professor at Wright State in Dayton, Ohio. That was in
23 the fall of 1993.

24 Q And because your title is -- your title is different
25 now, or the same now?

DAN E. KRANE

581

1 A It is different. I was promoted, my recollection is

2 three years ago, from assistant to associate professor.

3 Q And does that mean you have tenure? Is that what that
4 means?

5 A Among other things. That's included with that
6 promotion, yes.

7 Q Okay and could you describe your work at the university?

8 A Certainly. The university actually has some rather
9 specific suggestions as to what it is that I should do
10 during the course of my daily routines. Overall the
11 expectation is that approximately 50 percent of my time
12 should be spent doing research, basic research in areas
13 in which I have training; molecular evolution,
14 population genetics, molecular biology. Another 40
15 percent of my time is expected to be spent associated
16 with things relating to teaching, instruction, and so I
17 teach a variety of classes. And then the remaining 10
18 percent is supposed to be set aside for service
19 activities, and service is defined fairly broadly. It
20 includes things such as serving on committees, for
21 finding new faculty members, for evaluating the
22 performance of other faculty members, for deciding
23 whether or not students should be granted degrees or
24 not. It also includes things such as giving seminars
25 and lectures and educating the public, as well as other

DAN E. KRANE

582

1 scientific professionals, at meetings.

2 Q What sort of classes do you teach?

3 A Well, there's actually a fairly good variety of classes
4 that I teach. At the present time I'm teaching the
5 introductory freshman biology course that we offer to
6 our majors at Wright State, the biology majors at Wright
7 State. There are approximately 370 students in that
8 class at the present time and it covers a fairly broad
9 range of topics ranging from structures of cells to
10 principles of genetics. That's again a freshman-level
11 course.

12 In the winter I will be teaching, and I have
13 ever since I've been at Wright State, every winter, been
14 teaching a sophomore level molecular genetics course.
15 It's essentially a course on the regulation of gene
16 expressions. In other words, how genes get turned on
17 and turned off during the life of an organism.

18 And then we're on a quarter system so we have a
19 spring quarter as well. In spring quarter I've taught a
20 fairly good range of courses. Most recently I've taught
21 a senior and graduate level human genetics course in the
22 spring. I've also taught a bioinformatics course in the
23 spring. I have taught molecular evolution and a
24 population genetics course in previous spring quarters.
25 This upcoming spring I'll be teaching a bioinformatics

DAN E. KRANE

583

1 course and I believe also a senior level laboratory
2 experience for our graduating seniors where they have a

3 lot of hands on laboratory experience performing
4 experiments such as PCR, gel electrophoresis, actually
5 we'll have them generate some DNA profiles during the
6 course of that training experience that they have as a
7 capstone course before they graduate.

8 Q Is that part of the lab -- I don't remember if you
9 actually referenced earlier when you were talking about
10 your research, is that your lab?

11 A No, actually that instructional lab is separate and
12 apart from the research laboratory that I also direct,
13 and again, the majority of my time is supposed to be
14 spent, at least a small majority, 50 percent of my time
15 is supposed to be spent doing things relating to the
16 conducting of basic research and toward that end I have
17 a separate research laboratory in which I supervise the
18 work of graduate students as well as undergraduates and
19 technicians where they generate data and we go about the
20 process of answering fundamental questions about
21 biology.

22 Q And what type -- could you be more specific, perhaps, on
23 what those fundamental questions might be and more
24 specifically what type of work is being done in the
25 laboratory?

DAN E. KRANE

584

1 A Certainly. I would say that the term that summarizes
2 all the work that's being done in the lab is molecular
3 biology. I suspect that I think of molecular biology a

4 bit differently than many do in that I see molecular
5 biology as a set of tools that we can use to answer a
6 wide variety of questions. It's not necessarily a
7 discipline in its own right like astrophysics that might
8 be interested in how stars evolve, but rather it's a set
9 of tools that we use to answer a variety of questions.

10 The types of questions that I'm particularly
11 interested in answering and that my laboratory has been
12 involved in doing research with are those that tend to
13 pertain particularly to molecular evolution and
14 population genetics. And those are studies of how gene
15 frequencies change over the course of time within
16 populations of organisms.

17 Molecular evolution is a study of how gene
18 frequencies change over long periods of time, many
19 generations, millions, tens of millions of years, for
20 instance, whereas population genetics is a study of how
21 gene frequencies change over short periods of time, one
22 or two generations as opposed to many or thousands of
23 generations.

24 And so, again, there are a variety of molecular
25 evolution and population genetic questions that we've

DAN E. KRANE

585

1 been addressing. They include things such as the effect
2 that pollution has on genetic diversity of naturally
3 occurring populations of organisms. We've found that

4 organisms that live in polluted environments tend to
5 have lower levels of genetic diversity than those that
6 live in pristine environments. So that turns out to be
7 a very useful and effective measure of the extent to
8 which a site has been impacted by pollution.

9 Again, the way we found that is by asking some
10 very basic questions and going out in the field and
11 generating data that would help us arrive at an answer
12 to those questions. So that's an example of a
13 population genetics type of question that my lab's been
14 involved with, and again there are many others I'd be
15 happy to tell you about if you'd like but it could take
16 some time. Just what would you like?

17 Q When you say you're generating data, where does that
18 data come from?

19 A Well actually the data can come from a variety of
20 sources. A large portion of the data that we analyze is
21 data that we literally create within the laboratory. We
22 use the tools of molecular biology to extract
23 information from living organisms to determine DNA
24 sequences of their genes, to determine the relative
25 frequency of one version of a gene as opposed to another

DAN E. KRANE

586

1 version of a gene. But also we're not shy about using
2 data that's been generated by others as well and, for
3 instance, the Human Genome Project has resulted in an
4 explosion of information and data that's available about

5 our own genetic makeup as human beings, and while we
6 could have generated those DNA sequences ourselves,
7 certainly it's much more cost effective for us to simply
8 use that data that's been generated by others. And so
9 we analyze the data of others as well as generating some
10 of our own.

11 Q I guess one thing that I don't think is really clear on
12 this record, Dr. Krane. Do you do DNA testing in your
13 laboratory?

14 A Well, I think a short answer is yes. We extract DNA
15 from tissues of organisms, we quantitate that DNA, and
16 we do in fact do PCR amplification of the DNA toward the
17 end of generating a DNA profile. And in fact the
18 environmental impact study that alluded to earlier is
19 exactly that. We were generating DNA profiles of these
20 organisms that we had been collecting and comparing
21 those DNA profiles to get a feel for how genetically
22 distinct those organisms are. If their DNA's are very
23 similar to each other we interpret that as evidence that
24 they have low levels of genetic diversity and if those
25 DNA profiles are very different from each other we

DAN E. KRANE

587

1 interpret that as meaning that they have high levels of
2 genetic diversity in those populations.

3 Q Okay, and have you published any papers, Doctor?

4 A Yes, quite a few. It's generally known, I suppose, that

5 in academic settings one should publish or perish. So
6 it's certainly an expectation that I demonstrate that my
7 laboratory is productive and doing useful -- answering
8 useful and interesting questions by publishing the
9 results of our studies.

10 Q Are those papers, I see you have quite a list here, are
11 they published in peer-reviewed journals?

12 A Certainly for the most part. There maybe one or two
13 that I've had published in journals that are not peer
14 reviewed, but the overwhelmingly is peer-reviewed
15 publications.

16 Q Have you published any textbooks or manuals?

17 A Well, I have published a laboratory manual that we use
18 for our freshman biology courses. It is also used by
19 the -- or at least portions of that manual are used by
20 other institutions as well. We're in the third addition
21 of that book now, or that manual now.

22 But actually just recently my first widely
23 applicable book, aside from just a laboratory manual,
24 has been published. It's called Fundamental Concepts of
25 Bioinformatics and it's been available for sale through

DAN E. KRANE

588

1 Benjamin Cummings since September or October of this
2 year. So very recently it's been available for sale at
3 book stores and such. But so yes, I published both a
4 laboratory manual as well as a textbook.

5 Q Okay. And this textbook, Fundamental Concepts of

6 Bioinformatics -- let's start a little earlier.

7 Can you define for us, please, what
8 bioinformatics is?

9 A Yes. That's a common question I get, actually.
10 Bioinformatics is the application of computer science
11 tools to analyze biological data and particularly to
12 analyze molecular biological data, such as the type of
13 data one obtains when doing DNA sequencing analyses or
14 STR analyses in forensic cases.

15 Computers lend themselves very well to doing
16 large-scale and detailed analyses that human beings
17 would not be able to do in a reasonable time frame and
18 those types of analyses often give us some very
19 important fundamental insights as to how it is that
20 biological systems are working.

21 So again, bioinformatics is using computers
22 effectively to analyze molecular biological data.

23 Q Okay. Is this something that you invented or it's not a
24 term that we hear very frequently. Is it a new sort of
25 science?

DAN E. KRANE

589

1 A Well it's an increasingly important area of work. I
2 suppose I first heard the term bioinformatics myself
3 five or seven years ago, somewhere about there, and that
4 book does happen to be the first book that caters to an
5 undergraduate level of bioinformatics training, but

6 there are a number of other books that are available at
7 graduate or postgraduate types of level that have been
8 on the market for a few years now. So I wouldn't say I
9 invented the field but we certainly utilize those tools
10 extensively in the course of our work.

11 Q Okay. Dr. Krane, you actually have testified in this
12 case previously, is that correct?

13 A That is correct.

14 Q And do you recall, prior to testifying, coming to
15 Minnesota to review some documents at the BCA
16 laboratory?

17 A I do.

18 Q Do you also recall, Dr. Krane, comparing an affidavit by
19 Ms. Ann Gross which contained some summary results of
20 the validation tests you looked at?

21 A Comparing it to the documents that are maintained at the
22 laboratory?

23 Q Yes.

24 A Yes, I do.

25 Q And are you aware that since the time of your testimony

DAN E. KRANE

590

1 Ms. Gross has filed another affidavit which contains
2 some information modified from the Dishmon information,
3 are you aware of that?

4 A Actually just today. I saw portions of that modified
5 affidavit, yes.

6 Q And I'm going to -- weren't you also -- were you

7 questioned about some of that information at a different
8 hearing, do you recall?

9 A Yes, I was. At least several months ago, so I don't
10 recall specifically when, but that was in Minneapolis.

11 Q Okay. And I'm just going to offer you Exhibit 7 and I
12 don't know that you necessarily need to look at it at
13 this moment, but I'd ask you to -- do you recall --
14 looking at and subsequently testifying in this case
15 about a BCA study referred to as Study 30-A that
16 discussed, in the Dishmon affidavit, referred to
17 approximately 80 samples being reviewed?

18 A I do recall that, yes.

19 Q And could you summarize just briefly for us what you
20 recall doing after looking at both the affidavit, the
21 original affidavit, and the study?

22 MR. FRISTIK: Objection, Your Honor.
23 Relevance. It pertains to prong two, specifically
24 whether or not the BCA laboratory has acceptable --
25 apparently in this witness's view has done acceptable

DAN E. KRANE

591

1 work in their validation studies or in terms of their
2 standard operating procedures or protocols. All of that
3 going to prong two. I object to any testimony in that
4 regard.

5 THE COURT: Ms. Funk?

6 MS. FUNK: The direction of this testimony,

7 Your Honor, is going to be fairly brief, but more
8 importantly is specifically directed towards the
9 statement that are contained in this affidavit which
10 were modified. I guess I wanted the foundation to be
11 clear that Dr. Krane has looked at this information, has
12 commented on this information, and now presented to this
13 Court for consideration is an affidavit which contains
14 information modified from the original affidavit and I
15 only want to talk about three things, each of which --
16 and I think it does go to the broader prong of general
17 acceptance. The State offered the exhibit and now we're
18 talking about a specific portion of the exhibit.

19 MR. FRISTIK: Your Honor, if I could respond?

20 THE COURT: Yes, please.

21 MR. FRISTIK: I did offer that exhibit, Your
22 Honor. I understand that there are several sections of
23 that exhibit that talk about the BCA's validation
24 studies. I offered the exhibit, perhaps I didn't make
25 it clear at the time. I offered the exhibit because

DAN E. KRANE

592

1 there is a great deal of information in that exhibit,
2 specifically we're talking about Ms. Gross's affidavit,
3 that focuses directly on prong one. Maybe I should
4 have, at the time I offered it, explained the purpose
5 for which I was offering it or I suppose I could have
6 just offered the first, I think -- I think the items
7 that pertain specifically to prong one are contained

8 probably like in the first, I don't know, five to six
9 pages of the affidavit, and I would have just offered
10 those.

11 I didn't offer that to suggest in any way that
12 I was opening the door to having this become a prong two
13 hearing and that was never my intention. So if
14 necessary at this point I'll withdraw that portion of
15 the exhibit that deals with what I believe to be issues
16 concerning prong two.

17 THE COURT: Go ahead, Ms. Funk.

18 MS. FUNK: I'm not intending to pursue a prong
19 two purpose, Your Honor. I'm not going to be talking
20 about the test results in this case. I'm talking about
21 whether the evidence in this case which was offered by
22 the State as purported scientific evidence is actually
23 scientific evidence and to do that we need to look at
24 some foundational issues and some of those foundational
25 issues include whether the validation studies that were

DAN E. KRANE

593

1 done -- Dr. Budowle talked about we do validation
2 studies to stress the system, to see how far we can push
3 the system, and to see whether or not the system works
4 for our testing setting. So we need to look at those
5 validation studies and see if in fact they do what they
6 purport to do. And I don't think that's a prong two
7 issue.

8 THE COURT: Well, it's a close call. For the
9 purpose of limiting the argument here I'll just simply
10 say that I'm going to accept what you're presenting or
11 your argument here, Ms. Funk, and let you proceed,
12 noting Mr. Fristik's objection and subject to the
13 possibility of striking it from the record later if I
14 determine that it's really prong two information.

15 MS. FUNK: Well what I would request the Court
16 to consider in the alternative to striking it, Your
17 Honor, is I'd ask that I be allowed to pursue this on a
18 fairly limited basis, and --

19 THE COURT: That's what I'm saying.

20 MS. FUNK: -- the Court can give it whatever
21 weight it feels is appropriate after having heard all
22 the evidence. But I'd like it to remain in the record.

23 THE COURT: Okay.

24 MS. FUNK: Thank you.

25 BY MS. FUNK:

DAN E. KRANE

594

1 Q Dr. Krane, directing your attention back to that Study
2 30-A, and I appreciate -- well what can you tell us
3 about that study and these affidavits?

4 A The Study 30-A is one that was specifically designed to
5 assess the comparabililty of DNA testing results as they
6 were generated with one machine as opposed to a new
7 machine that the laboratory was using and is using to
8 this day. We're talking specifically about a switch

9 from a machine that's known as a 377 machine to a
10 machine that's known as a 310 machine. And what was
11 done in that study was simply the retesting of samples
12 that had previously been tested on the 377 machine but
13 now on the 310 machine to assure that they gave
14 equivalent results.

15 Q And do you recall a number being provided in the
16 original affidavit that you had at the time that you
17 were at the BCA?

18 A Yes. It stuck in my memory because it seems to be an
19 odd way to state how many samples were re -- were tested
20 for that reproducibility. The original affidavit
21 summarized the study as saying that there were
22 approximately 80 samples that were retested in that way.

23 Q And why does, as a scientist, Doctor, why does that
24 strike you as unusual or stick in your memory?

25 A Well, in a peer-reviewed journal, for instance, or some

DAN E. KRANE

595

1 other scientific study that was being presented to other
2 scientists, a number such as approximately 80 would not
3 have been described as an approximate number but as the
4 actual count. Certainly when one is talking about one
5 million or some very large numbers approximate estimates
6 might be more reasonable, but it wouldn't -- I would
7 have thought it would not have been difficult to have
8 provided a precise count of exactly how many samples

9 were retested in that way and from which that conclusion
10 was drawn as opposed to an approximation as to how many
11 were looked at in that way.

12 Q And based on that reaction can you tell us when you were
13 looking at the validation status what you discovered?

14 A Well, I actually went through the trouble of carefully
15 counting the number of samples that were rerun that had
16 previously been typed using the 377 machine but then
17 were retyped on the 310 machine and found that the
18 actual number was in reality 57, at least that's what
19 was documented in the laboratory's files that I was
20 allowed to review while I was there.

21 Q Okay. And you are aware, based on prior testimony and
22 the review today that in this new affidavit that number
23 has been modified to approximately 60?

24 A I see that in this exhibit before me, yes.

25 Q Moving on to Study 30-I do you recall reviewing that

DAN E. KRANE

596

1 study at the BCA?

2 A Yes, I do.

3 Q And do you recall what you discovered about that study
4 at the BCA at that time?

5 A The 30-I study was described in the affidavit, as well
6 as in the summary information associated with it at the
7 BCA's lab, as an evaluation of previously adjudicated
8 casework. Essentially the purpose of the study was to
9 see that this new typing system, the Profiler Plus and

10 Cofiler kits for instance, would generate equivalent or
11 similar results or lead to similar conclusions and
12 generate similar results to those that had been
13 generated using previously accepted methodologies such
14 as the DQalpha or Polymarker tests, a previous
15 generation, of sorts, of DNA testing or even earlier
16 generation of DNA testing, RFLP or VNTR type testing.

17 Q And what did you find in reviewing the data at the BCA?

18 A Well again, I was -- my attention was drawn to, at least
19 initially, the number of cases that were involved. My
20 recollection is that the original affidavit said that
21 there were approximately 12 samples or 12 cases for
22 which that validation study had been performed. When I
23 actually reviewed the documentation that they had there
24 I think it's -- well it -- actually only four would have
25 met the criteria of that, well, what the purpose of that

DAN E. KRANE

597

1 study was to have addressed.

2 Q Meaning specifically that only four had both a prior
3 type of DNA testing and this new STR type of testing?

4 A Exactly.

5 Q And the balance?

6 A The balance either had just the old type of testing or
7 just the new type of testing, but my recollection is the
8 balance were largely just the old type of testing
9 without any of the new type of testing included.

10 Q Doctor, when you were here in the spring in the Hennepin
11 County case were you provided more information about
12 that study?

13 A That study was mentioned in the early part of my
14 testimony and during the break, I believe the lunch
15 break, the BCA lab provided me with more information
16 related to that validation study. Effectively what
17 happened is a representative of the lab brought the
18 binder that I had reviewed, essentially a year prior, to
19 the Court and allowed me approximately 20 or 30 minutes
20 to go through that binder again and I found that in fact
21 there were a number of additional cases that qualified
22 under the original purpose of that study. So the number
23 was now actually greater than four and my recollection
24 is is that it was something like 18.

25 Q So just so I understand it, this study was then

DAN E. KRANE

598

1 supplemented after your initial review?

2 A Well there was no documentation of supplementing in the
3 binder that I was reviewing, but nonetheless there
4 definitely were more cases that met those criteria
5 within that binder than what I had originally observed a
6 year prior.

7 Q You point out that there's no documentation of
8 supplementation. Would that be expected in the
9 scientific community for a study to be supplemented that
10 there be some documentation?

11 A Yes, I would say that's a strong expectation that there
12 would be some note of amendments to the study or
13 modifications to the study. There was a cover page
14 associated with the study that outlined what was
15 intended by the study and how it is that the tests were
16 to be performed and the original documentation said that
17 approximately a dozen or 12 cases would be analyzed and
18 yet in the modified version of the report that page had
19 actually been removed and replaced with another that had
20 a different number associated with it, and again it
21 would have been my expectation that there would have
22 been some notation that this was an ongoing study or
23 that this work -- that the conclusions that had been
24 drawn by subsequent or additional tests were consistent
25 with the previous tests. Yes, that's certainly a very

DAN E. KRANE

599

1 standard practice in scientific settings to document
2 that type of amendment or ongoing work.
3 Q Okay, and finally I wanted to speak with you about the
4 BCA study 30-J which you reviewed. Do you recall 30-J?
5 A I recall from the original affidavit, as well as from
6 the binder that I observed at the BCA's laboratory, that
7 the 30-J validation study was one that was meant to
8 address the effects of environmental insults on the
9 integrity of DNA that's to be tested.
10 For instance, is exposure to sunlight something

11 that might be expected to cause a DNA profile to become
12 less reliable or more difficult to interpret, or
13 alternatively would contact with the material that's
14 used to make blue jeans have some similar types of
15 effect.

16 And so when I was at the laboratory I again saw
17 the three-ring binders that they maintain those
18 validation studies in and that particular three-ring
19 binder that contained the validation study 30-J happened
20 to be the same three-ring binder that contained the
21 validation study 30-I that we've just been talking
22 about, but all that was present was a leaf essentially
23 in the binder that said 30-J and that was effectively
24 the last page of the material that was present within
25 that binder, so there was nothing related to that

DAN E. KRANE

600

1 validation study that was actually present in the
2 laboratory when I inspected it.

3 Q Did you ask if there were any additional documents that
4 the BCA hadn't provided you with when you were there?

5 A I specifically drew that study, as well as the 30-A and
6 30-I studies, to the attention of the person from the
7 laboratory who was bringing me binders and pointing me
8 to which binder contained which validation study and was
9 told that what the laboratory had was present for me to
10 review there and if it wasn't there they did not have
11 it.

12 Q Okay. And I'd ask you, Doctor, to look at page 9 of the
13 exhibit -- I'm sorry, labeled page 9 of 32 which I think
14 technically would be page 11 because there's a CV.
15 attached as well. And do you see a section on
16 environmental studies?

17 A I do.

18 Q I'd ask you to take a minute and read that.

19 A I've read it.

20 Q Is it true that it represents that there was a BCA study
21 as well as there's some reliance on some other published
22 studies?

23 A Yes. It cites three specific studies performed by
24 others aside from the BCA, but the first study in
25 support of that is one that's ostensibly been performed

DAN E. KRANE

601

1 by the BCA itself.

2 Q It's entitled?

3 A (a) Environment Insult Study using the AmpFLSTR Blue kit
4 (loci D3S1358, VWA and FGA which are also part of the
5 Profiler Plus kit).

6 Q All right, and so this -- based on your conversations
7 with the lab personnel and your personal observations,
8 is it your understanding that this particular study
9 referenced in this affidavit does not exist at the time
10 that you were at the laboratory?

11 MR. FRISTIK: Objection. Foundation.

12 THE COURT: Overruled.

13 THE WITNESS: That is -- well, I asked
14 specifically to see documentation related to that study
15 and was told that if it was not there it did not exist
16 and I certainly did not see any there as part of that
17 study.

18 BY MS. FUNK:

19 Q Okay, and just as a follow-up detail, this Blue kit
20 that's referenced, do you know if that's the test kit
21 that's currently being used?

22 A No, I do not think that that is the test that's
23 currently being used by the BCA. Instead they're using
24 the other kit that's mentioned, the Profiler Plus kit.

25 Q And this Blue kit is part, has some of the loci that the

DAN E. KRANE

602

1 Profiler Plus kit has?

2 A That's right.

3 Q All right. Dr. Krane, are you familiar with the term
4 primer binding site mutation?

5 A Yes, I am.

6 Q Could you tell what that means, please?

7 A Certainly. The DNA profiling that's done by most
8 laboratories today is one that involves initially a PCR
9 amplification. PCR is short for polymerase chain
10 reaction. And what PCR does is it allows a molecular
11 biologist to start with a very small amount of DNA in a
12 sample and amplify up specific regions of interest to

13 the point at which they're simply more amenable to
14 detection and analysis.

15 At the heart of the PCR technique, and what
16 allows the specific amplification of one region as
17 opposed to all DNA, is the fact that DNA sequences
18 called primers are used. These are synthetically
19 synthesized, you can order them to be produced at
20 approximately 50 cents per nucleotide that you'd like to
21 have added on to that chain, and again they're chosen
22 because of their sequence specificity. Typically
23 they're in the ballpark of 20 to 30 nucleotides in
24 length to assure that they will bind to only one place
25 within the entire human genome or whatever genome one is

DAN E. KRANE

603

1 interested in amplifying.

2 These primers have their specificity because
3 again, we have a single-stranded bit of DNA that we
4 synthesized which is capable of then base pairing with,
5 specifically interacting with, complementary DNA
6 sequences. The sites to which those primers interact,
7 with which they interact and have that specific
8 interaction of base pairing are called primer binding
9 sites.

10 If a mutation occurs within a primer binding
11 site the primer will be less likely, and in many
12 instances unable, to bind to that site and as a result

13 the PCR process itself will fail. It will not be
14 possible to amplify up that particular region.

15 So very briefly, I suppose in summary, a primer
16 binding site mutation would be a change to an
17 individual's DNA that would prevent a particular locus
18 of their DNA from being amplified and detected by the
19 PCR process.

20 Q And the practical application of that is that you
21 wouldn't see an allele if you ran a test?

22 A Yes.

23 Q You'd miss one or more alleles because you didn't
24 amplify that allele because the primer didn't fit at
25 that locus?

DAN E. KRANE

604

1 A That's a fair summary. Again, the method of detection
2 of DNA in these forensic tests involves typically an
3 amplification step. It is possible to detect DNA
4 without that amplification step, but the Profiler Plus
5 and COfiler kits, for instance, rely fundamentally upon
6 amplification for detection. If the PCR process fails
7 for a particular locus, then at least one version of
8 that gene will not be detected for an individual.

9 Of course we all inherit two copies of our
10 genes; one copy from our mother and one copy from our
11 father. If the mutation to a primer binding site
12 occurred only in the maternal copy, the copy from our
13 mother, but not in the paternal version of the gene,

14 then instead of seeing two versions of the gene during
15 the PCR amplification and subsequent detection, we would
16 instead see just one. We would see only the paternal
17 contribution to our genetic makeup and not the maternal
18 one because the primers were unable to bind and
19 therefore unable to amplify that particular region.

20 Q When this primer binding site mutation occurs, and so
21 let's say with your example, then the end result would
22 show a single allele which could be interpreted as a
23 homozygote, is that right?

24 A Actually that would be the standard interpretation that
25 if only one allele was detected in the reference sample

DAN E. KRANE

605

1 of an individual it would be interpreted as meaning that
2 the individual was homozygous. In other words, that
3 they had two copies of the same version of a gene.

4 Q Is there a way that you can tell if someone has a primer
5 binding site mutation as opposed to being a homozygote
6 at a single locus?

7 A Certain -- well yes, there would be ways to do that. It
8 would be possible to do exhaustive sequencing of the
9 individual's genome, of their DNA, a sequence to
10 determine the nucleotide sequence of all the DNA
11 surrounding the region of interest and so forth.

12 You might also get some hint that that was the
13 case through things such as peak height imbalance. If a

14 peak appeared to be of lower height than
15 corresponding -- than other homozygous loci within that
16 individual, that might be a suggestion that there had
17 been a primer binding site mutation but would probably
18 not be interpreted as proof of a primer binding site
19 mutation.

20 So certainly there are ways to detect it and
21 get that impression but the sequencing of an
22 individual's DNA around these loci is both -- well, it's
23 prohibitive both in terms of time and cost and the peak
24 height imbalance issue is one that probably would not
25 have gotten much attention because it would be so much

DAN E. KRANE

606

1 more likely to expect that a single peak was due to the
2 fact the individual was a homozygote as opposed to a
3 heterozygote with one allele that was amplified and
4 another allele that failed to be amplified.

5 Q Would having the primer sequences of a given kit assist
6 a scientist in determining whether there was a primer
7 binding site mutation that was occurring with any rate
8 of frequency?

9 A Definitely, yes. Having -- knowing the sequences of the
10 primers that are used for the amplification process
11 specifically states what those primer binding sites are
12 and would then allow a review to be, or an experiment to
13 be conducted to determine if those sites were in fact
14 prone to mutation, more prone than other regions were.

15 Would also allow an assessment to be made as to how
16 often those mutations had occurred in typed samples and
17 thereby give a feel for how frequently erroneous
18 conclusions had been made about an individual being a
19 homozygote when in reality they were a heterozygote with
20 an allele that was typed and an allele that had failed
21 to amplify.

22 Q Dr. Krane, I assume that you are aware that the primer
23 sequences for the COfiler and Profiler Plus kits have
24 not been published? Are you aware of that?

25 A That is certainly my understanding. That there has been

DAN E. KRANE

607

1 an issue regarding the availability of those sequences.

2 Q And Dr. Krane, as a scientist, typically in the -- when
3 you are in the scientific community, what is the
4 practice about -- does the scientific community have a
5 practice regarding publication of data?

6 MR. FRISTIK: Objection, Your Honor. May I
7 inquire to lay foundation?

8 THE COURT: Sure.

9 BY MR. FRISTIK:

10 Q Dr. Krane, do you see yourself as a member of the
11 forensic scientific community?

12 A Could I ask you to define forensic science community or
13 would you like me to do that?

14 Q I'm asking you if you can answer the question. Do you

15 see yourself as a member of the forensic scientific
16 community?

17 A I'm hesitating in my answer because I know there's a
18 wide range of interpretation as to what qualifies as
19 forensic science community. I feel that I have
20 expertise that would qualify me to be a member of that
21 community at least with regard to the answering of this
22 question.

23 MR. FRISTIK: Well, Your Honor, my objection is
24 foundation. His equivocal answer suggests that he
25 doesn't know if he's a member of the forensic scientific

DAN E. KRANE

608

1 community or not and based on the question that was
2 asked I don't think there's foundation to provide an
3 answer so it's objected to.

4 THE COURT: I'll overrule the objection and
5 allow the answer.

6 BY MS. FUNK:

7 Q In case you've forgotten, Dr. Krane, my question is in
8 the scientific community at large does the scientific
9 community have a standard position on publication or
10 keeping things secret when it comes to scientific
11 methods?

12 A Definitely it does. It's a fundamental precept of the
13 scientific method is that experiments can be repeated by
14 others. And to facilitate that repetition and
15 confirmation there must be complete disclosure of the

16 underlying principles upon which an experiment was
17 conducted. And in the context of a primer binding site,
18 that certainly qualifies as something that's
19 fundamentally important to the performance of that
20 exercise of amplifying DNA.

21 THE COURT: My search now is for a logical
22 breaking point.

23 MS. FUNK: Actually, Your Honor, I think I'm at
24 a logical breaking point.

25 THE COURT: Very well, we will recess until

DAN E. KRANE

609

1 1:00, is that good for you? 1:05?

2 MS. FUNK: 1:05, please.

3 THE COURT: Will that work for the State,
4 Mr. Fristik?

5 MR. FRISTIK: That's fine, Judge.

6 THE COURT: Okay, 1:05. Thank you.

7 (Noon recess at 12:02 p.m.)

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DAN E. KRANE

610

1 (1:10 p.m.)

2 THE COURT: Okay, when we recessed for lunch
3 Dr. Krane was on the stand. You may come forward,
4 Dr. Krane.

5 In about an hour I'm going to be asking
6 everybody to give me an estimate of how long it's going
7 to be going, not only with Dr. Krane if he's still on
8 the stand at that time, but for all of the other
9 witnesses or any other witnesses today so that we can
10 inform people who will be staying so they can make their
11 plans and those who are here can make plans.

12 All right, go ahead please, Ms. Funk.

13 BY MS. FUNK:

14 Q Dr. Krane, in preparation for your testimony today did
15 you prepare for us some overheads to look at?

16 A Yes, I did.

17 THE CLERK: Exhibit Number 25 marked.

18 BY MS. FUNK:

19 Q I'd ask you to take a look at Exhibit Number 25 and tell
20 me if that is a representation of those overhead slides?

21 A Yes, they is. These are paper copies of the overheads
22 I've prepared.

23 MS. FUNK: Judge, I made an extra copy for you.

24 BY MS. FUNK:

25 Q And could you tell us -- let me put it this way, do some

DAN E. KRANE

611

1 of the pages of this exhibit represent hypothetical
2 situations that you yourself composed?

3 A Yes.

4 Q And do some of the pages reflect data obtained from the
5 Minnesota Bureau of Criminal Apprehension's population
6 database?

7 A They do.

8 MS. FUNK: I'd offer this exhibit, Your Honor.

9 MR. FRISTIK: Object to that data that pertains
10 to BCA's population database. At this point I'm not
11 sure what the further discussion is going to be, but
12 again Your Honor, it seems to be getting into an area
13 about specific ways in which the BCA may have conducted
14 their business or ways in which they should have
15 conducted their business in comprising their population
16 database. I would object on that basis. It gets into

17 prong two.

18 THE COURT: Okay. Well, I understand the
19 objection. Overruled. We'll proceed.

20 BY MS. FUNK:

21 Q Dr. Krane, I appreciate that you were not here for
22 yesterday's testimony. Well let's back it up even
23 further.

24 MS. FUNK: I'm sorry, Your Honor, has the
25 exhibit been received then?

DAN E. KRANE

612

1 THE COURT: Yes.

2 BY MS. FUNK:

3 Q Essentially could you give us a topic for what these
4 documents illustrate?

5 A Well I think in very brief some of the problems that are
6 associated with mixture interpretations and analyses and
7 essentially they illustrate to a large extent why
8 there's lack of consensus within the scientific
9 community about a standard approach to dealing with
10 mixture analyses of forensic DNA profiles.

11 Q Okay. And I appreciate, as I said, that you weren't
12 here for the previous testimony. I can represent to you
13 that we have had a considerable amount of discussion on
14 this topic already so I would ask, Dr. Krane, that you
15 start with the first overhead that you've prepared but
16 bearing in mind that we are at least somewhat educated
17 on some of these initial issues. And let's just proceed

18 from there.

19 A All right.

20 Q If it's easier for you to stand, as long as you're not
21 standing in the line of vision of the people in the jury
22 box.

23 A If I need to speak louder please let me know.

24 Would you like me to say a few words about it?

25 Q Please.

DAN E. KRANE

613

1 A Well all that I'd really like to do is discuss some of
2 the issues associated with mixture interpretations, so
3 for instance if we have an individual we can distinguish
4 one individual from another quite often on the basis of
5 the DNA profiles that we observe in them.

6 Typically crime laboratories and people doing
7 DNA typing will look at 12 or 13 different loci. This
8 is just illustrative of what might be observed at one of
9 them, a locus that's frequently abbreviated and called
10 the D3 locus, but it's possible we might find an
11 individual who is typed 16, 17 and another individual
12 who is typed 14, 16 and be able to distinguish them on
13 the basis of the alleles that we observe for that
14 particular locus.

15 If DNA genetic material from both of these
16 materials were to be mixed together, a mixture profile
17 would be observed.

18 Q I just want the record to reflect when you switch to a
19 new overhead.

20 A And the second overhead in the series illustrates
21 essentially the genotype that would be observed in such
22 a mixture. Where again if we had a mixture of
23 individual one with individual two we would expect to
24 see some evidence of that 14 allele from individual two,
25 the 16 allele from both individuals one and two, and the

DAN E. KRANE

614

1 17 from individual one. But again, we'd said a genotype
2 that now had three alleles present as opposed to two.
3 The one firm conclusion that can be drawn is that two or
4 more individuals have contributed to this sample.

5 Now if we go to the next overhead and try to
6 move through them as quickly as I can, the way that that
7 would actually be detected would be through an analysis
8 of some electropherograms. This is the output of the
9 ABI 310 or, to some extent the ABI 377 machines using
10 the Profiler Plus kit. It turns out that the genotypes
11 that I've described for D3 locus are the same ones that
12 appear in these electropherograms. You can see that
13 contributor one, as it's labeled here, essentially
14 individual one in the previous overheads, could be
15 genotyped as being 16, 17, they have a peak that's got
16 that 16 tag and the 17 tag underneath them. Whereas
17 individual two or here contributor two, would be
18 genotyped as 14, 16. And yet when we mix the DNA of

19 contributor one and contributor two, what's observed is
20 a DNA profile that's consistent with a mixture. Where
21 now we see a peak that corresponds to the 14, the 16,
22 and the 17.
23 Q Dr. Krane, we can't see that.
24 A I'm sorry.
25 Q Thank you. Just so the record is clear, we've got those

DAN E. KRANE

615

1 boxes with the numbers that you've referred to.
2 Underneath there's another box. Could you just give a
3 very brief explanation as to the significance of those
4 lower boxes?
5 A The lower box is what's known as the peak height. It's
6 measured in units called RFU's and it's reflective of
7 how much material is present associated with each of
8 those particular peaks. So the 14 has 746 RFU's, the 17
9 has 877, and you might be able to see from the graph
10 that the 17 peak is a little bit higher than the 14
11 peak. Again, the RFU values are measures of those peak
12 heights.
13 Q Okay.
14 A Okay? So again, this is essentially just a summation or
15 the underlying data that would be associated with what
16 I'd just been talking about for those individuals.
17 But again, when we're talking about a mixture,
18 interpretations of mixtures can be very challenging.

19 The mixture that we observed on that previous set of
20 electropherograms, the 14, 16, 17, could have come from
21 a mixture of DNA that came from individual one with type
22 16, 17 and individual two with type 14, 16, but it could
23 have just as easily have come from a mixture of an
24 individual who was completely different, actually two
25 individuals completely different from the previous two

DAN E. KRANE

616

1 individuals. For instance somebody who is typed 16, 16
2 mixed with somebody who is typed 14, 17. The mixture
3 would be indistinguishable between the first pair and
4 the second pair.

5 By the same token we could invoke a completely
6 different individual still, now labeled individual five
7 whose typed 17, 16, mix them with somebody whose 14, 16,
8 and again get the very same mixture. Indistinguishable.
9 And still a fourth pair of individuals could be combined
10 to give that exact same mixture profile.

11 So when confronted with a mixture there's this
12 challenge of determining not only which pair of
13 individuals might have contributed but then also, it
14 turns out, how many individuals may have contributed.

15 Q Dr. Krane, if I could just -- if you would put that
16 slide back up. I believe the slide reflects, in your
17 individual number five, having a 17, 17 profile. I
18 thought I heard you say 17, 16 profile?

19 A If I did I was in error. Individual five on the chart

20 or on the overhead is 17, 17.

21 Q Okay, thank you. I just wanted the record clear on
22 that.

23 A Sure. Another way of describing that is that individual
24 five is a homozygote for the 17 allele. They're
25 homozygous 17.

DAN E. KRANE

617

1 Again, not only is it difficult to distinguish
2 what pair of individuals might have contributed to a
3 mixture, there's also challenges to determining how many
4 individuals may have contributed to a mixture.

5 At the top of this next overhead we still see
6 the original pair of individuals that were portrayed in
7 those electropherograms that gave us that original
8 mixture, but now see a group of three individuals that
9 might give exactly the same mixture. Now somebody who
10 is typed 16, 16 mixed with somebody whose typed 14, 17
11 mixed with somebody whose typed 17, 17 would still give
12 us the 14, 16, 17 mixture. So again, not only do we
13 have problems deciding what pair of individuals might
14 have contributed, there are now becoming some issues as
15 to how many individuals might have contributed to a
16 mixture like the one that I showed in an
17 electropherogram a few overheads ago.

18 And it's not just three-way mixtures that are
19 in issue, it's entirely possible in this instance, for

20 example on this next overhead, that you might get six
21 individuals that have contributed to a mixture that
22 still yield just 14, 16, 17 as the mixture profile
23 that's observed.

24 So in the end what we have here then is a
25 situation where not only do we have a hard time

DAN E. KRANE

618

1 determining what pairs of individuals might have
2 contributed to a mixture but there's some serious
3 questions as to how many individuals might have
4 contributed to that mixture.

5 Q Now Doctor, going back to that third slide, the
6 electropherogram, if you could perhaps put that one back
7 up for a minute. We've had some testimony that while
8 it's hypothetically possible to mix three people and
9 obtain, as you suggest, a profile that could be limited
10 to simply two people or mixed here in this last slide,
11 six people, and obtain that three allele profile, if we
12 look over into that other locus, the one on the far
13 right --

14 A FGA.

15 Q -- FGA, don't we see four alleles for that mix that you
16 were talking about?

17 A For this particular mixture if we have contributor one
18 mixed with contributor two in fact you do observe four
19 alleles in the mixture. Essentially for the FGA locus
20 we see a 21, a 22, a 24, and a 25.

21 Q All right. I didn't mean to interrupt. If we could go
22 back to your slide show.

23 A Well so the FGA locus in this mixture would suggest
24 quite clearly that there are at least two contributors
25 to the sample. But we might be confused by looking

DAN E. KRANE

619

1 simply at the VWA locus as to how many contributors
2 there are because there we observe in the mixture simply
3 a 16, 17.

4 And again, I understand that you've heard
5 testimony about this already, but in case this didn't
6 get explicitly mentioned, the expectation is that every
7 individual should have not more than two versions of
8 these genes; one copy from their mother, one copy from
9 their father. It's possible for the mother and the
10 father to have contributed the same gene and therefore
11 we'll observe only one as we do for the VWA locus and
12 contributor two where we see just that 16. But it's
13 also possible that you would observe two, such as we see
14 in contributor one for VWA where we see a 16, 17. The
15 point, though, is that if ever we see more than two
16 that's a clear indication that there must be at least
17 two individuals contributing to that sample.

18 So at the D3 locus and the FGA locus we're
19 seeing evidence here of at least two contributors, but
20 there's still an open question as to how many

21 contributors exactly. It's at least two but, as some of
22 those other overheads illustrated, it could be as many
23 as six or substantially more that would have contributed
24 and given the exam same mixture profiles.
25 Q Okay, and back to what was going to be your next slide

DAN E. KRANE

620

1 in the series.

2 Did you do some research into how often it
3 would occur that you could have three people in a
4 mixture and see a limited lower number of alleles?

5 A Well yes I did and it turns out that that's still
6 something of an open question that I think we might be
7 able to make some -- provide some light onto what the
8 answer to that question might be through some of the
9 analyses that we've performed.

10 The issue is this: If a DNA profile, a mixture
11 profile, is observed to have four or fewer alleles
12 across 12 or 13 loci, is that tantamount, is that
13 equivalent to saying that there were only two
14 contributors?

15 An argument has been made quite frequently that
16 if there was a third contributor that at least at one of
17 those loci, and probably many more, a fifth or a sixth
18 allele would also have been observed. Not just four or
19 three or two or one, but rather five or six. That would
20 be taken -- that's an expectation when one has a
21 three-way mixture. At least a common expectation.

22 So what we did was take the actual BCA's
23 database, 649 individuals, and perform all possible
24 three-way mixtures with that database to assess how
25 frequently we might be misled into thinking that there

DAN E. KRANE

621

1 were only two contributors when in fact there were three
2 contributors to a particular mixture.

3 Q And did you write these all out by hand?

4 A Definitely not. Again, we're talking about 649
5 individuals for whom DNA profile information was
6 available to us from the BCA for 12 loci. The minimum
7 of two characters per locus times 649 individuals,
8 that's a large number of characters to keep track of and
9 to perform the three-way mixtures that I'm suggesting,
10 what I'm suggesting needs to be done and what we've
11 performed is examine the profiles that would result from
12 a mixture of all possible three-way mixtures. Talking
13 about mixing the DNA profile of individual one with two
14 and three; combining individual one with two and 4;
15 individual one with two and five; and again, all
16 possible three-way mixtures. And in the end that's 649
17 times 649 times 649 or, to be precise, 45,349,524
18 different possible three-way mixtures of the 649
19 individuals in the BCA's database. So again, in excess
20 of 45 million combinations, far beyond what any human
21 being could reasonably be expected to perform in a

22 lifetime actually.
23 Q And so --
24 A Without assistance.
25 Q How did you analyze the data?

DAN E. KRANE

622

1 A Well we applied some of the tools of bioinformatics. We
2 used computers to help us generate these samples or
3 these mixtures and then extract from those
4 computationally generated mixtures the results that we
5 were interested in observing.

6 Q I see. Okay.

7 A So --

8 MR. FRISTIK: Your Honor, I want to object.
9 Again renew my objection. This is not relevant to prong
10 one of the Frye-Mack test. The witness is up there
11 essentially criticizing what the BCA did in their
12 population database and he is suggesting to the Court
13 that what they did was incorrect and that he, by that
14 testimony, is well beyond the scope of prong one and
15 this has no relevance to this hearing and I object to
16 it.

17 THE COURT: Ms. Funk?

18 MS. FUNK: I don't think that up to this point
19 he has testified that the BCA did anything incorrect. I
20 will note a couple of things. Dr. Budowle testified
21 specifically about the Minnesota database and
22 Mr. Fristik introduced a published paper talking about

23 the Minnesota database, and again, I am not talking
24 about the prong two issues of whether or not things were
25 done correctly in this case. The issue is whether or

DAN E. KRANE

623

1 not the scientific evidence the State sought to offer,
2 including the number of 63 trillion for a profile
3 frequency, the question is whether or not that's based
4 on valid scientific principles. And in coming up to a
5 statistical calculation offered to a jury in a case you
6 rely on the database.

7 MR. FRISTIK: Your Honor, if I can respond?

8 THE COURT: Sure.

9 MR. FRISTIK: No, we're not here to discuss or
10 go over again the evidence that was offered in this
11 specific Roman Nose case about 1 in 63 trillion. That's
12 not the reason we're here. That issue was litigated at
13 prong two, that issue was litigated at trial. We're not
14 here to specifically talk about the evidence and what
15 she means by that is the evidence we introduced in the
16 Roman Nose prosecution about the results that were
17 obtained by the BCA, the specific evidence they analyzed
18 using DNA. That has already been litigated at prong
19 two, that's been litigated at the trial, and that is not
20 appropriate for litigation at this hearing.

21 MS. FUNK: And perhaps I was unclear, Your
22 Honor. There will be no presentation of the statistical

23 calculations used in this case. We're only talking
24 about A, what's in the Minnesota database and B, concept
25 we've talked about repeatedly, which is masked alleles

DAN E. KRANE

624

1 and three-way mixtures. It's difficult because it's
2 already happened, but what we're litigating is whether
3 the State can introduce scientific evidence and
4 scientific evidence is comprised of conclusions about
5 DNA profiles and DNA matches and statistical frequencies
6 and those conclusions in every DNA case are come to in
7 reliance on the database.

8 MR. FRISTIK: We're not here to discuss what I
9 can introduce in evidence. The evidence has already
10 been introduced. It's been received by the Court.
11 We're not here to revisit that issue. The evidence is
12 in.

13 THE COURT: It is.

14 MR. FRISTIK: We're here for prong one. She's
15 trying to go over again, have another bite at the apple,
16 of the evidence we introduced and have witnesses comment
17 on that and why, what the evidence that was introduced,
18 why it's shaky or something. It's not appropriate for
19 this hearing, Your Honor.

20 MS. FUNK: The evidence was introduced and the
21 Supreme Court made a ruling that said, came down with a
22 ruling that said when a party seeks to introduce this
23 type of evidence a prong one hearing must be held. And

24 again, I can assure the Court there's no discussion
25 about the specifics of this case. The conversation is

DAN E. KRANE

625

1 limited to the database. Mr. Fristik brought in the
2 document purporting to establish the validation of the
3 Minnesota BCA's database, Ms. Gross talked about the
4 validation of the BCA's database and so did Dr. Budowle
5 and that is what this is in response to.

6 THE COURT: Okay. I'll permit you to proceed.
7 The objection is overruled. This is a close call. I'm
8 going to let you put it in so there is a record
9 preserved. Go ahead. I'll decide what it's worth.
10 Thanks. Or if it's relevant.

11 MS. FUNK: It's understood, Your Honor, that
12 the Court will give -- make its own determination about
13 the weight of each piece of evidence.

14 THE COURT: Of course.

15 MS. FUNK: At the conclusion.

16 THE COURT: Of course, that's what I'm here
17 for.

18 THE WITNESS: So if I recall where I left off I
19 was suggesting that an interesting question might be how
20 often might we be misled by the number of alleles that
21 are present across all 12 loci in terms of making an
22 inference as to how many contributors had contributed to
23 a mixture.

24 BY MS. FUNK:

25 Q And Dr. Krane, if I could interrupt, it looks like

DAN E. KRANE

626

1 you've actually written on that overhead so it's
2 slightly different than the exhibit which was offered
3 and received.

4 A Actually I made the same mark on the exhibit as well.
5 There's a typographical error, essentially.

6 Q Okay.

7 A Such that the word allele is used where it should be
8 have been loci, or alleles in place of loci.

9 So again, it's quite, it has been quite
10 frequently asserted that if there are no instances of
11 five or six alleles observed across 12 loci, that it's a
12 reasonable conclusion -- a reasonable conclusion to be
13 drawn is that there are only two contributors to a
14 mixture.

15 To test that directly we constructed,
16 artificially or conceptually, all possible three-way
17 mixtures to see how often we would observe an instance
18 of four or fewer alleles across all 12 loci that would
19 be consistent on the surface with just the mixture of
20 two individuals but in reality arose from a mixture of
21 three real individuals.

22 Again, altogether there are 45,349,524 possible
23 three-way mixtures that can be constructed from varying
24 I combinations of 649 individuals and what we found was

25 a rather surprisingly high number of 2,505,650 three-way

DAN E. KRANE

627

1 mixtures that across all 12 tested loci never had more
2 than four alleles. And in fact there are even 310
3 three-way mixtures that had never fewer than three
4 alleles across all 12 tested loci.

5 So in essence approximately 5.5 percent of all
6 three-way mixtures using the DNA profiles of known
7 individuals who were typed as part of the database here
8 for the State of Minnesota, approximately 5.5 percent of
9 three-way mixtures could have easily been confused as
10 actually having been due to just two-way mixtures, a
11 sizable fraction, and actual number, again, is in excess
12 of 2.5 million three-way mixtures.

13 Q Okay, go ahead.

14 A So, that number struck me as quite large. I've heard it
15 frequently again described as being exceedingly unlikely
16 that any three-way mixture would have four or fewer
17 alleles across 12 different loci. And to get a feel for
18 how large that number actually was and if it might be
19 something that's due simply to the database, something,
20 some unique aspect of the Minnesota BCA's database as
21 opposed to some sort of randomly generated database,
22 what we did, and I again have corrected "alleles" on
23 this overhead with the word "loci" and have done the
24 same on the exhibit as well. On the left-hand columns

25

here you can see again the very same numbers from the

DAN E. KRANE

628

1 previous overhead but on the right-hand column is the
2 results of the same analysis performed using five
3 different randomly generated sets of 649 individuals,
4 the same 649 from the original database.

5 Let me explain exactly what those randomly
6 generated individuals were like. What we did is we took
7 the exact allele frequencies from the original database
8 and used those to construct an exact equivalent database
9 in terms of allele frequencies but did so in a random
10 fashion so that we broke any possible associations that
11 there might have been between the alleles at one locus
12 and the alleles at another locus or even the alleles
13 within a locus. This is entirely random shuffling of
14 the alleles that we had observed in the original
15 database but in a way that doesn't alter the frequencies
16 in any way. The frequencies are the same but the
17 associations have been broken.

18 We did that five separate times and what you
19 see in the columns to the right of this overhead are the
20 results of that analysis on average. So the total
21 number of three-way mixtures remains the same because on
22 average we looked at five times this -- we looked at
23 five times this number but the average was five times
24 that number divided by five or the same number we had
25 looked at before, and now we observe that the number of

1 three-way mixtures with three or fewer alleles is
2 actually significantly, or the very least substantially
3 smaller than it was in the actual database.

4 And the same is also true for number of
5 individuals that had -- or the number of loci with four
6 or fewer alleles. Previously we had seen 2,505,650, now
7 on average we're observing 2,409,121.6.

8 So this caused me to suspect that there was
9 something about the Minnesota BCA's database that was
10 nonrandom in terms of the way the alleles were
11 associated with each other. That the numbers change
12 when we look at a truly random database and they're
13 different from those that we observed in a nonrandom
14 database or the actual original database.

15 That prompted me to then want to take a look at
16 what's some of those actual mixtures were, these
17 hypothetical or computer-generated mixtures. And I've
18 got an overhead here now that simply shows you five --
19 or actually six different three-way mixtures where
20 across all 12 loci we've never observed more than three
21 alleles in the mixture profile.

22 Q And Doctor, are these computer-generated profiles or are
23 these actual profiles of DNA from the BCA's database?

24 A These are the actual profiles from the BCA database.
25 What's been computer generated is the combinations of

1 them, pairing individual BCA identifier PB0005 with
2 PH0070 and PH0138. That has been -- we've had computers
3 help us with that. But the actual genotypes for those
4 individuals are the ones that come straight from the
5 BCA's database.

6 Q And this is an example of six of those combinations?

7 A It is. Six of 310.

8 Q Did you also generate for the Court copies of all of
9 those 310?

10 A I did generate a printout of all 310 three-way mixtures
11 at which three or fewer alleles were observed across all
12 12 loci.

13 THE CLERK: Exhibit Number 26 marked.

14 BY MS. FUNK:

15 Q I'd ask you to take a look at this Dr. Krane. Is
16 that --

17 A Yes, this is that compilation of all 310 three-way
18 mixtures.

19 MS. FUNK: I'd offer Exhibit 26, Your Honor.

20 MR. FRISTIK: No objection.

21 THE COURT: All right, 26 is received.

22 MR. FRISTIK: Well I shouldn't say -- renew an
23 objection the Court's --

24 THE COURT: Subject to your prior objection,
25 you don't have any objection to this. In other words --

1 MR. FRISTIK: Not specifically. This pertains
2 to the previous objection which is on the record
3 already.

4 THE COURT: Understood.

5 MR. FRISTIK: All right, thank you.

6 THE WITNESS: One of the things that was
7 particularly curious after an inspection of those
8 three-way mixtures in which there were, again, three or
9 fewer alleles across all 12 loci, is that many of them
10 contained recurring pairs of individuals. That makes
11 some sense, actually, because if a pair of individuals
12 share many alleles in common, to some extent it's not
13 that different from having just one individual's DNA
14 profile. We're seeing the same DNA profile occur two
15 times. The more alleles they share in common the closer
16 it is to us to perhaps being confused that they were the
17 same individual.

18 And so we took a close look at those pairs of
19 individuals that kept recurring in those three-way
20 mixtures and found that of those 310 three-way mixtures
21 at which there were three or fewer alleles across all 12
22 loci, that there was one pair in particular that showed
23 up quite frequently. Database ID numbers PN0036 and
24 PN0154 accounted for actually, or were present in a
25 total of 21 of the 310 three-way mixtures that I've been

1 talking about. And there were some other pairs also
2 shown on this overhead that showed up a rather large
3 number of times compared to other pairs of individuals.

4 And so when looking at those particular
5 individuals something really, well, quite striking I
6 would say, emerges. If we simply now look at those
7 particular pairs of individuals, and I apologize because
8 the print on this particular overhead is very small, but
9 to get all the alleles for these genotypes as well as
10 the ID numbers on it was necessary to reduce it to some
11 extent, but I think it's still legible, at least in the
12 printed version.

13 The very top of the list shows side by side a
14 pair of individuals, BCA ID number PH0113 and PN0056,
15 that actually share, across all 12 loci, 19 of 24
16 possible alleles. Again, only two alleles possible per
17 locus, 12 loci being considered, these individuals were
18 indistinguishable from each other at 19 of those 24
19 positions.

20 To a geneticist that extent of shared alleles
21 says something quite significant. There are two ways
22 that one can share alleles. You can share them by
23 chance or you can share them by descent. In genetics
24 terms we're talking about the difference between
25 identity by state versus identity by descent. To have

1 19 of 24 alleles shared between a pair of individuals is
2 strongly suggestive that those individuals share those
3 alleles, that large number of alleles, because of
4 identity by descent. That means that there's a strong
5 probability, a high likelihood, that that pair of
6 individuals are in fact related to each other and
7 probably in fact very closely related to each other; in
8 genetics terms first degree relatives, things like a
9 mother and a daughter or two siblings.

10 And the same sort of conclusion could probably
11 also be drawn from the next two pairs of individuals in
12 this list where we see 18 out of 24 alleles are shared
13 and in fact one of those pairs is the pair that I was
14 pointing out previously, the PN0036, PN0154, where they
15 appeared in 21 of the 310 three-way mixtures where there
16 were three or fewer alleles across all 12 loci.

17 To get a feel for how likely it was that those
18 individuals were related to each other, again we turned
19 to a randomized database where here we took, we
20 generated random DNA profiles in the same fashion that
21 was generated before, did that process five different
22 times, turns out that there are 210,276 different pairs
23 of individuals that can be generated from a database
24 with 649 individuals within it.

25 Again we did that five times and this, the

1 spreadsheet, is telling us the number of times that we
2 observed, for instance, just one allele of the 24
3 alleles across all 12 of those loci and down at the
4 bottom for the original data set again there's that one
5 instance of 19 alleles shared by that one pair of
6 individuals.

7 In the randomized data set, five times we've
8 done this process randomized, not once do we ever
9 observe an individual or a pair of individuals that
10 share 19 or more alleles like we observed in the actual
11 data set.

12 In the original data set we observed two pairs
13 of individuals that share 18 alleles of 24. In the
14 randomized data set we see, on average, only .8 share 18
15 of the 24 alleles, and again, this suggests very
16 strongly that there's something different about the
17 distribution of the alleles in the original data set as
18 opposed to the randomized data set. That difference,
19 again, seems to be associations or linkages or
20 correlations that are strongly suggestive of there being
21 closely related individuals in the original data set and
22 then when we randomize the data set we break those
23 associations and no longer observe them.

24 And there's one other overhead but I think
25 actually I've pretty much made the points that I would

DAN E. KRANE

1 like to make with the ones that I've discussed.

2 BY MS. FUNK:

3 Q Fine. Thank you, Dr. Krane.

4 THE COURT: I don't think I said that 26 was
5 received. It is, so the record's clear.

6 MS. FUNK: Thank you, Your Honor.

7 BY MS. FUNK:

8 Q Dr. Krane, do you know why there are 649 individuals in
9 the BCA's database?

10 A To a large extent, yes. I know that at one point there
11 were 650 individuals within the database but that there
12 was -- it was found that there was a duplicate entry
13 within the database, where a single individual's DNA
14 profile was represented two times, that one of those
15 entries was removed after it was demonstrated that it
16 was a duplicate entry, and as a result 649 were left.

17 Q And we had some testimony about that specific issue from
18 Dr. Budowle and he indicated, as you did, that upon
19 discovery it was removed. And I'm asking you,
20 Dr. Krane, is that a scientifically valid or appropriate
21 thing to do?

22 A Yes, it is.

23 Q Okay, and why is that?

24 A Well again, the purpose of these databases ultimately is
25 to get an assessment of the relative frequency of these

DAN E. KRANE

1 different genes and genotypes in a relevant population,
2 in this case the population was chosen to be individuals
3 living within the State of Minnesota, or at least
4 donating blood in the State of Minnesota, and to have
5 one individual represented twice would effectively over
6 represent that individual's alleles within the
7 population such that it may be less reflective of the
8 general population's allele frequencies.

9 Q And likewise if the database contained two individuals
10 who are closely related -- well, should those closely
11 related individuals be in the database?

12 A The logic, the reasoning is precisely the same with
13 regard to closely related individuals and identical
14 individuals. The difference is a matter of degree.
15 Identical individuals are identical across and therefore
16 there's a nonrandom sampling of the alleles of the
17 population. Closely related individuals are giving you
18 a feel for perhaps the allele frequencies of that
19 particular family but not necessarily of the allele
20 frequencies across the entire state.

21 And so again, just as it's appropriate to cull
22 or to remove duplicate entries I would think that a
23 reasonable solution might be to remove obviously related
24 individuals from a database as well.

25 Q Dr. Krane, are you aware that the Minnesota BCA's

DAN E. KRANE

637

1 database was subjected to Hardy-Weinberg and linkage

2 equilibrium analysis?

3 A Yes.

4 Q Can you explain for us why it is that these allele
5 similarities weren't discovered during that analysis?

6 A Well, the Hardy-Weinberg test is widely known as being a
7 statistically weak test. And what that means is that
8 it's possible to have some very substantial and quite
9 significant departures from random association of
10 alleles and yet still have the Hardy-Weinberg test tell
11 you that there was no observed problem.

12 The linkage equilibrium tests are effectively
13 the same as the Hardy-Weinberg test but instead of being
14 within a locus they now look at correlations across loci
15 and by the same token are also effectively statistically
16 weak, but in fact it was my understanding that some
17 discrepancies or departures from linkage equilibrium
18 were observed within the Minnesota database or some
19 portions of it and I think in fact that the fact that we
20 now have some evidence that there are related
21 individuals could easily explain why those departures
22 were observed.

23 Q Thank you, Dr. Krane.

24 MS. FUNK: I don't have any other questions,
25 Your Honor.

DAN E. KRANE

638

1 THE COURT: Okay, cross-examination?

2 Before we start with that let's check and see
3 if anybody has an estimate, starting with you,
4 Mr. Fristik, about how much, first of all how much
5 cross-examination time you're going to take and then if
6 you have any indication of how far we should be planning
7 on going later this evening?

8 MR. FRISTIK: Well the only thing I can tell
9 the Court in terms of my cross-examination of this
10 witness, I'll be as conservative as I can understanding
11 that the figure I give the Court may, I may end up using
12 less than that time, but I'm going to tell the Court an
13 hour and maybe a little bit more. I don't know what it
14 will turn out to be, it might be less than that, so I'll
15 error on the side of caution and say at least an hour,
16 maybe more, in terms of my cross of this witness.

17 THE COURT: Okay, and let's talk now, I don't
18 know if you will have any indication at this time about
19 redirect, Ms. Funk, but if you have anything on that or
20 how long it will take to do your direct on your next
21 witness?

22 MS. FUNK: I can't speak to redirect, Your
23 Honor, but I can represent I haven't saved any
24 questions. I'm not planning a redirect at this time.

25 As to Dr. Mueller, I'm thinking an hour and a

DAN E. KRANE

639

1 half.

2 THE COURT: Okay.

3 MR. FRISTIK: And my cross of Dr. Mueller, I'll
4 error on the side of caution, I'll say an hour.

5 THE COURT: All right, so I think what we're
6 saying is we'll perhaps be done with Dr. Krane by 3:00
7 to 3:15, and if we break until 3:30, with Dr. Mueller,
8 direct, 5:00 and cross, 6:00. That sound about right so
9 far? Reasonable? Within an hour one way or another?

10 MR. FRISTIK: Yes.

11 MS. FUNK: Yes.

12 THE COURT: All right. Go ahead, Mr. Fristik.

13 MR. FRISTIK: Thank you, Your Honor.

14

15 CROSS-EXAMINATION

16 BY MR. FRISTIK:

17 Q Dr. Krane, I want to begin by contrasting some
18 information that we find in your CV and I'm contrasting
19 your current CV that was just offered and received by
20 the Court today with your CV that was offered and
21 received in your testimony in May of 2001.

22 I'll begin by asking or just pointing out
23 something that we find under the section "current
24 research funding" and I note that in your CV that was
25 offered in today's hearing you've left out a section

DAN E. KRANE

640

1 that was in your CV that you offered in May of 2001 and
2 the section you left out states as follows: Under the

3 heading current research funding, support from contract
4 work totaling \$93,400 for consultations in the area of
5 forensic DNA profiling, and that goes from 1993 to
6 present, which would be May of 2001.

7 Do you recall that being in your earlier CV?

8 A Yes, I do.

9 Q In your current CV I note that you've left that out, is
10 that correct?

11 A That is correct. Let me also mention that this is not
12 necessarily a totally up-to-date CV. I would say it's
13 perhaps two months out of date. But in the most current
14 version it's also not listed as part of my current
15 research funding.

16 Q Well how often do you update your CV, let's ask that?

17 A Well, not as often as I should but approximately once
18 every six months.

19 Q Okay. Do you recall then updating your CV after you
20 testified in May of 2001?

21 A Yes.

22 Q Do you recall the next time you updated your CV after
23 May of 2001?

24 A I don't recall specifically. I think it may have been
25 in March of this year.

DAN E. KRANE

641

1 Q And in March of this year when you updated your CV did
2 you include that section under current research funding?

3 A No, I did not.

4 Q When's the next time you updated your CV after March of
5 this year?

6 A I have not formally updated it since. I have a few
7 small modifications but I have not made that available
8 to anybody yet.

9 Q So the only formal update you did in your CV was in
10 March of 2002?

11 A That's right.

12 Q And in March of 2002 you left that section out, correct?

13 A That's right.

14 Q And in comparing your CV's I find that, correct me if
15 I'm wrong, I find that that's the only area that you
16 left out of your March, 2002, updated CV?

17 A Well certainly there have been additions.

18 Q I don't disagree with that.

19 A But it is possible that that may be the only thing that
20 was removed. But you're right, it was removed.

21 Q Do you do the updates on your CV or do you give it to a
22 support person and have them do it and tell them what to
23 modify and what not to modify?

24 A I do it personally.

25 Q So you updated the CV from May of 2001 to March of 2002

DAN E. KRANE

642

1 and when you were doing it you left that section out,
2 right?

3 A I felt it wasn't consistent with what was present in the

4 rest of that, so yes, that was deleted.

5 Q Okay. And let me talk to you about that because we
6 talked about this before when you testified, that the
7 amount of money you make, and again it's reflected in
8 your old CV, the May of 2001 CV, you make -- not you,
9 your university, your research funding accrues a
10 significant amount of money as a result of you doing the
11 outside forensic DNA consulting, true?

12 MS. FUNK: Objection. That's irrelevant, Your
13 Honor.

14 THE COURT: I think it's relevant. Overruled.

15 BY MR. FRISTIK:

16 Q Is that true?

17 A I suppose it depends on how you define significant but
18 yes, at least as of that previous version of my CV it
19 was approximately \$93,000 over ten years.

20 Q And in fact since -- well let me ask you then, because
21 you testified that you only spend, according to your
22 testimony, 10 percent of your time doing what's called
23 community service or something like that, true?

24 A That's a good approximation, yes.

25 Q And your outside consulting in DNA cases, in forensic

DAN E. KRANE

643

1 DNA cases, would fall within that category, that 10
2 percent of community work or service work?

3 A That's how I would characterize it and I think that's
4 how the university perceives it, yes.

5 Q So, and by the way, the figure of \$93,400 has of course
6 since that time increased because you've also been
7 involved in some additional cases where you've either
8 consulted and/or testified on behalf of criminal
9 defendants, true?

10 A Yes.

11 Q And as a matter of fact when you testify in your outside
12 consulting and forensic DNA cases you testify almost
13 exclusively on behalf of criminal defendants, is that
14 true?

15 A Almost exclusively is correct, yes.

16 Q Except for one time?

17 A That's correct. That number has not changed since we
18 last spoke.

19 Q What has changed since we last spoke is that you've
20 testified in -- actually there's another area in your CV
21 that I think you left something out?

22 A I wouldn't be surprised that there are omissions or
23 mistakes, yes.

24 Q Since you first testified in the Roman Nose hearing in
25 May of 2001 you've testified in Massachusetts versus

DAN E. KRANE

644

1 Greineder, Indiana versus Wilburn, and South Dakota
2 versus Luce, correct?

3 A Yes, I have.

4 Q And all on behalf of defendants?

5 A That's correct.

6 Q And what you left out was you testified in May of this
7 year in Minnesota versus Kromah, is that correct?

8 A Actually that name is not familiar to me but again this
9 CV is as of March of this year as opposed to May.

10 MR. FRISTIK: Approach the witness?

11 THE COURT: You may.

12 BY MR. FRISTIK:

13 Q Take a look at that transcript. Does that refresh your
14 recollection?

15 A You know, again that particular defendant's name is not
16 one that I recall but I did testify in Hennepin County
17 in May and it was -- it was portrayed to me as a
18 combined case where there were a number of different
19 defendants and that particular name does not ring a bell
20 to me, but again, I wasn't testifying about the specific
21 results of the testing in any particular individual case
22 there, so it's possible that that is in fact the
23 transcript. I think you're right.

24 Q You'll take my word for it?

25 A Yes.

DAN E. KRANE

645

1 Q What you do remember is testifying in Hennepin County in
2 May of 2002?

3 A Yes.

4 Q Okay. And we'll talk about your testimony in that case
5 in a minute because I have some questions for you.

6 Let me address, once again, and to some extent
7 I probably asked you this before on the first time you
8 testified in this case but it's significant and I want
9 to ask you about it.

10 You list in your CV, again, areas where you
11 have done some publications and those are acknowledged
12 in your CV, is that correct?

13 A Yes.

14 Q And in looking through your CV I don't find, correct me
15 if I'm wrong, I don't find any specific publications
16 that were a part of a peer-reviewed forensic scientific
17 journal. Did I miss that?

18 A There certainly are publications that are pertinent and
19 related directly to forensic science. In fact some in
20 very prominent journals such as the Proceedings of the
21 National Academy of Science who in effect commissioned
22 the NRC studies that frequently get a cited as authority
23 in these types of cases, so I don't think that's a fair
24 characterization.

25 Q Are you referring specifically there to the 1992

DAN E. KRANE

646

1 publication Genetic Differences in Four DNA Typing Loci?

2 A That is the one I was referring to specifically, yes.

3 Q All right. Other than that publication are there any
4 publications that appear in any peer-reviewed forensic
5 scientific journals?

6 A There's a 1993 publication titled Unresolved Issues in
7 the Forensic Use of DNA Profiling that I think would
8 qualify as being pertinent to forensic DNA profiling
9 published in a journal, Accountability and Research.

10 Beyond that I think that -- I think those are
11 the two that would be most directly relevant to a
12 forensic science application.

13 Q Just those two, we'd agree on that?

14 A Those certainly are the two that are most directly
15 relevant. There may be others peripherally relevant,
16 but those are certainly focused primarily on a forensic
17 science audience.

18 Q Dr. Krane, you acknowledge several presentations you've
19 made to various professional groups and societies and I
20 ask you if you've ever offered or made a presentation to
21 a forensic based scientific community or society? For
22 example, have you ever made a presentation to the
23 Promega International Conference?

24 A No, I have not.

25 Q Have you ever made any presentations on behalf of or at

DAN E. KRANE

647

1 a conference sponsored by the American Academy of
2 Forensic Scientists?

3 A No, I have not.

4 Q Have you made any presentations to any other
5 organizations that could be be characterized as forensic
6 science groups or societies?

7 A Yes, quite a few.

8 Q Okay, and just go ahead and point those out, what you're
9 referring to?

10 A Well, my understanding of the word forensic means that
11 we're talking about issues that are discussed in court.
12 And forensic science would be scientific issues
13 described in a courtroom setting.

14 Q Can I interrupt you? I probably should have narrowed
15 the question.

16 A Great.

17 Q When I say forensic science what I'm referring to
18 specifically is the forensic use of DNA typing in a
19 forensic setting. Let's narrow it down.

20 A Well I think it seems to me that's consistent with what
21 I just said, the application of scientific methods in a
22 fashion or in a way that's relevant or discussed in a
23 courtroom setting or helping to resolve issues
24 pertaining to law or courtroom types of issues. And
25 so --

DAN E. KRANE

648

1 Q So what have you got there?

2 A Well again, there are quite a few.

3 Q Would they be those that would fall into the category of
4 presentations you've given on behalf of a particular
5 defense attorney or public defender organizations in
6 various states?

7 A There surely would be quite a few that would fall under
8 that categorization, yes. There are also others' such
9 as posters and presentations at meetings like the
10 American Society of Human Genetics as well as invited
11 seminars at universities around the country interested
12 in these types of issues as well.

13 Q And I think you testified -- well maybe you didn't
14 testify to this, but the number of times in which you've
15 offered consultations or testimony as to DNA profiling,
16 I think, totals about 40 occasions, is that right?

17 A Well --

18 Q Is that about current?

19 A Actually I think you've cast a bit of a broader net
20 there in terms of consultations as well as testimony.
21 What's listed in my CV are those instances where I've
22 been called upon to testify. The number of cases in
23 which I've been called as a consultant is actually
24 substantially larger and quite frequently the defense
25 has apparently found that my testimony would not be

DAN E. KRANE

649

1 helpful to them and has chosen to not call me as a
2 witness. Quite frequently cases were resolved before it
3 was necessary to testify and there certainly are a good
4 number of occasions in which I have consulted with
5 prosecuting attorneys but again it has not been
6 necessary for me to come in and actually give testimony.
7 So what I list in my CV are simply those where I've

8 actually been on the witness stand.

9 Q Cases where you've actually testified?

10 A That's correct.

11 Q And that numbers total 40?

12 A It's between 40 and 50, yes.

13 Q And far more, far greater number in which you've been

14 asked to consult?

15 A The number in which I've been asked to consult is a much

16 larger number than the number in which I've actually

17 given testimony.

18 Q That's what I'm asking?

19 A Yes.

20 Q Thank you. Have you ever taught any courses at Wright

21 State on forensic applications of DNA typing?

22 A I've certainly not taught any course that has that title

23 but I certainly have taught many courses in which DNA

24 typing and DNA manipulation methods that are suitable

25 and appropriate in a forensic setting were within the

DAN E. KRANE

650

1 subject matter that was covered.

2 Q So it would be a portion of another course that has a

3 broader title?

4 A Yes.

5 Q As it pertains to your current research at Wright State

6 University, you, by profession you're a biochemist or --

7 A I have a degree in biochemistry.

8 Q By profession what do you tell people?

9 A When people ask what I do my standard response is I'm a
10 molecular biologist. If they still have interest beyond
11 that I'll tell them that I'm a molecular biologist with
12 an interest in population genetics molecular evolution.

13 Q What's the current focus of the research that you're
14 presently doing at your laboratory?

15 A As I mentioned in my earlier testimony, I suspect I'm
16 different than many or most molecular biologists in that
17 I like to apply those tools to a variety of different
18 questions, so I wouldn't say that there's a single focus
19 to my research, unlike most molecular biologists who
20 tend to focus on one very specific issue. In my
21 laboratory we're answering and addressing questions in
22 at least four or five different areas at the present
23 time.

24 Q And what areas at the present time are you addressing
25 questions?

DAN E. KRANE

651

1 A As I alluded to earlier, one active area of research is
2 still the effects of environmental stressors, pollution
3 for instance, upon the genetic diversity of naturally
4 occurring populations of organisms. Another -- would
5 you like me to clarify?

6 Q Let me ask you, if I could, on that specific topic. The
7 effects of environmental pollution on various organisms.
8 What kind of organisms?

9 A We are nondiscriminatory in terms of the organisms that
10 we perform those analyses upon.

11 Q What are they?

12 A There's a large range. Earth worms, crayfish, minnows,
13 fresh water shrimp, bald eagles, garlic mustard plants,
14 violet plants, maple trees.

15 Q So primarily --

16 A Quite a large variety. That's a partial list.

17 Q Okay. But limited to plants and animals?

18 A Yes.

19 Q Okay. What's another area that you're currently
20 questioning?

21 A From a molecular -- that's a population genetics study.
22 From a molecular evolution perspective I am now and I
23 have been for quite some time very interested in the
24 effect of context upon nucleotide substitutions
25 particularly within primates and most particularly

DAN E. KRANE

652

1 within humans. I'd love to go on at great length about
2 those studies. I find them very interesting. But in
3 essence what we've got is a bioinformatic approach
4 looking at large amount of sequence data available
5 through the Human Genome Project. And there's a
6 particular DNA sequence known as an Alu repeat, A-l-u,
7 that is found scattered throughout the human genome in
8 approximately a million copies. Accounts for almost 10

9 percent of all of our DNA. That simple repeated
10 sequence is something whose sequence we know what it
11 started as and now can look to see what it's become in
12 all the different possible contexts in which it's fallen
13 within the human genome. So by studying those types of
14 substitutions we can get some very interesting and very
15 important and very medically relevant insights in
16 terms of where mutations are likely to occur and what it
17 is that might allow us to predict where to look for
18 important mutations.

19 Q So that part of your current work seems to be, at least
20 a portion of it, focuses on some human identification
21 issues?

22 A Alu repeats are used for human identification in some
23 settings. They've been used anthropologically to trace
24 human migrations patterns and such and as a result it's
25 also turned out that they've been applied in human

DAN E. KRANE

653

1 identification, in forensic settings as well, but again,
2 we're not so much looking at them for identification
3 purposes as we are for maybe --

4 Q Evolution purposes?

5 A Evolution and medicinal prediction types of purposes;
6 where it is mutations are likely to occur within
7 important genes.

8 Q So you're really not doing strict human identification,
9 you're looking at them for other purposes?

10 A Yes.

11 Q Any other part of your work that you're currently doing
12 that is looking at human identification?

13 A Well, the analysis that I described earlier with some
14 overheads I think would be considered to be directly
15 relevant to human identification issues, so using
16 bioinformatics tools to answer population genetics and
17 particularly population substructure issues that we
18 observe in STR profile databases as well as VNTR profile
19 databases, the '92 paper we had mentioned earlier was a
20 VNTR type of analysis. Now we're moving into the STR
21 types of analyses. There are at least two independent
22 projects along those lines that I am supervising and
23 that my research group is involved with.

24 Q In those projects the analysis you're doing is
25 computer-based statistical analysis, it's not research

DAN E. KRANE

654

1 at the lab bench using extracted DNA?

2 A That's correct. For those analyses that's certainly
3 true. The other analyses it turns out we do a lot of
4 our DNA extractions and amplifications and such, but for
5 those we're talking about for STR testing we're relying
6 on data that have been generated by others.

7 Q All right. For that portion of your work where you are
8 looking at some human DNA, now like you said you're not
9 looking at it for purposes of human identification,

10 you're looking at it for more so for purposes of
11 evolution and things like that. Are you still having to
12 extract human DNA and do some laboratory analysis of it?
13 A Yes, we do.
14 Q I think that right now you're using the 310, correct?
15 A We have access to a 310, yes.
16 Q Do you use it in your work, though? I'm talking about
17 when you do extraction of human DNA do you use the DNA
18 sequencer?
19 A All the DNA sequencing that gets performed by my
20 laboratory, be it on human DNA or eagle DNA or any other
21 is performed upon a ABI 310 machine.
22 Q It is?
23 A Yes.
24 Q How long have you been using the ABI 310?
25 A I actually first encountered an ABI 310 machine during

DAN E. KRANE

655

1 my postdoctoral studies at Washington University in St.
2 Louis. I believe that would have been in '91 or '92
3 when they were being beta tested there by the company.
4 Q Now, have you -- I take it that you're using the 310
5 because you're satisfied that it's the kind of
6 instrument that's going to give you, for the purposes
7 you're using it for, it's going to give you reliable and
8 valid results, right?
9 A That's correct.
10 Q And again, for at least a portion of your work you are

11 using it for some human DNA, correct?

12 A Oh yes, definitely.

13 Q And it works well for you, true?

14 A I do not know of any better or more affordable

15 alternatives.

16 Q And you also know that the 310 is used not only in this

17 country but it's used worldwide for purposes of forensic

18 DNA typing, correct?

19 A Yes.

20 Q And you have absolutely no qualms about saying right now

21 that the 310 would be a instrument that is generally

22 accepted in the forensic scientific community for giving

23 valid and reliable results, right?

24 A I think that's correct, yes.

25 Q The samples that you're looking at when you're doing

DAN E. KRANE

656

1 human DNA, the samples you're looking at, I assume

2 they're pristine?

3 A As pristine as we can get them, yes.

4 Q So unlike the forensic setting you don't have to worry

5 about degraded or contaminated samples?

6 A It's less of a concern for us.

7 Q I've always wondered, is there an issue when you're

8 looking at a nonhuman DNA like with an eagle or an

9 earthworm or something, that can you come across

10 situations where you run into degraded or contaminated

11 DNA?

12 A Well, if you're curious let me tell you that pill bugs
13 are especially difficult to obtain good quality DNA
14 from. There's something intrinsic about crustaceans,
15 which pill bugs are related, that causes their DNA to
16 degrade very quickly upon their death. So we have
17 substantial difficulty when we want to do DNA profiling
18 of some organisms dealing with those issues of
19 degradation.

20 Q But you still proceed with your attempts to get the DNA
21 to amplify and then run further testing on it I take it?

22 A What we do is shorten as much as possible the amount of
23 time that the DNA has resided in that dead organism from
24 the time we're amplifying its DNA to the point at which
25 we perform our DNA profiles on pill bugs on legs that

DAN E. KRANE

657

1 have been pulled off of still living pill bugs and place
2 them into the PCR tube for the amplification. So we
3 cannot possibly have a shorter time between the death of
4 the tissue and the time the amplification has occurred.

5 Q Enough about the pill bug. Let's talk about the human
6 DNA. What are you using besides the 310? Are you using
7 a particular kit?

8 A The type of DNA profiling that we're doing is one that's
9 called rapid PCR, far more than any other type of
10 characterization of the DNA except for DNA sequencing.
11 Rapid PCR is actually abbreviated RAPD. It's short for

12 randomly amplified polymorphic DNA. And there are kits
13 that are available, in a sense, for that. We do use
14 commercially provided primers that I suppose could be
15 construed as a kit, but we do not have occasion to use
16 the Profiler Plus or the COfiler kits that have been
17 used, for instance, in the original Roman Nose trial.

18 Q Or which are used throughout the country and throughout
19 the world in forensic DNA laboratories, right?

20 A Yes.

21 Q That was a yes?

22 A That was a yes, yes.

23 Q So you don't use any specific commercially available
24 kits when you're doing your human DNA studies?

25 A We use -- I'm not sure how the producer would

DAN E. KRANE

658

1 characterize them. I suspect they would call them a
2 kit. We use materials provided by Operon technologies
3 for our particular DNA profiling experiments.

4 Q And what do they provide you, just the primers --

5 A They provide --

6 Q -- or any other reagents?

7 A They do provide primers, that's the primary thing that
8 they provide, but I believe they also would be happy to
9 provide us with other reagents that would be involved.

10 We find that we can get our reagents more affordably by
11 purchasing them directly from the manufacturers of those

12 reagents as opposed to that sort of secondhand assembly
13 into a kit.

14 Q Now the primers that you purchase, do you know the
15 primer sequences?

16 A Absolutely, yes. Not off the top of my head, but we
17 certainly do know them, yes.

18 Q Are they provided by the manufacture?

19 A They most definitely are, yes.

20 Q But have you ever used the COfiler or the Profiler?

21 A I wouldn't claim extensive experience but I've certainly
22 had those amplification performed within my lab and I've
23 overseen they're injection and such into capillary
24 electrophoresis machines, so to some extent I have, yes,
25 not an inordinate amount.

DAN E. KRANE

659

1 Q Let me make sure I understand you. The COfiler-Profiler
2 kits have been used by individuals in your lab?

3 A On at least two separate occasions, yes.

4 Q Just a couple of times?

5 A Yes. And actually again, I mentioned earlier that I'm
6 beginning to do some mental preparation for a class that
7 I'll be teaching in the spring quarter for us, a
8 senior-level class, and my intent is to utilize the
9 COfiler and Profiler kits in that class as well in an
10 instructional setting.

11 Q Well let me ask you then, based on your understanding
12 would it be fair to say that the COfiler-Profiler kits

13 are generally accepted in the forensic community to give
14 valid and reliable results?

15 A The kits generate reliable DNA profiles, it's possible
16 to generate genotypes from those kits quite reliably and
17 reproduceably.

18 Q Okay. I think you said in some of your research that
19 you've relied on data from the Human Genome Project?

20 A Yes, definitely.

21 Q And you know that the Human Genome Project utilized the
22 310 -- actually they utilized the bigger one, the 31 or
23 37 hundred, right?

24 A 3100's most definitely, yes.

25 Q Those are all capillary electrophoresis instruments,

DAN E. KRANE

660

1 right?

2 A That's right.

3 Q We've already established that those are reliable, valid
4 instruments as far as you're concerned?

5 A Yes, in terms of the results that they yield, I think
6 you can certainly draw conclusions from them, yes.

7 Q You were asked some questions about Ms. Gross's
8 affidavit and you still have it in front of you there?

9 A I do, yes.

10 Q She indicates on page four up at the top, number 19?

11 A All right.

12 Q She indicates: I am aware that a large number of

13 forensic laboratories throughout the United States,
14 Canada, and Europe have validated the Profiler Plus and
15 COfiler kits and the ABI Genetic Analyzer 310 for
16 forensic testing. To my knowledge, none of these
17 studies have raised any questions concerning the ability
18 of these kits or instruments to produce accurate and
19 reliable DNA typing results.

20 Do you agree with that statement?

21 A Well I suspect that perhaps it's just my nature, but I'd
22 probably want to put in a few qualifiers there, but the
23 general sentiment I do agree with. The qualifiers I
24 might like to include would be things such as none of
25 these studies have raised any questions concerning the

DAN E. KRANE

661

1 general ability, as opposed to the ability. Certainly
2 one of the purposes of a validation study is to push a
3 kit or a machine to its limits and see where it is that
4 it fails to provide reliable results. And I think that
5 at those limits the machine fails to provide accurate
6 and reliable results. So certainly validation studies
7 -- well validation studies are not very useful if they
8 don't determine at what point the method is no longer
9 valid and so the validation studies do find problems
10 with the kits, but in the process of doing a validation
11 study you limit the application of the technique then to
12 where you expect the valid result to be found.

13 So again, I think that the phrasing there might

14 be a little bit too simplistic and not quite give credit
15 to what goes on in a validation study, but the general
16 sentiment is something that I do agree with.

17 Q You are aware that there are numerous validation studies
18 that have been conducted concerning the COfiler-Profiler
19 kits, right?

20 A Yes.

21 Q And are you suggesting that in your opinion the numerous
22 studies that have been conducted still do not yet go far
23 enough in testing the limits of those kits?

24 A That is not what I'm suggesting. I'm suggesting that
25 those validation studies, at least those that are

DAN E. KRANE

662

1 designed well, are ones that determine -- are ones that
2 determine what the limits of the reliability of those
3 kits are and they do in effect have limits. It would be
4 unreasonable to expect that they have unlimited
5 reliability or capacity.

6 Q Right.

7 A Yes.

8 Q And in fact that's why laboratories do their own
9 internal validations, to test the limits of the kits and
10 they're going to use them within those confines and not
11 push them any further, right?

12 A Precisely.

13 Q That's what laboratories do?

14 A That's what they should do, yes.

15 THE COURT: Excuse me, Mr. Fristik. For the
16 benefit of all of us, but especially the court reporter,
17 let's take about 15 minutes right now.

18 MR. FRISTIK: Thank you.

19 (Short recess.)

20 THE COURT: Okay, Mr. Fristik, you were
21 proceeding with your cross-examination. Go ahead.

22 MR. FRISTIK: Thank you, Judge.

23 THE COURT: I think you were asking a question
24 about the Gross affidavit.

25 MR. FRISTIK: Right. Thanks, Your Honor.

DAN E. KRANE

663

1 BY MR. FRISTIK:

2 Q I want to continue with that, Dr. Krane. I was asking
3 you about item 19 on her affidavit. I want to go to
4 item 20 and just ask you about that.

5 Item 20 indicates: I have attended numerous
6 scientific meetings and seminars at which I shared
7 information with scientists and laboratories that use
8 the Profiler Plus and COfiler kits and the ABI 310. I
9 have never received any information concerning the
10 results obtained which would cause me to alter my
11 opinion that accurate and reliable DNA typing results
12 are obtained when using the kits and instruments.

13 Would you agree that statement she makes in her
14 affidavit?

15 A You know, I think my answer would be essentially the
16 same as my answer regarding point 19 --

17 Q All right.

18 A -- the general sentiment, but I think I might add or
19 change one word saying the results can be accurate and
20 reliable as opposed to essentially are accurate and
21 reliable.

22 Q In what way in your opinion might they not be reliable?

23 A It depends a great deal on the type of testing that's
24 being performed. Testing on mixed samples, for
25 instance, as I suggested, might be very open to

DAN E. KRANE

664

1 misinterpretation or prone to misinterpretation and as a
2 result might not be considered as accurate and/or
3 reliable. But certainly typing of known or pristine
4 reference samples, absolutely, this is a good method.

5 Q I know that you raised concerns about mixed samples. I
6 think you said that, and other witnesses have said that
7 mixed samples are a challenge, but that doesn't mean
8 that mixed samples can't be -- can't be typed and
9 interpreted, isn't that true?

10 A Well they certainly can be typed. Again it's the
11 interpretation that's very challenging and poses some
12 particular problems and for which I would say there is
13 not a general consensus or a commonly accepted solution
14 for how to deal with those problems. But again they

15 certainly can be typed and I would say typed reliably.
16 Q Finally item 21, if you'd refer to that. And item 21
17 indicates: I am aware that a significant amount of
18 research has been conducted and published by the
19 scientific community. As of today, and the date that's
20 referred to in the affidavit is April 17 of 2002, there
21 are 974 peer-reviewed articles listed on the NIST STR
22 website. I am not aware of any published articles that
23 question the reliability of the Profiler Plus and
24 Cofiler kits or the ABI 310.

25 Would you agree that statement?

DAN E. KRANE

665

1 A Well I feel I'm in a position to personally attest to
2 the number, 974. Actually in the previous testimony
3 that you'd alluded to there was some confusion that I
4 had about that number but I've since gone back and
5 confirmed that it is in fact, at least as of that date,
6 974.

7 Again, I think she may be painting with a bit
8 of a broad brush about any published articles that
9 question the reliability. Again, all these validation
10 studies, to some extent that's inherent to them, they're
11 probing the extent to which they're reliable and
12 different papers have reached different conclusions
13 about precisely where those end points are, so it's not
14 fair to say that none of them question the reliability.
15 I would say that the validation studies invariably

16 question the reliability. But nonetheless the consensus
17 seems to be that they can be used within certain
18 tolerance ranges to generate reliable typing results,
19 particularly with single-source samples.

20 Q And there are studies that not only reflect upon the
21 single-source samples but there are in fact studies that
22 focus on the mixed samples, right?

23 A Yes, there are.

24 Q And as a matter of fact you know that the BCA itself has
25 done a mixed sample study?

DAN E. KRANE

666

1 A Yes, and in fact in my original testimony, when this
2 trial first transpired as I understand it, I had quite
3 positive comments to say about that validation study. I
4 thought it was well done and as well as it could be
5 performed in sort of a clinical, sterile setting.

6 Q Why don't you take a look at Exhibit 3. Are you
7 familiar with that study, Dr. Krane?

8 MS. FUNK: I'm sorry, what exhibit number?

9 MR. FRISTIK: 3. It's the NIST 1 and 2.

10 THE WITNESS: Yes, I am.

11 BY MR. FRISTIK:

12 Q Now this was a study that was designed to test some
13 limits of the kits by looking at mixed samples, is that
14 right?

15 A Yes.

16 Q Okay. And turn to the conclusion, which would be the
17 last page, I think, or the second to the last page.

18 Are you there?

19 A I am.

20 Q Okay. And midway into that paragraph why don't you read
21 where it indicates, starting with the word "none." None
22 of the relatively few.

23 A It says: None of the relatively few analysis problems
24 encountered can be attributed to abnormal STR multiplex
25 performance; all DNA application anomalies reported are

DAN E. KRANE

667

1 associated with inefficient DNA extraction, inaccurate
2 DNA quantitation, and/or analytical threshold policies.

3 Shall I finish?

4 Q Go ahead, finish.

5 A Given an appropriate total amount of DNA in the reaction
6 mixture current STR multiplex systems reliably amplify
7 multiple-source DNA.

8 Q And do you know how many labs participated in NIST
9 Number One?

10 A I don't recall the specific number. It was a
11 substantial number, but over a dozen is my recollection.

12 Q And in fact in NIST 2 there was even more labs that
13 participated in that study is that correct?

14 A That's my recollection.

15 Q Would you agree then that the conclusions reached by
16 NIST 1 and 2 would be that there's nothing to indicate

17 that there's any problems with the COfiler and the
18 Profiler in resolving mixtures? Would you agree with
19 that statement based on what you're looking at here in
20 NIST 1 and 2?

21 A You know I don't think that's what the conclusions say
22 at all, that there's -- I think you said that there's no
23 problem or they suggest that there's no problem with
24 resolving mixture interpretations. That's not the case
25 at all. What the conclusions --

DAN E. KRANE

668

1 Q Maybe I misphrased the question.

2 MS. FUNK: Could he finish, Your Honor?

3 THE COURT: Well, it's an interesting situation
4 because he may be trying to answer a question that
5 wasn't asked or wasn't intended to be asked.

6 Why don't you ask another question,
7 Mr. Fristik, and then if the witness thinks it's
8 appropriate I'll let him amplify on it if he thinks it's
9 appropriate to do so in light of the former question.
10 Go ahead.

11 MR. FRISTIK: Thank you, Judge.

12 BY MR. FRISTIK:

13 Q Let me rephrase the question. Maybe I didn't clarify it
14 enough.

15 With respect to the COfiler and the Profiler,
16 those kits being able to resolve mixtures, the study

17 doesn't tell us that the use of those kits results in
18 any concerns or problems in resolving mixtures would you
19 agree that?

20 A There's one word that you said that I'm having a problem
21 with and that is resolve mixtures. Amplify the DNA in
22 mixtures I have no problem with. Generate genotypes for
23 mixtures I have no problem. But in terms of resolving
24 possible contributors to those mixtures, I think there's
25 substantial potential for problem.

DAN E. KRANE

669

1 Q And the resolution of the mixtures really isn't done by
2 the kits or the instrument, it's done by the analyst,
3 right?

4 A It's an interpretation issue, yes.

5 Q So the use of the kits themselves doesn't create
6 difficulties in interpreting mixtures. The kits are
7 doing what they're supposed to be doing, right? It's
8 the analyst, as I understand your answer, that may be
9 the problem in interpreting a result of these mixtures,
10 right?

11 A I would agree that there are -- there's considerable
12 room for problems with the analysts and I don't know
13 that it's fair to say the kits do as well as they could
14 in terms of providing the information that's available.
15 It might be -- I can imagine ways to design kits that
16 might give the analysts more information that would help
17 facilitate their interpretation and their analysis to

18 make it less likely to be problematic, but again, the
19 kits are performing as advertised.
20 Q Right.
21 A In the sense that they generate a genotype, they
22 generate genotypes with peak height differences that are
23 not necessarily as useful an indicator of mixtures or
24 contributors to mixtures as is sometimes assumed, but
25 the kits do not say that they should be interpreted that

DAN E. KRANE

670

1 way. Again, the analysts are the ones that are making
2 those interpretations.
3 Q Scientific analysis -- well, leave off the scientific.
4 Analysis of data by an analyst involves some
5 subjectivity, right?
6 A Well I suppose if you leave the scientific modifier off
7 it could, but in a scientific setting the objective is
8 to minimize subjectivity as much as is possible and in
9 fact to the point of eliminating it.
10 Q You were testifying about concerns relating to primer
11 binding site mutation and the primers are engineered or
12 designed to be compatible or bind with certain segments
13 of the DNA, correct?
14 A Very specific segments, yes.
15 Q Yes. And I think as you testified, you know, if there
16 was mutation at a particular location on the genome then
17 the primer's going to have -- not going to be able to

18 sit down or bind with that particular region of the DNA,
19 right?

20 A I think I was careful to say that it would have
21 diminished capacity or diminished specificity,
22 potentially to the point where it would no longer bind.

23 Q But it could?

24 A Well again, it's dependent upon the primers and the
25 primer binding sites. The longer the primer binding

DAN E. KRANE

671

1 site, the less problematic a single mutation would be.
2 But for a relatively short primer, 20 or 21 nucleotides
3 long, for instance, a single mutation could effectively
4 prevent the primer from binding to that site.

5 Q And your testimony, I think, was if the primer sequences
6 were known you could tell if the primer binding site
7 mutation is present; that's where you're having the
8 problem. Was that your testimony?

9 A I don't think that's an accurate specific
10 characterization.

11 Q What did you say?

12 A Knowing the primer binding sites would be an important
13 first step in conducting a study to determine if those
14 sites might be especially prone to mutation, and further
15 that if mutations were to occur at those sites the
16 relative likelihood that they would be problematic
17 because again, as I mentioned in the answer to my
18 previous -- your previous question, some mutations to

19 primer binding sites might not be as problematic as
20 other. Some can be completely devastating and some can
21 be somewhat innocuous. But in absence of the
22 information associated with the specifics of those
23 primer binding sites it's not possible to address that
24 issue in anything other than a conjectural way.
25 Q And are you saying therefore that that's why you need to

DAN E. KRANE

672

1 know the primer sequences?
2 A That's the -- from my background and perspective that's
3 the one thing that I would find interesting about the
4 primer sequences. There may be others who would have an
5 interest in them for other reasons, but for my
6 perspective that's what I would find particularly
7 interesting.
8 Q I want to ask you about that, that you would find it
9 interesting to know the primer sequences, but are you
10 saying it's not necessary to know the primer sequences?
11 A Necessary for what purpose?
12 Q Well versus interesting, you know?
13 A Well, you know again, I'm afraid necessary is too broad
14 of a term. In certain circumstances it would become
15 necessary. Certain -- to answer certain questions it
16 would transcend from interesting to absolutely necessary
17 to be able to get a reliable answer to that question.
18 So there are circumstances where it would be absolutely

19 essential. There are some questions for which knowing
20 the primer binding site is an absolute necessity.
21 Q But not knowing the primer sequences doesn't remove the
22 kits from their -- from being able to give accurate and
23 reliable results?
24 A Certainly the presumption is that what you say is
25 correct, but in the absence of the specific information

DAN E. KRANE

673

1 it's really not possible for me to give you an absolute
2 answer yes or no about that. Again, it's easy for me to
3 conceive of a variety of different types of mutations to
4 those primer binding sites that would in fact give rise
5 to unreliable STR testing results. How frequently that
6 is a problem in reality is still an open question
7 because I do not know nor does -- nor do others who are
8 interested in answering that question, have that
9 knowledge.
10 Q The forensic scientific community has not raised any
11 concerns about not knowing what the primer sequences
12 are, have they?
13 A I understand other scientists who have testified about
14 DNA testing and using these kits have in fact raised
15 those concerns in courtroom settings and so I would say
16 that forensic scientists have raised those concerns.
17 Q Who?
18 A Well, I suppose I would qualify in that sense.
19 Q Other than you?

20 A I understand that Professor Shields, who testified
21 earlier, has similar concerns.
22 Q Who else?
23 A Actually those are the only two that I have personal
24 knowledge of from listening to testimony and from having
25 observed, so I would leave it at that.

DAN E. KRANE

674

1 Q You and Dr. Shields and that's it as far as you know?
2 A That I have personal direct knowledge of, yes.
3 Q I mean seems to me that you would know if there were
4 others the more you interact with the forensic
5 scientific community, i.e., go to meetings, go to
6 symposia, go to poster sessions, you would learn that
7 stuff; if there were others out there expressing an
8 interest or concern in not knowing the primer sequences
9 you would hear those voices and you would interact on a
10 larger scale with the forensic community, wouldn't you?
11 A Well certainly, yes.
12 Q Okay. And finally one more question about primer
13 sequences and about primer binding site mutation. I
14 think that you would agree the statement that the primer
15 binding site mutation, to the extent that it does exist,
16 would never lead to a false positive result, is that
17 true?
18 A I don't think that that's a fair characterization. I'm
19 trying to think of a scenario in which it would not lead

20 to a -- it could not lead to a false characterization.
21 Again, what we're talking about here is a
22 misinterpretation of a DNA profile, an interpretation
23 that a profile is that of a homozygote individual as
24 opposed to a heterozygote individual. It's certainly
25 possible that the perpetrator of a crime was in fact

DAN E. KRANE

675

1 homozygous and a defendant was in fact heterozygous but
2 because of a primer binding site mutation appeared to be
3 homozygous at that locus. That would be a false
4 positive inclusion.

5 Q I asked you that question because isn't that how you so
6 testified in Hennepin County in State versus Kromah?

7 A Again, I think if you could refresh me with the context
8 and such. It's possible that my -- that I'm -- I have
9 thought of an example today that I have not before, but
10 if I could see the context that might help.

11 Q I'm showing you a portion of your cross-examination.
12 Your name's at the top, Dr. Dan Krane. This is
13 cross-examination from State versus Kromah. At the very
14 bottom, line 22, you were asked the question: And this
15 test would never give a false positive, would it? Your
16 answer: Primer binding site mutation would not provide
17 a false -- could not provide a false positive result.

18 Is that what you testified to?

19 A That is a direct quote, yes.

20 Q All right.

21 A Would it be all right if I just looked at the rest of
22 the context to help refresh my memory?

23 Q Sure.

24 MS. FUNK: I would object in he's only being
25 given one additional page. I read that transcript this

DAN E. KRANE

676

1 morning, Your Honor. My recollection is this is a
2 rather lengthy discussion. If Dr. Krane needs more than
3 that following page --

4 THE COURT: We'll see what he needs.

5 THE WITNESS: Well, and actually it does go on
6 to talk about an exception to a false positive. The
7 following question elicits an answer that talks about
8 lack of comparability perhaps between testing kits.
9 There are in fact two widely used testing kits; one
10 available by -- well, two different manufacturers. One
11 who has published their primer sequences and one who
12 has not. It's possible that the other manufacturer uses
13 different primer binding sites and would recognize --
14 would have primer binding site mutations that the other
15 kit did not have and that in turn could also result in
16 some false positives and another specific example would
17 be the one that I enumerated just a bit ago where a
18 sample could be mistyped because of a known allele being
19 dropped.

20 BY MR. FRISTIK:

21 Q So you would choose to qualify your answer in that way?

22 A Yes.

23 Q Okay. On that issue of the primer sequences that are
24 contained in the COfiler-Profiler kits as opposed to the
25 primer sequences that are in the Promega PowerPlex --

DAN E. KRANE

677

1 you're familiar with the Promega PowerPlex?

2 A That was the alternative manufacturer that I was
3 alluding to.

4 Q Right. Your understanding is Promega has released their
5 primer sequences?

6 A That is correct.

7 Q Is it also your understanding that Promega released
8 their primer sequences only after a court order told
9 them they had to do it?

10 MS. FUNK: Relevance, Your Honor.

11 THE COURT: Overruled.

12 THE WITNESS: I'm afraid I don't know what
13 prompted them to release those sequences. I do know
14 that they are available.

15 BY MR. FRISTIK:

16 Q You would agree, Dr. Krane, that the DQalpha and the
17 Polymarker kits came to be accepted in the forensic
18 scientific community as providing valid and reliable
19 results, is that true? Would you agree with that?

20 A Again I would say that the results can be considered
21 reliable, but again there's the potential of problems

22 with the interpretation and perhaps the presentation of
23 the significance of those results. But certainly the
24 tests themselves do as they say they will do.
25 Q And you never knew -- I mean the scientific community

DAN E. KRANE

678

1 never knew what the primer sequences were in the DQalpha
2 and Polymarker kits, did they?
3 A Not to my knowledge, no.
4 Q And that's also true with the -- with the ABI -- the CTT
5 kit, the blue kit. You never knew what the primer
6 sequence were there, did you?
7 A I don't believe so. Not that I know.
8 Q And that kit was validated in numerous areas, in
9 numerous studies which showed that it gives reliable and
10 valid results, right?
11 A Yes.
12 Q Okay. It strikes me that your biggest concern in this
13 area of PCR-STR technology as it's used for forensic DNA
14 typing lies with the analyst who's giving the
15 interpretation. It's not so much with the instrument
16 and the kits, your biggest concern is with the analyst
17 who's doing the interpretation, is that a fair
18 statement?
19 A I think you characterized what I've testified to today
20 quite well, yes. That's correct.
21 Q Okay. I mean after all, let me go through a couple more

22 things here to kind of cement in what I'm talking about.
23 You know that the kits, the COfiler and Profiler, are
24 being used worldwide? As a matter of fact they're being
25 used to identify the victims of the World Trade Center

DAN E. KRANE

679

1 disaster, do you know that?

2 A Yes?

3 Q They were used to identify the remains of the Swiss
4 aircraft off Nova Scotia a few years ago?

5 A Yes.

6 Q They're used in a medical setting in bone marrow
7 transplants, did you know that?

8 A Quite well, yes.

9 Q Okay. Bone marrow transplants can involve, at times,
10 life and death decisions and they're relying on the
11 results of these kits to make those decisions, right?

12 A They do indeed.

13 Q Let me ask you --

14 A Perhaps just to help you, the primer binding sites --

15 Q Wait a minute, I don't have any question any more.

16 We're going to move on to something else.

17 Let me ask you about, you had a rather lengthy
18 discussion, put up some overheads, that focused on the
19 BCA population databases. What's your concern? Can you
20 give it to me in a nutshell? What's your concern about
21 BCA's population databases?

22 A I'd like to include all the things in the nutshell that

23 I can, so as briefly as I can, I think that the alleles
24 that are represented in that database may not be a fair
25 representation of the general population that it was

DAN E. KRANE

680

1 intended to represent and as a result it raises some
2 interesting questions about mixture interpretations and
3 also raises some important questions about the
4 reliability of inferences from those frequencies such as
5 those that come from a product rule calculation or some
6 of the alternative calculations, that the underlying
7 numbers that are being used in those statistical
8 calculations are not reliable, the final statistics also
9 have some lack of reliability as well.

10 Q And you came to this conclusion, as I understand it, by
11 employing or importing your biometrics or what's it
12 called?

13 A Bioinformatics.

14 Q By bioinformatics? You came to this conclusion by
15 employing your bioinformatics technique to analyze their
16 population data, is that right?

17 A I wouldn't say call it a bioinformatic technique, I'd
18 call it a tool, much like the tools in molecular
19 biology. We used some of the tools that are available
20 in the discipline of bioinformatics to analyze that
21 data, yes.

22 Q Doctor, with the concerns you expressed, being that you

23 believe or you have concerns that the alleles may not be
24 a fair representation of the populations that they were
25 intended to represent and that this may raise questions

DAN E. KRANE

681

1 regarding mixture interpretations and frequency
2 calculations, those are some big concerns, aren't they?
3 You'd agree this is a major concern?
4 A That's why I felt it was helpful and necessary to have
5 the opportunity to talk about them today, yes.
6 Q Being a member of the forensic scientific community as
7 you kind of said earlier that you kind of think you are,
8 don't you think that it would be important to let the
9 rest or others in the forensic scientific community know
10 about those major concerns you have about the BCA's
11 population database?
12 A I wholeheartedly concur, and I wish --
13 Q Have you told anybody what your concerns are?
14 A I would hope this venue is one means of communicating
15 this information to them and I would like to publish it
16 in a broader arena so other forensic scientists can see
17 the perils associated with the presumption that four or
18 fewer alleles across as many as 12 loci is evidence of
19 only two contributors to a sample, but I'm actually,
20 when I was provided with the data by the BCA, was
21 specifically prohibited and forbidden from publishing
22 any analyses that I performed upon those databases. And
23 I'm hoping that in this public forum, where I'm being

24 asked direct questions about them, that perhaps we're
25 moving toward an opportunity for me to publish them in

DAN E. KRANE

682

1 the a broader forum so that the general scientific
2 community can be made more of aware of this. Because I
3 agree, this is a potentially very important issue that I
4 think the forensic science community would be intensely
5 interested in knowing about.

6 Q Okay. Wouldn't you want to begin, though, by composing
7 a letter and sending it to the BCA? Wouldn't that be a
8 good place to begin? I appreciate that because of
9 restrictions that may have been imposed upon you by the
10 BCA your efforts to publish are limited or maybe
11 nonexistent, but wouldn't you want to at least write a
12 letter to the BCA? I mean I know this is a public forum
13 here but, you know, wouldn't it make sense to write a
14 letter to the BCA and say I looked at this stuff and
15 these are my concerns. Hey, I'm a forensic scientist
16 and you guys are forensic scientists, gosh darn it,
17 these are my concerns. Here. Have you done that?

18 A I think it's an excellent idea and frankly if I had had
19 these results more than a week or so ago I would have
20 done that very thing. And actually as I sit and think
21 about the need to publish these results, that's going to
22 be one of the steps that we'll take. I intend to
23 contact the BCA, unless I can find an alternative data

24 set that's more easily available to me, I will contact
25 the BCA and inquire as to whether or not they would be

DAN E. KRANE

683

1 receptive to being a co-author or a participant in the
2 study because, frankly, I think it would lend more
3 credibility in the forensic science community if a
4 number of people got on board and pointed out this
5 problem as opposed to a lone individual such as myself.

6 Q So you do intend to write a letter to them?

7 A In time as my schedule permits. Certainly if we publish
8 any results based on this study I would -- I would, as a
9 point of honor, want to give the BCA an opportunity to
10 participate in the study more directly and that would
11 come by way of either a phone call or a letter in which
12 we describe those results.

13 Q Would you copy me on that letter, too?

14 MS. FUNK: Your Honor, I think we're getting
15 beyond the testimony of this hearing.

16 MR. FRISTIK: I'll withdraw the question.

17 BY MR. FRISTIK:

18 Q You're aware of the fact that the BCA's population
19 databases have been validated, though? You know that?

20 A I testified to that, yes.

21 Q But now that you've run these new computations you're
22 finding problems with their database, right?

23 A Now that we're employing a much more sensitive and
24 powerful technique than what had been available in the

25 past we're finding what's potentially a problem, yes.

DAN E. KRANE

684

1 Q Do you intend to offer your technique to others in the
2 forensic scientific community so they can employ it in
3 looking at their individual databases in their
4 laboratories?

5 A I would be delighted to employ it on any database where
6 there was an interest in having us use it.
7 Computationally it takes approximately a day to do that
8 three-way mixture simulation with 649 individuals, so we
9 might not be able to take care of them all, you know,
10 right away but I think that would be an extremely
11 important service and I'd be delighted to be able to
12 provide it.

13 Q Maybe at the next Promega International meeting? Or you
14 don't go to those?

15 A Those are difficult for me to fit into my schedule
16 because of my teaching and the times they have those
17 particular meetings, but again I think intrinsic to any
18 publication we would have we would include such an offer
19 as part of a publication in a peer-reviewed journal and
20 that should be a sufficient way to get the message out
21 to the broader community.

22 Q Did you testify -- I know you testified about
23 Hardy-Weinberg and linkage equilibrium. I don't
24 remember what you said. Did you say that the BCA's

25 population databases are -- they shouldn't be using

DAN E. KRANE

685

1 those corrections?

2 A Not so much a correction as a test for population
3 substructure. There's certainly, well, you know those
4 would be the first tests that come to mind to anybody
5 whose taken a population genetics course, but again
6 those are not the most powerful tests that are available
7 and certainly what we've got available to us now is
8 substantially a more powerful statistical test.

9 Q You know that those, I believe, those are the ones
10 recommended by NRC-2, right?

11 A Again because those are fairly simple to implement and
12 certainly at the very least a database should meet that
13 threshold, but in the absence of a more powerful,
14 readily accessible test, that was all that was
15 available.

16 Q Finally, Dr. Krane, in your opinion is PCR-STR as it's
17 used for forensic DNA typing a generally accepted method
18 in the forensic scientific community?

19 A As I've been saying, I think the methodology is
20 generally accepted. There may be problems with the
21 interpretation and the presentation of those
22 interpretations, but the underlying techniques I would
23 say are sound.

24 MR. FRISTIK: Thank you. Nothing further.

25 THE COURT: Redirect?

1

2

REDIRECT EXAMINATION

3 BY MS. FUNK:

4 Q

Dr. Krane, let's talk about the interpretation. Is there a single analyst problem or is this a sort of forensic lab wide interpretation problem as you see it?

7 A

I would say more of a forensic lab wide type of problem as opposed to a specific individual.

9 Q

Do you have some validation studies that you could point to that would support that, Dr. Krane?

10

11 A

Well the NIST studies actually speak to misinterpretations of mixed samples where forensic DNA testing laboratories arrived at known-to-be erroneous conclusions about the contributors to mixtures.

14

15 Q

Are you also aware, Dr. Krane, of a study done by Carll Ladd on this issue?

16

17 A

I've spoken with Carll Ladd about a study on this type of issue. I actually have on my computer his PowerPoint presentations on this issue. And it has been presented to me or purported to me to be essentially something of a NIST 3 study that has not yet been completed or published.

22

23 Q

Okay. And Dr. Krane, I believe that you have Exhibit 3, the NIST study, up there with you, is that right?

24

25 A

I do.

- 1 Q And I'd ask you to turn to the second to the last page,
2 okay?
- 3 A I'm there.
- 4 Q Just above the conclusion where Mr. Fristik had you read
5 into the record the references to problems associated
6 with interpretation which included inefficient
7 extraction, inaccurate quantitation and/or analytical
8 threshold policies, I'd like you to look above that
9 where the heading is policy issues?
- 10 A Yes.
- 11 Q I'd ask you to read that first paragraph just to
12 yourself.
- 13 A I've read it.
- 14 Q Okay, and is it fair to say that this particular
15 paragraph expresses some concern about stutter peaks?
- 16 A That's a fair characterization, yes.
- 17 Q We've had some extensive definitions provided about what
18 stutter is but could you read for us the last sentence
19 of that paragraph?
- 20 A It reads: In any case, we believe some consensus policy
21 on the evaluation and reporting of stutter would benefit
22 the entire forensic community.
- 23 Q And is that because stutter can make interpretation a
24 difficulty in a mixture?
- 25 A Absolutely, yes.

1 Q And would you agree as a scientist that were there a
2 consensus policy in the forensic scientific community
3 about stutter that that would resolve some of the issues
4 involved in mixture interpretation?

5 A It would resolve a large fraction of them, yes.

6 Q Looking at the next paragraph, Dr. Krane, I'll give you
7 a chance to read it first.

8 A I've read it.

9 Q All right. First it begins by talking about -- why
10 don't you tell us. Could you summarize the concerns of
11 this paragraph for us?

12 A Well, it seems in general it's talking about problems
13 associated with what would be peak height imbalance, the
14 fact that alleles are not always associated with
15 fluorescence or RFU's that are consistent with their
16 relative abundance in a sample.

17 Q And does it express any concerns? Why don't we skip
18 down to the last sentence of that paragraph and could
19 you read that into the record?

20 A Sure. It's something of a conclusion of sentence. It
21 reads: When multiple interpretations cannot be
22 excluded, "moderate stringency" profiles unique where
23 possible and explicitly describing the ambiguities where
24 required should be specified.

25 Q If that was the standard across the board in the

1 forensic scientific community when it came to presenting
2 the typing results in terms of interpreting those
3 results, do you believe that that would go at least some
4 way towards resolving the concerns that you have about
5 the current interpretation in mixed samples?

6 A I think they would -- that speaks explicitly to the
7 concerns I've been raising today to a large extent, yes.

8 Q Okay. Finally looking at that last paragraph of this
9 study, the National Institute of Science and Technology
10 -- I'm sorry, I'll give you a chance to read it.

11 A I've read it.

12 Q Okay. The National Institute of Science and Technology
13 actually expresses surprise at the number of
14 participants who indicated that they were unable to read
15 a mixed sample without a reference sample -- excuse me,
16 I mischaracterized that. Surprised at the number of
17 participants who indicated that providing a genotype or
18 specifying a profile in the absence of a reference
19 sample was against their laboratory's policy.

20 Are you also surprised? Well, are you
21 surprised that there are laboratories that use reference
22 samples in interpreting mixtures?

23 A Perhaps I've become cynical, but I've encountered that
24 on a number of occasions. I think it is an appalling
25 practice that is, to some extent, putting the cart

1 before the horse in terms of these analyses. It's
2 tantamount to saying unless you tell me what the answer
3 should be I won't venture a guess or draw my own
4 conclusion because I'm afraid that my answer might be
5 inconsistent with yours and I'll be proven to be wrong.
6 That's not good scientific practice.

7 Q And illustrated in your presentation where we were
8 talking about any number of combinations of individuals
9 who could contribute to a mixture, if a known suspect
10 was provided as one of those combinations, perhaps is it
11 true in a lab that uses known samples to declare
12 genotypes in mixed samples there would be a strong
13 temptation to declare that particular profile as opposed
14 to any other possible profiles that could be in that
15 mixture.

16 A I agree.

17 Q And would you agree that this study not only expresses
18 concerns about the practice of interpreting mixed
19 samples but also offers some suggested solutions as to
20 how to avoid misinterpretation in the future?

21 A We've spoken about three of them in the paragraphs that
22 I've just been asked to read.

23 Q Okay. And now, Dr. Krane, it came to my attention that
24 there was an overhead that you had prepared that we
25 didn't discuss and I'd just ask you to put it up there

1 briefly, if you would.

2 A It actually speaks to the issue of analysts's discretion
3 in these interpretations.

4 Shall I talk about it?

5 Q Please. Perhaps you could provide the title first.

6 A Unfortunately I didn't put titles on these, but it shows
7 four panels essentially with original data being the
8 words first on the upper left and randomized data
9 average being in the upper right. And the bottom part
10 is talking about consideration of different -- well, let
11 me tell you what the bottom part is. Again there's this
12 use of alleles where loci would have been more
13 appropriate, so let me make that correction here.

14 But it, again, I think this really speaks to
15 the issue of how the ability of an analyst to invoke
16 some discretion or flexibility in their interpretation
17 as opposed to using very objective rigorous guidelines
18 can dramatically compound a problem. I had earlier been
19 testifying that, again, there are over two million
20 three-way mixtures of known individuals in the Minnesota
21 database that, when combined, give a mixture profile
22 that has four or fewer alleles across all 12 loci that
23 were typed.

24 Well, if an analyst were to observe a profile
25 that had four or fewer alleles across 11 of 12 loci, but

DAN E. KRANE

1 perhaps five at a twelfth locus, many laboratories'
2 guidelines would allow an analyst to exercise their
3 discretion and say that that fifth allele at the twelfth
4 locus was most likely to be an anomalous result. If I
5 could put quotation marks around anomalous, because in
6 reality it might be reflective of a third contributor
7 but if the analyst is presuming, as the general forensic
8 science community seems to presume, that three-way
9 mixtures with four or fewer allele across 12 loci are
10 exceedingly rare to the point of being hypothetically
11 possible but not realistic to ever encounter, unlike
12 seeing over 2.5 million of them in this one database
13 that we've tested, if exercising that discretion, saying
14 that it's unreasonable that there would be only one
15 locus with five or six alleles if there were three
16 contributors, there should be been two or three
17 therefore the one with the five or six must be some sort
18 of anomaly, the result of a technical artifact --

19 Q Like stutter?

20 A Conceivably stutter or any of a number of other kinds of
21 technical artifacts, if they're allowed to discard that
22 one anomalous result, now the false classification would
23 go from 2,505,650 to 11,566,249. Such that it's now
24 approximately a quarter of the possible mixtures that
25 were actually three-way mixtures might be misinterpreted

DAN E. KRANE

1 as a two-way mixture.

2 So again, I think this really illustrates how
3 there needs to be extraordinary caution in allowing
4 analysts to use discretion or nonobjective measures or
5 methods for interpreting these results. It can give
6 rise to essentially a large number of mistaken
7 interpretations, literally millions of mistaken
8 interpretations that would not have occurred in the
9 absence of that ability to exercise the discretion.

10 Q Okay, thank you. And as to, Mr. Fristik asked you about
11 how many forensic scientists you could name. I'm not
12 going to ask you to name any scientists, Dr. Krane, but
13 I'm going to ask you how many scientists do you
14 personally know? Approximately?

15 A Oh a few hundred. Maybe a hundred fifty.

16 Q And how many of those people that you know who are
17 scientists would find the refusal to release scientific
18 data and the insistence upon keeping it secret to be an
19 accepted scientific practice?

20 A A very small number. That's generally considered
21 exceptionally bad form in the scientific community.

22 MS. FUNK: Thank you. I don't have any further
23 questions.

24 THE COURT: Recross?
25

DAN E. KRANE

694

1

RECOSS-EXAMINATION

2 BY MR. FRISTIK:

3 Q Was that statement you just made that there can be
4 millions of mistaken interpretations in mixtures? Is
5 that what you said?

6 A If an analyst is allowed to exercise discretion
7 regarding the number of contributors to a mixture and
8 further exercises discretion about what they perceive to
9 be anomalous results, that can easily result in a large
10 fraction of the interpretations being made incorrectly.

11 In the specific instance of the analyses that I
12 was talking about where there were a total of 45,349,524
13 possible different three-way mixtures, that combination
14 of instances would have resulted in as many as
15 11,566,294 mistaken inferences or incorrect conclusions.

16 Q You're referring to the data that you looked at from the
17 BCA?

18 A Yes.

19 Q So you've identified by crunching these numbers 11
20 million mistakes they've made in interpretation of data?

21 MS. FUNK: Objection. That's a total
22 mischaracterization.

23 THE COURT: He's asking a question. He's
24 asking for clarification.

25 THE WITNESS: That is not a fair

DAN E. KRANE

695

1 characterization. It's the potential for that many

2 mistakes --

3 BY MR. FRISTIK:

4 Q It's the potential?

5 A -- given misunderstandings about the relative frequency
6 of three-way mixtures that have four or fewer alleles
7 across 12 loci, and again that seems to be very standard
8 practice for that to be considered to be a very rare
9 phenomenon whereas with the real data set we see that
10 happens at least 5.5 percent of the time that three-way
11 mixtures might occur, and then compounding that with an
12 analyst's discretion or the ability of an analyst to
13 exercise discretion about a single, what they perceive
14 to be a single anomalous result, if they're allowed to
15 discount just one anomalous result and attribute it to a
16 technical artifact such as stutter or pullup or any of a
17 number of other technical artifacts, that dramatically
18 compounds the possibility that an error would be drawn
19 in the terms of the number of contributors to a mixture
20 such that it goes from 2,505,650 to, in this instance,
21 11,566,294.

22 Q Seems to me that you're not taking into account, and
23 maybe you are and maybe you just don't like the way it's
24 done, but you're not taking into account what a
25 laboratory has done to not only validate the use of the

DAN E. KRANE

696

1 kits and the equipment and the instruments but the
2 protocols that they've established for their analysts to

3 identify things like artifacts, stutter, and those type
4 of things and to recognize that and to know when it is
5 stutter and when it's not a true allele and you're not
6 giving enough credit to the analyst who's been trained
7 and experienced in interpreting this data, which they
8 have to do; that you're simply not crediting them in
9 their professional ability to do do that. You're saying
10 they're not capable of doing that. Is that a fair
11 statement?

12 A I would say, again, that the validation studies speak
13 quite a bit about the reliability of the underlying
14 methodology but again, the interpretations are a
15 separate issue. And I understand that there's been
16 testimony given in this hearing by another forensic
17 scientist that three-way mixtures with four or fewer
18 alleles across 12 loci, while hypothetically possible,
19 are exceedingly unlikely, or something to that effect.
20 That, in my survey and attempts to get a feel from the
21 rest of the forensic sign community, seems to be a very
22 commonly held opinion that influences interpretations
23 and I have presented here evidence that that is a
24 substantially incorrect basis upon which to make an
25 inference and therefore the interpretations that would

DAN E. KRANE

697

1 arise from it have the potential to be erroneous as
2 well.

4 spelling your last name for the record, please.

5 THE WITNESS: Sure. My whole is name is
6 Laurence Dochez Mueller, the last name spelled
7 M-u-e-l-l-e-r.

8 THE COURT: Ms. Funk please.

9

10 DIRECT EXAMINATION

11 BY MS. FUNK:

12 Q Dr. Mueller, where are you currently employed?

13 A I'm a professor at the University of California at
14 Irvine.

15 MS. FUNK: If I could approach the witness,
16 Your Honor?

17 THE COURT: Yes.

18 BY MS. FUNK:

19 Q Showing you what's been marked as Exhibit 27, do you
20 recognize this, sir?

21 A Yes.

22 Q Would you tell the Court what it is, please?

23 A It's a current copy of my curriculum vitae.

24 MS. FUNK: I would offer Exhibit 27, Your
25 Honor.

LAURENCE D. MUELLER

699

1 MR. FRISTIK: No objection.

2 THE COURT: 27 is received.

3 BY MS. FUNK:

4 Q Dr. Mueller, could you tell the Court your educational
5 experience, please?

6 A Sure. I was an undergraduate at Stanford University in
7 1974. I graduated with a Bachelor of Science in
8 chemistry and a Master's Degree in biology. Then from
9 1975 to 1979 I was a graduate student in the department
10 of genetics at the University of California-Davis and in
11 '79 graduated with a Ph.D. in the general field of
12 ecology. Then from 1979 to 1983 I was a postdoctoral
13 fellow back at the department of biological sciences at
14 Stanford University. During that period I worked on a
15 variety of problems in theoretical population genetics.

16 Q And how long have you been at the University of
17 California at Irvine?

18 A Since the summer of 1988.

19 Q And prior to that were you employed at another
20 university?

21 A Yes.

22 Q Could you tell us about that?

23 A My first faculty position was at Washington State
24 University in the program in genetics and the department
25 of zoology. That was from 1983 to 1988. And I was an

LAURENCE D. MUELLER

700

1 assistant and then later an associate professor there.

2 Q Doctor, I see on your CV you list outside referee and
3 then you list a series of publications. Could you just
4 define for us what an outside referee is?

5 A Sure. In science referees are used to review both
6 scientific papers that are submitted to journals for
7 publication and they're also used to review grant
8 applications to different agencies that have money to
9 give to people. Anyway, the purpose of the referee is
10 to look at, in the case of scientific publications, the
11 research, the conclusions reached, the information that
12 was used to reach those conclusions, and then make
13 recommendations that the editor of the journal can use
14 to decide whether to publish a paper or not or ask for
15 revisions.

16 With a grant application the referee serves a
17 similar function, although this isn't about completed
18 work but proposed work, and based on those reviews again
19 the granting agencies decide who will get money to do
20 research.

21 Q Okay. And then you've listed those journals and places
22 where you do outside referee work, is that right?

23 A Yes.

24 Q Also reflected in your CV is, it indicates review
25 panels. Could you tell us what that is, a review panel?

LAURENCE D. MUELLER

701

1 A Sure. In some cases granting agencies, like the
2 National Science Foundation, will just send me and other
3 people a grant to review, which we do and send back the
4 review. In other instances organizations like the

5 National Science Foundation or the National Institutes
6 of Health will convene panels of scientists to review
7 many grants and the panels may even have access to these
8 outside reviews in making their deliberations. So I've
9 been on several panels at the National Institutes of
10 Health, mostly in the Institutes of Aging and also in
11 the Population Biology Panel for the National Science
12 Foundation.

13 Q And you've also listed research articles that you've
14 published in your CV?

15 A Yes, I have.

16 Q We haven't had discussions about many of the ones that
17 are listed here. Are these, for the most part,
18 peer-reviewed journal publications?

19 A Of the 70 or so publications there's probably about two
20 or three that were not peer reviewed, but all the others
21 are.

22 Q Okay. Now there's been a little confusion about this
23 with some of our other Ph.D.'s. I see yours is in
24 ecology. Does that make you an ecologist, Dr. Mueller?

25 A Well some of my research certainly overlaps into that

LAURENCE D. MUELLER

702

1 field. At a place like the University of
2 California-Davis there are many different kinds of
3 programs that confer Ph.D.'s. Within those programs,
4 though, there's oftentimes very diverse types of
5 research. So as it turns out I worked in the genetics

6 department. My research was on genetic changes that
7 accompany life in different densities. So it had both
8 an ecological component but certainly had a population
9 genetic and evolutionary component to it. As it turned
10 out the degree-granting organization at UC-Davis only
11 gave out degrees in ecology, so that's the name of my
12 degree, but doesn't certainly describe very precisely
13 the kind of research I was doing.

14 Q What title would you give to the kind of research that
15 you do now?

16 A Well, it is in several fields but certainly population
17 genetics is the primary area of my research but that's
18 related to evolution and I also do work in population
19 biology.

20 Q Okay. And as a professor at the University of
21 California at Irvine could you tell us what your
22 responsibilities or job duties are and how you divide
23 your time?

24 A Well, generally all professors do research, teaching,
25 and service. The research obviously is under their own

LAURENCE D. MUELLER

703

1 direction and, as I said, I do research in population
2 genetics, evolutionary biology.

3 The teaching is both at the undergraduate and
4 graduate level and I also have undergraduates and
5 graduate students that do work in my lab.

6 Service is basically within the university
7 service and also the university considers things like
8 what I'm doing today is a service activity where their
9 faculty members who have expertise do work or consult
10 outside of the university.

11 Q You've referenced a lab. Could you tell us a little bit
12 about what goes on in your laboratory?

13 A In my lab currently what -- the kinds of things we do is
14 we look at experimental evolution, we put populations in
15 different conditions and watch how they change, and
16 change can be measured in many ways. It can be measured
17 at a visible level, that is with traits you can measure
18 like a behavior or other physical characteristics, or we
19 can also look at underlying genetic changes and in my
20 lab we're doing both of those. Some of the genetic work
21 I do in conjunction with other colleagues that have labs
22 that are set up to do more detailed types of genetic
23 analysis. But that's the kind of stuff we do. The
24 experimental populations we use are a species of insect
25 known as the fruit fly which has been used almost the

LAURENCE D. MUELLER

704

1 last hundred years for genetic research.

2 Q Do you do DNA testing in your laboratory?

3 A I do not, no.

4 Q Okay. Could you explain to us how the principles of
5 population genetics can be applied to forensics?

6 A Sure. Well certainly forensic DNA typing as a field can

7 really be broken down into two intellectual disciplines;
8 one we would call molecular genetics or molecular
9 biology. It's the principles and methods of molecular
10 genetics that help us how to decide how to isolate DNA
11 from evidence samples, how to visualize genetic patterns
12 that are there, and then how to compare those patterns
13 and different samples and make some conclusions or
14 inferences about possible identity and other things.

15 However, once that process has been gone
16 through, and let's say in a typical sample where
17 identity is an issue, it's been decided that two samples
18 may be from the same source, we need then to borrow from
19 the principles and techniques of population genetics to
20 assess how rare or common that genetic pattern is that
21 we're using to identify a person is. After all, there
22 are many characteristics that can be used that are
23 genetic in origin to identify people, some being more
24 useful than another.

25 As an example, a person might see a criminal at

LAURENCE D. MUELLER

705

1 a crime scene, see he has brown hair, and a suspect may
2 also have brown hair and hair color is determined by our
3 genes if it hasn't been altered and in that instance you
4 have a form of identification but we know it's not
5 terribly useful since lots of people in this country can
6 be described as having brown hair. At the same level

7 just saying two DNA patterns match or are consistent
8 with each other doesn't tell us much until we go one
9 step further and say how many people might have had that
10 genetic pattern or be identified as having that genetic
11 pattern.

12 Q Have you been involved with other cases in the court
13 system that involved the use of DNA?

14 A Yes.

15 Q And statistical calculations?

16 A Yes.

17 Q And during the course of the involvement you've had,
18 have you had the opportunity to review the database from
19 the Bureau of Criminal Apprehension in Minnesota?

20 A Yes.

21 Q Have you -- and are you personally aware that that
22 database has been subject to the Hardy-Weinberg
23 analysis?

24 A Well it's been tested for agreement with Hardy-Weinberg
25 and linkage equilibrium, yes.

LAURENCE D. MUELLER

706

1 Q Are you aware of the results that were arrived at by
2 Dr. Carmody?

3 A Yes, I reviewed a document he prepared summarizing his
4 results.

5 Q Are you in agreement with his results?

6 A Not entirely, no.

7 Q And could you tell us what your concern -- let me ask

8 you this: Have you testified before today about your
9 thoughts on the BCA's database in regards to
10 Hardy-Weinberg and linkage equilibrium?

11 A Yes, I have.

12 Q And your views on the BCA database are not particularly
13 secret, is that fair to say?

14 A Sure.

15 Q Could you tell us the concerns that you have with that
16 database?

17 MR. FRISTIK: Objection, Your Honor. Renew my
18 objection. Relevance. Beyond the scope of this
19 hearing.

20 THE COURT: I understand your objection.
21 Objection's overruled. You may answer the question.

22 THE WITNESS: So I've also examined the BCA
23 databases for these two major principles of independence
24 which have names from the theory of population genetics.
25 One form of statistical independence is known as the

LAURENCE D. MUELLER

707

1 Hardy-Weinberg Law. That's a description of how genetic
2 markers at a single gene location behave in a
3 population. And the second principle of independence is
4 called the condition of linkage equilibrium and that's a
5 description of how genetic markers at different gene
6 locations interact with each other within a population.

7 It's really the second form of independence

8 where my conclusions differ from Dr. Carmody's because
9 in both the BCA Caucasian and the BCA Indian database,
10 that is Native American database, I have found, applying
11 statistical tests that are really the best ones around,
12 significant departures from independence, meaning that
13 the properties of the population are not those that we
14 would expect if the population indeed was behaving as
15 this principle called linkage equilibrium required.

16 As a result any methodology that relies on
17 multiplying frequencies across multiple genetic markers
18 is dubious because that key assumption appears to be
19 violated, certainly in those two databases. And the
20 black database gave no indication of this in the BCA's
21 sample, but Caucasians and Indians did.

22 BY MS. FUNK:

23 Q Now were you referring to the product rule or were you
24 referring to any -- we've talked about the product rule
25 as well as the probability of exclusion. Both of those

LAURENCE D. MUELLER

708

1 involve multiplication, is that right?

2 A That's right.

3 Q Of the allele frequencies found in a sample?

4 A That's correct.

5 Q And are you saying that the fact that there was not
6 linkage equilibrium in the Caucasian and the Native
7 American databases, your position is and has been that
8 it's inappropriate to use either of those statistical

9 calculations with those particular databases?

10 A Right, they both rely on the essential elements of the
11 product rule which are multiplication across multiple
12 loci, multiple genetic markers. The probability of
13 exclusion simply does that over many different genetic
14 patterns whereas the standard product rule does that to
15 just one genetic profile or pattern.

16 Q You indicated that you discovered this by using a
17 statistical test which I believe you characterized as
18 one of the best ones around. Could you tell us what
19 statistical test you applied?

20 A The name of the test, it's called the exact test. Its
21 properties were actually compared to several other kinds
22 of tests of independence by Bruce Weir in a paper --
23 Bruce Weir and some of his colleagues, in a paper in
24 1995 in the journal *Genetica*, and it was found that this
25 particular test had properties that were superior to the

LAURENCE D. MUELLER

709

1 others. And one of the important properties of this
2 test is that if in fact a population did not conform to
3 actually either Hardy-Weinberg or linkage equilibrium
4 the exact test would be more likely to discover that
5 than many of the other existing tests; that that could
6 also be used to look at this problem.

7 Q Are you aware that Dr. Carmody recognized that there
8 were some problems with the Minnesota database?

9 A Yes.

10 MR. FRISTIK: Objection to that question as
11 leading.

12 THE COURT: Overruled. It seems to be moving
13 to a slightly different topic. Go ahead.

14 BY MS. FUNK:

15 Q Are you aware that he offered a way to fix that?

16 A Yes.

17 Q Could you tell us about what you know about that?

18 A Well, he made the suggestion, which is also similar to
19 what the second NRC committee suggested, that certain
20 genetic patterns or profiles called homozygotes, we
21 could alter their frequency with a parameter called
22 theta and in his mind applying that type of mechanism or
23 correction to the product rule would overcome any
24 difficulties that might be there.

25 I can talk more about that, but that was the

LAURENCE D. MUELLER

710

1 essentially his suggestion for fixing some of the
2 problems he saw. I don't agree with it, but
3 nevertheless it's what he suggested.

4 Q And why don't you agree it?

5 A Well, the application of this correction, and this was
6 discussed and pointed out in NRC-2, will fix problems of
7 independence within single genetic markers, that is the
8 things we called the Hardy-Weinberg equilibrium, because
9 the major phenomena that may cause departures from

10 Hardy-Weinberg always result in errors in one direction.
11 They tend to make the homozygotes too rare and the
12 heterozygotes more common than they should be. So the
13 theta factor will inflate the frequency of these
14 homozygotes thus avoiding producing a statistic that's
15 rarer than it should be.

16 The problem is that the issues that I had with
17 the BCA didn't involve Hardy-Weinberg, they actually
18 involved this other form of independence known as
19 linkage equilibrium. That problem can't be fixed simply
20 and it certainly can't be fixed by theta. Theta doesn't
21 deal with departures from linkage equilibrium. So it's
22 a much thornier problem to get at and in fact all of the
23 dialogue and NRC-2 says assuming there is no departure
24 from linkage equilibrium we can do the following to fix
25 any problems with Hardy-Weinberg. So even NRC-2

LAURENCE D. MUELLER

711

1 realizes that theta doesn't fix those problems. So
2 that's why I don't see this as a solution to the kinds
3 of problems I observed.

4 Q How long have you been aware of this problem with the
5 lack of linkage equilibrium in the Minnesota database?

6 A I'm trying -- I probably did this analysis on their
7 database a couple of years ago.

8 Q Okay. Did you have any thoughts over the last couple
9 years as to how this could be explained?

10 A Sure. I mean this is an issue I've thought about a lot
11 over the last 12 or 13 years, so sure, I've thought
12 about why it might be that the BCA or any population
13 database used in forensics might not conform to these
14 rules.

15 Q Could you give us some possible explanation?

16 A Sure. Well, one which -- the explanation that's often
17 offered, which is a biological explanation, so it has
18 some real, you know, sort of biological meat to it, is
19 the notion that a population like US Caucasians is not a
20 single homogeneous genetic entity but in fact is a
21 collection of peoples from different areas of Europe and
22 maybe even North Africa which are themselves genetically
23 different from either other, at least for the genetic
24 markers used here. And it's a very well-known fact that
25 when you pool together genetically different groups into

LAURENCE D. MUELLER

712

1 a single entity, that that pooled population will show
2 both departures from Hardy-Weinberg and linkage
3 equilibrium. So one explanation could be the pooling of
4 different racial subgroups into these convenient broad
5 categories that forensic labs use for creating their
6 databases.

7 A second reason is that it is also well known
8 that the samples that are used to create these databases
9 have not been randomly sampled. They're typically
10 samples of convenience from blood banks or other sources

11 and, as a result, may include artifacts that could cause
12 these problems, for instance, if they had relatives in
13 them. Relatives end up donating blood or contributing
14 in some way to these data banks, then the inclusion of
15 relatives in these populations would also produce the
16 kinds of effects I've seen in these kinds of departures
17 from independence.

18 Then finally, there are other kinds of
19 artifacts that can result from sloppy handling of the
20 data. This is sort of independent of picking the
21 people, but if you pick people and then you misclassify
22 them in your handling of the data according to race,
23 that could clearly screw things up. Or if you
24 occasionally include, for instance, duplicate samples.
25 Now this has happened once in the BCA and that type of

LAURENCE D. MUELLER

713

1 problem can be readily identified. But, you know, a
2 duplicate is like an identical twin. It's the most
3 extreme form of a relative. But the BCA -- well other
4 labs have in fact included duplicates, in some cases
5 large numbers of them.

6 So any or some combination of all these
7 problems actually might contribute to the kinds of
8 problems I've seen. And it's not easy to tease them
9 apart because there are no real easily diagnostic clues
10 for one problem versus another.

11 Q You've referenced a couple of times NRC or NRC-2. Could
12 you define for us what those -- what that terminology
13 means?

14 A Sure. NRC stands for the National Research Council
15 which is a division of the National Academy of Sciences.
16 National Research Council is often asked to create
17 committees to review scientific issues that usually have
18 broad public importance. It's turned out in the last
19 ten years the National Research Council has created two
20 different committees to review forensic DNA typing, each
21 committee has issued a report, one which came out in
22 1992 is called and is referenced typically NRC-1, and a
23 second committee which issued a report that came out in
24 1996.

25 Q And do these reports address statistical calculations to

LAURENCE D. MUELLER

714

1 be used in forensic settings?

2 A Yes, they both do.

3 Q And I take it you are familiar with and have read both
4 these reports?

5 A Yes.

6 Q Do you recall the recommendations of NRC-1?

7 A Yes.

8 Q And are they different than the recommendations of
9 NRC-2?

10 A On a number of issues they are, yes.

11 Q Okay. Could you tell us first what NRC-1 recommended?

12 A Well, NRC-1 considered all aspects of DNA typing. I'm
13 just going to restrict myself to the statistical and
14 population genetic aspects of their recommendations.
15 And in that regard NRC-1 suggested that forensic labs
16 should base their statistics on a collection of 15 to 20
17 different ethnic groups or populations rather than the
18 standard three to four. And when I say different
19 groups, you know, I don't mean Caucasians from New York
20 and Los Angeles and Miami, but I mean Italians and Irish
21 and Swedes. I mean really teasing apart these big
22 groups into smaller categories.

23 And they also recommended that, even when those
24 15 populations were in place, rather than using the
25 product rule in each one of them, a different statistic,

LAURENCE D. MUELLER

715

1 known as the ceiling principle, should be used with that
2 collection of information.

3 And then thirdly, they also recommended that in
4 every case, every forensic case, that alongside a number
5 produced by this ceiling principle, which would
6 represent the chance that a person chosen at random
7 would have the profile seen in the evidence, that the
8 laboratories also should estimate what's called a lab
9 error rate, that is the chance that the lab would
10 incorrectly say two samples match when in fact they
11 didn't.

12 Q All right. I think I'd like to go on to NRC-2, then
13 come back to a little more on error rate. Did NRC-2
14 also address what they thought was appropriate
15 statistical calculations in a forensic setting?
16 A Yes.
17 Q If you know, the people who comprised this -- the people
18 -- you know if there were a -- the group of people that
19 sat on the board to, or wrote this study?
20 A I've certainly seen all their names. I did talk to the
21 committee, so I've met them all. I'm familiar with the
22 professional records and history of the population
23 geneticists on that committee. I'm less familiar with
24 the people that were professional statisticians.
25 Q Okay. Do you know if any of the people who sat were

LAURENCE D. MUELLER

716

1 forensic scientists? Let me qualify what I mean by
2 forensic scientists, people who work in crime labs doing
3 this type of DNA analysis.
4 A In that case none of the people on the committee were,
5 on the second NRC committee, were forensic scientists.
6 Q If you broaden the definition of that is there somebody
7 that would fit in?
8 A Yes. There's someone who does academic-related research
9 in forensics, George Sensabaugh. He was on the second
10 committee and he would be like the next tier up in one's
11 definition of forensic scientists, but the rest of the
12 people didn't even have that. I mean none of the rest

13 of the people would be identified as working in areas of
14 forensic-related research at all.

15 Q Okay. Did they also come out with recommendations as
16 far as what to do with the statistics in forensic DNA
17 cases?

18 A Yes.

19 Q Could you tell us what those recommendations were?

20 A Well, they had a couple of different ones but certainly
21 their primary recommendation was that the product rule
22 could be used, at least variants of the product rule
23 could be used both with a type of genetic testing known
24 as RFLP testing or the kinds of PCR testing that was
25 available, commonly available then which included

LAURENCE D. MUELLER

717

1 markers like DQalpha and Polymarker.

2 For the RFLP testing the changes in the way you
3 would do the calculations are that any time an
4 individual had at a particular gene just a single band
5 or single allele, rather than use the standard
6 Hardy-Weinberg formula you would take the frequency of
7 that allele and double it. And that ended up being a
8 recommendation that was required because of certain
9 artifacts that happened with RFLP testing.

10 With PCR testing that first recommendation
11 wasn't needed but they did say, though, is that again if
12 you have at any particular genetic marker a profile that

13 has only a single form of the gene, again we call those
14 people homozygotes, that you should use this theta term
15 to inflate the frequency that you would get from the
16 product rule to try to accommodate any departures from
17 Hardy-Weinberg that might exist, but you would otherwise
18 be using the product rule. That was their two major
19 recommendations on estimating the frequency of profiles.

20 They also say, coming to the second major
21 statistical issue of lab error rates, they found that it
22 was either going to be -- their opinion was that it was
23 either going to be too hard to estimate error rates or
24 that the error rates that you could estimate from
25 proficiency tests would not be applicable to the rate of

LAURENCE D. MUELLER

718

1 error you would make in real forensic cases so for that
2 reason estimating error rates ought not to be done and
3 that was their recommendation on that particular issue.

4 Q As to the product rule, is the product rule used in a
5 random -- or excuse me, in a probability of exclusion?

6 A Yes.

7 Q And the product rule is also used in a calculation as
8 far as random frequency in the population?

9 A That's right.

10 Q Is that the proper term?

11 A It can be called the random match probability for a
12 single, you know, profile which is a word used to
13 describe the genetic pattern from one individual in

14 forensics often. Population geneticists would typically
15 call that profile a genotype, but it's the same thing.

16 With the probability of exclusion you typically
17 have many profiles or many genotypes that are all
18 potential contributors and so you're using the product
19 rule with all of them but you are adding up many numbers
20 together rather than just a single one.

21 Q After you multiply out -- you take each genotype and
22 multiply it out and then add those final statistics
23 together?

24 A That's right. With probabilities of exclusion where,
25 for instance, with mixtures you can have multiple

LAURENCE D. MUELLER

719

1 donors, you would in principle, although you don't
2 actually do this in practice, but in principle you would
3 apply the product rule to all the different possible
4 contributors then add up all those numbers together.

5 Q Okay. But if I understood your earlier testimony, you
6 can only use the product rule with a data base that has
7 linkage equilibrium?

8 A That's right.

9 Q And your belief is that this theta correction factor
10 isn't going to address the linkage equilibrium problem?

11 A That's right.

12 Q Are there other scientists that would agree with that?

13 A Well I think there certainly would be other scientists

14 that agree that theta does not fix linkage equilibrium.
15 That's a well-established fact and in fact, as I said,
16 even NRC-2 prefaces their recommendations about theta
17 with a statement assuming there is no or very little
18 linkage -- departures from linkage equilibrium we can do
19 the following. So I don't think that's a really -- that
20 the role of theta is not something under dispute in
21 population genetics. Its role and what it does is
22 pretty well understood.

23 Q I see. Okay. So if I understand now correctly, NRC
24 says first you have to have linkage equilibrium then you
25 should apply theta if there's problems with

LAURENCE D. MUELLER

720

1 Hardy-Weinberg and only if you can meet those two
2 criteria can you go on to use the product rule in
3 calculating a statistic to associate with the frequency
4 of a profile?

5 A Well that's certainly the logic of their conclusion.
6 They in fact say for certain systems they think we can
7 assume there's linkage equilibrium, like DQalpha and
8 Polymarker, and however the application of the theta
9 factor they basically say let's just do it in general,
10 you know, for all PCR-based markers just to be safe.
11 That was basically their final recommendation. You
12 don't pick and choose when to do it, you just would do
13 it all the time.

14 Q All right. And let's go back to error rate. How would

15 you define that term for purposes of this discussion?
16 For the statistical calculations, what's an error?
17 A Obviously there are lots of different kinds of errors
18 people can make in a forensic testing situation but the
19 one that's obviously very important in, I won't say all
20 but many many forensic cases, since you're looking at
21 identify between two samples, could two samples have
22 come from the same source, that's usually the important
23 and interesting question, there the error that I am
24 concerned about and others are concerned about is well,
25 what if those two samples are in fact not from the same

LAURENCE D. MUELLER

721

1 person? What if those two samples in fact have
2 different genetic profiles but the lab nevertheless
3 reaches the wrong conclusion and says they're the same.
4 That's clearly an error and is the error we're concerned
5 about because when we come to court we usually have two
6 samples that the lab's saying match. So we need to know
7 not only if those kinds of errors can happen but if they
8 can how often do they happen? Do they happen one in ten
9 times or one in a quadrillion times? And I say
10 quadrillion simply because that's a number that can come
11 up with the other statistics we're dealing with.

12 So that's sort of like the range of interest
13 and if it can happen in those ranges certainly in the
14 lower end of the range it's an important factor to keep

15 in mind.

16 Q Well then let me ask you this: Could you also consider
17 -- you talked specifically about mishandling a sample
18 that certainly the genotypes would appear to be
19 identical but it's an inaccurate reflection of what the
20 evidence was when collected. What about if, in a mixed
21 sample, a scientist incorrectly pulled out or declared
22 something to be a genotype that wasn't actually
23 reflective of the true contributors of the mix? If
24 there was a way you could determine how frequently that
25 happened could you consider that as part of the error

LAURENCE D. MUELLER

722

1 rate?

2 A Well again, to the extent that when you -- when you have
3 a mixture if you pull out a profile or say there's a
4 profile there which you then say is consistent with a
5 particular person so you're in essence including someone
6 in that mixture when in fact that profile is not there
7 and that person should have been excluded, then that's
8 actually a similar kind of error because you're falsely
9 including someone and in this case he's being included
10 with lots of other people because it's not a -- it's a
11 mixed sample, but it's still an error of inclusion.
12 You're saying this person could have left this -- could
13 have contributed to this mixture when in fact he
14 couldn't have. So it's the same kind of error,
15 obviously, which would require different kinds of tests

16 to see how frequently it happens.
17 Q More specifically are you aware of the NIST Mixed Stain
18 Studies?
19 A Yes, I've seen the paper and have reviewed it some time
20 ago, yes.
21 Q I guess what I -- certainly if you're going to use a
22 probability of inclusion-exclusion there will be
23 profiles in that calculation that aren't actually in the
24 mixed sample, but what I was talking about was where a
25 lab as a practice will look at a mixture and declare,

LAURENCE D. MUELLER

723

1 you know, this allele and this allele belong to suspect
2 number one and we can match these other two alleles to
3 suspect number two within this mixed sample,
4 inaccurately declaring genotypes that way such that the
5 product -- or the random match statistic is used.
6 A Right. So this is --
7 MR. FRISTIK: I'm going to object. That wasn't
8 a question, that was a statement.
9 BY MS. FUNK:
10 Q So based on that, and the studies we have two in
11 evidence which would -- which do suggest or purport up
12 to 30 percent of the time labs pick the wrong profile,
13 between 10 and 30 percent depending on whether we're
14 talking about the major or minor contributor.
15 A Uh-huh.

16 Q But could that also be factored in as part of an error
17 rate?

18 A Well, I -- it's a problem. I would not consider this
19 something that would -- should be handled with error
20 rates. I would in fact say this is something that
21 should be handled by just changing the overall protocol
22 of the lab not to make those kinds of calls that can be
23 ambiguous and subject to incorrect interpretation.
24 Because that would completely avoid that problem.
25 Whereas the kinds of errors I'm mentioning, these are

LAURENCE D. MUELLER

724

1 errors that happen that no one sees. So you get a
2 result, it looks perfectly fine, yet in fact the
3 result's erroneous and by definition those are not
4 things that we can simply wish away or change one
5 protocol and have disappear, so the possibility of those
6 kinds of errors are always present and they need to be
7 taken account of, whereas the kinds of problems you're
8 mentioning could be dealt with by a change in protocol
9 quite directly. So my point of view would be no, don't
10 use error rates to handle that problem, just change your
11 protocols in the way you interpret mixtures.

12 Q Then we come back to what you referenced and NRC
13 expressed concern about. How does one figure out an
14 error rate when many of these things that occur we
15 wouldn't catch or wouldn't know what actually happened?

16 A Sure. So in cases it's very tough. I mean it's very

17 tough to look at casework and say yah, that's the right
18 answer or no, this one is wrong, although I should say
19 there actually now are a number of documented cases
20 where people have uncovered false matches. However, the
21 easiest way to do this is in a test where someone
22 actually creates an evidence and known samples where you
23 know what contributors donated the blood or other
24 biological fluid. So someone knows the answer, the lab
25 doesn't. You give the lab the test. The person that

LAURENCE D. MUELLER

725

1 knows the answer looks at how they did and says yah, you
2 got it right or you got it wrong, just like I do every
3 quarter at UC-I. We test people. And based on those
4 kinds of tests you can in fact figure out how often
5 these kinds of errors happen, and again, on tests labs
6 make these kinds of errors also. So that's the best way
7 to document it because if you do enough of these you can
8 quantify how often it happens and basically the results
9 are ambiguous about what the correct answer is.

10 Q What's a confidence interval?

11 A It's a statistical method for expressing uncertainty in
12 a number that you estimate. So for instance, this
13 random match probability is an estimate of how common a
14 particular profile is in a population and there's --
15 even if we ignore the potential problems caused by
16 having a lousy database or having relatives in a

17 database or even we ignore the problems of departures
18 from linkage equilibrium, if we assume all those things
19 are fine, that number you get from the product rule
20 still will not be the exactly right number because it's
21 based on estimates of allele frequencies from a database
22 of just a few hundred people. So the methods we have
23 for expressing the uncertainty in that number based on
24 the finite size of our database can generate what are
25 called confidence intervals and that will be a number

LAURENCE D. MUELLER

726

1 above and below your estimated frequency which will
2 express the uncertainty in that number because we didn't
3 sample all the Caucasians and Blacks and Indians in
4 Minnesota, we only took several hundred, so there's
5 uncertainty as a result of that. A confidence interval
6 is a way of letting us know how uncertain those numbers
7 are.

8 Q Is the confidence interval tied into error rates or is
9 that a separate --

10 A No, that's a completely separate issue and really the
11 methods for computing confidence intervals focus on a
12 very well-defined but narrow issue which is just sample
13 size; how big is your database. Any database that
14 hasn't sampled everyone in the population will have some
15 uncertainty and the confidence intervals will let us
16 know what that is.

17 Q Okay. As a population geneticist I want to go back to

18 error rates. Are you familiar with the position,
19 general scientific community's opinion as to the need
20 for providing an error rate?

21 A Yes.

22 Q And could you tell us what that is?

23 A Sure. I would say with a few exceptions, meaning
24 actually NRC-2, the overwhelming body of the scientific
25 community is in favor of reporting error rates in a

LAURENCE D. MUELLER

727

1 forensic setting. In fact in the literature almost
2 every published paper which includes some analysis of
3 this problem has concluded that error rates are an
4 important issue and these go back to letters in the
5 Journal of Forensic Science in 1990 up throughout the
6 90's and there's also been probably half a dozen papers
7 since NRC-2 criticizing NRC-2's position on this issue.

8 So there really is a very, I think, strong
9 consensus among the scientific community, meaning
10 population geneticists, statisticians who looked at
11 these problems, that lab error rates are a terribly
12 important part of evaluating any type of DNA evidence.

13 Q In your experience and with your knowledge of people you
14 know in the scientific community are there other areas
15 of science where error rates are presented to people?

16 A Sure.

17 Q Could you give us an example?

18 A Well, for instance in genetic testing counseling if
19 someone -- if a women's pregnant and wants to have the
20 fetus tested for genetic diseases like Down's Syndrome
21 with the possibility that she and her husband may be
22 considering termination of the pregnancy based on those
23 results, people that do genetic testing will typically,
24 along with their result of the status of the fetus, tell
25 you well, this percent of the time we say the fetus is

LAURENCE D. MUELLER

728

1 okay when in fact it isn't and this percent of the time
2 we say the fetus looks like it has Down's Syndrome when
3 in fact it doesn't. These are errors. And of course in
4 this kind of testing, since not all pregnancies are
5 terminated, they actually have a way of seeing how the
6 test works out in those cases where pregnancies go to
7 term. So they have data on how often they make errors
8 and they present these to people so that they can make
9 informed decisions realizing that science isn't always
10 correct, scientists screw up sometimes, and to the
11 extent that it impinges on their final decision they're
12 made aware of that information.

13 Q And would you be in favor of presenting an error rate to
14 the jury alongside of the statistical calculation for a
15 frequency?

16 MR. FRISTIK: Objection to the question.
17 Relevance. This hearing is isn't about what should be
18 presented to the jury.

19 MS. FUNK: I can rephrase it.

20 THE COURT: Very well.

21 BY MS. FUNK:

22 Q You're aware that currently in cases this type of
23 scientific evidence comes with, attached to it, a
24 number? A frequency number?

25 A Correct.

LAURENCE D. MUELLER

729

1 Q Does that give a person viewing this evidence or hearing
2 about this evidence, does it give the full story as to
3 the significance of the match?

4 A No.

5 MR. FRISTIK: Objection. Same objection.

6 THE COURT: Overruled. I'll let him answer the
7 question. I think I heard the answer no.

8 THE WITNESS: I said no, yes.

9 BY MS. FUNK:

10 Q Can you tell us why?

11 A Sure. As I said, I mean the really fundamental question
12 in our basic instance of where we're comparing two
13 samples to see if they may have originated from the same
14 source is, what's the chance of getting a genetic match
15 between an evidence sample and a known sample when in
16 fact the evidence sample didn't originate with that
17 known person?

18 Well there are really two different ways that

19 this can happen completely independent of each other.
20 The first way is that the defendant did not leave the
21 evidence sample, some other person did who
22 coincidentally has a matching genetic pattern to the
23 defendant. And the product rule or ceiling principle or
24 other methods are different ways from population genetic
25 theory we can go with trying to estimate how likely that

LAURENCE D. MUELLER

730

1 event is.

2 But secondarily, the evidence may not have
3 originated from the defendant and in fact the two may
4 not match but the lab has incorrectly concluded they do
5 because of a lab error. So you can get a match when a
6 defendant did not leave the evidence for either of these
7 causes.

8 So I think it only makes sense to anyone, I
9 mean you don't have to be a scientist to say geeze, it
10 makes sense that we ought to know how often each of
11 these things happen. And the analogy I sometimes give,
12 it's sort of like if you were a fighter pilot buying a
13 defensive missile system and, you know, a salesman for
14 the missiles came up to you and said well I have a
15 missile and it will, when it's fired, it only misses its
16 target one in a million times. If that's the only
17 information you have about that missile system you think
18 it's great, you go sure, let's get a million of them.

19 But then if the competing salesman comes up and

20 says well, you know, that statistic was right but what
21 he forgot to tell you is the missile only fires 50
22 percent of the time, then you realize that for the whole
23 system to work and be effective both parts have to be
24 reliable.

25 So in a case of a DNA match even if we assume

LAURENCE D. MUELLER

731

1 that genetic patterns are unique, there are no other
2 people on earth that will ever share genetic patterns
3 except for identical twins, if a laboratory will
4 incorrectly match different patterns, say one out of a
5 hundred times, then that would be the frequency with
6 which you'd expect innocent people to be incorrectly
7 matched to evidence and that ought to be, and it's a
8 statistical fact, that ought to be the weight that
9 dominates your final consideration of the evidence.

10 And so it's -- that's why it's so important.
11 That's why I think statisticians and population
12 geneticists recognize this and see that ignoring it or
13 saying it's zero, which in these settings when you have
14 a number like one in a quadrillion for the match
15 probability, when you say the error rates are zero or
16 small you're implying that they're actually smaller than
17 one in a quadrillion so you can effectively ignore them.
18 That's such a tiny number and there's absolutely no
19 empirical evidence to support anything close to that.

20 This is a big issue and I think that's why there's such
21 a -- such a body of support for it in the scientific
22 community.

23 Q If you take a database like the one we have in Minnesota
24 which isn't in linkage equilibrium, is there another
25 mathematical calculation provided by NRC-2 that we could

LAURENCE D. MUELLER

732

1 use to determine frequencies?

2 A It's not -- I won't say it's provided by NRC-2. They do
3 discuss another method. They of course reject it
4 because they think the product rule is okay, but they do
5 actually mention a method called a counting method which
6 can be used even for populations that aren't in linkage
7 equilibrium or Hardy-Weinberg. So those aren't the only
8 games in town, there are other ways of doing this, but
9 the counting method has it's own liabilities. It will
10 not produce exceedingly rare statistics because the
11 rarity of any profile is a function of how big the
12 database is. So if you only have a thousand people your
13 rarest frequency is going to be about one in a thousand.

14 Q Could the evidence be presented by frequency, allele by
15 allele? Rather than multiplying them together would it
16 be scientifically sound to present evidence as the
17 defendant, either allele by allele or locus by locus
18 given a database not in linkage equilibrium, such as the
19 defendant has an 8, 8, this combined allele pattern
20 occurs in 12 percent of the population or whatever?

21 A Sure. I mean you can certainly do that and of course
22 for a 12 or 13 gene or locus STR profile you've suddenly
23 got a lot of numbers and so it's sort of -- it avoids
24 multiplying but then the question is well what do you
25 tell people to do with these numbers? I mean those are

LAURENCE D. MUELLER

733

1 the raw information, though, and those estimates can be
2 made quite accurately.

3 Q Without worrying about -- the linkage isn't a problem?

4 A That's right, if you're not going to multiply things
5 together then you're just providing raw input data. We
6 have all these systems and here's how rare they are.
7 Sure, that avoids multiplying altogether.

8 MS. FUNK: Thank you. I don't have any further
9 questions.

10 THE COURT: Cross-examination?

11 MR. FRISTIK: Thank you, Your Honor.

12

13 CROSS-EXAMINATION

14 BY MR. FRISTIK:

15 Q Without going through all the details in your CV
16 Mr. Mueller -- Dr. Mueller, excuse me, it's fair to say
17 you're not a forensic scientist, correct?

18 A I would not call myself one because that's not my
19 primary research or teaching duties, no.

20 Q Right. Therefore you're not a member of the forensic

21 scientific community, correct?
22 A I have no idea how you even become a member of it, but I
23 don't consider myself a -- that's not my primary, like I
24 said, research and teaching.
25 Q Your work in population genetics is focusing on fruit

LAURENCE D. MUELLER

734

1 flies, is that right?
2 A No, fruit flies are a tool like a computer is. I use
3 computers and I use fruit flies but the focus of my
4 research is on things like the physiology and genetics
5 of aging or how population density affects evolution or
6 I do also do research on forensic databases and their
7 independence. So those are the ideas that I address. I
8 address them with computers, with fruit flies, with
9 other tools.
10 Q And you talked about your responsibilities and duties at
11 your university include teaching, research, and also
12 this outside service that you provide or outside
13 consulting, is that correct?
14 A Well service includes lots of things. Includes
15 committees at the university. It also includes outside
16 service, too, if you have the expertise to do that.
17 Q Consulting in criminal cases, is that part of it?
18 A It is a type of service, yes.
19 Q Do you do that?
20 A Yes.
21 Q And you do that -- this isn't the first time you've

22 testified on behalf of a criminal defendant in a case?
23 A That's correct.
24 Q You've been doing this for the better part of 13 or 14
25 years?

LAURENCE D. MUELLER

735

1 A Since 1989.
2 Q Okay. And in those cases in which you testified it is
3 always for criminal defendants, is that right?
4 A No. January this year I testified for the prosecution.
5 Q You did? What case was that?
6 A It was in Los Angeles. The defendant's name was
7 Ritchie.
8 Q Is that the only case in which you testified on behalf
9 of the prosecution?
10 A Yes.
11 Q And you indicated in your testimony that you do
12 absolutely no DNA testing, is that correct?
13 A In my own lab, that's correct.
14 Q Well in anybody else's lab?
15 A Well, yah. In fact I'm currently, we're taking some of
16 my populations into a colleague's lab where he has a
17 setup to do this and we're in fact extracting a related
18 molecule called RNA, turning that into a kind of DNA,
19 and looking at gene expression in these flies, so we're
20 basically doing work related to DNA analysis on my
21 populations. It's just not in my lab.

22 Q So that's DNA analysis on flies, correct?

23 A Yes, it is.

24 THE COURT: Excuse me, Mr. Fristik, I hate to
25 interrupt you but as I indicated to you and Ms. Funk

LAURENCE D. MUELLER

736

1 it's time for Mr. Roman Nose to have dinner.

2 MR. FRISTIK: I wonder this, Your Honor. I'll
3 just put this out. If I can tell the Court that I'll be
4 done in 20 minutes can we keep going? If we have to
5 break now I understand.

6 THE COURT: If it's a hot meal? It's a hot
7 meal. We'll break for about 20 minutes and I'll see you
8 back here about 5:20, 5:25, whenever we're ready.

9 (Short recess.)

10 THE COURT: Okay, Mr. Fristik?

11 MR. FRISTIK: Thank you, Judge.

12 BY MR. FRISTIK:

13 Q Do you have any idea how many cases you have testified
14 in?

15 A I don't have an exact count but since 1989 it's well
16 over a hundred.

17 Q And I think that you testified in Minnesota previously,
18 is that right?

19 A Yes.

20 Q In Hennepin County?

21 A Yes.

22 Q You were talking about something called the exact test

23 concerning population data, is that -- am I right about
24 that phrase?

25 A Yes.

LAURENCE D. MUELLER

737

1 Q What's the exact test?

2 A It's a statistical test for independence either within
3 or between gene loci and it actually relies on computer
4 simulation or computer sampling to achieve or arrive at
5 the final test statistic.

6 Q Is that a test that you developed?

7 A No. The version of this test was first developed
8 actually by R. A. Fisher around 1930 but has been
9 improved for use for testing genetic loci with many
10 alleles in the early 1990's by Elizabeth Thompson and
11 then later, as I said, in 1995 by Bruce Weir and his
12 colleagues.

13 Q But the NRC didn't adopt that test, is that right?

14 A Well they didn't adopt any statistical test, per se. I
15 mean they focused on should we or should we not use the
16 product rule and if so, how do we modify it. They
17 didn't have an extensive discussion of testing for
18 independence at all.

19 Q The NRC is an arm of the National Academy of Sciences,
20 is that right?

21 A Yes.

22 Q You would agree that the National Academy of Sciences is

23 probably the most esteemed body of scientists that are
24 collected in the country? I mean there's Noble
25 laureates on that group?

LAURENCE D. MUELLER

738

1 A The people that are members of the National Academy,
2 yes.

3 Q The National Academy of Science really does speak for
4 the mainstream of the scientific community in this
5 country, is that a fair statement?

6 A Well the National Academy of Science generally doesn't
7 speak. They have members, they have a publication, but
8 they don't offer pronouncements at weekly press
9 conferences. They don't speak for people. They are
10 just an organization.

11 Q Do they develop policy?

12 A No.

13 Q Do they have meetings?

14 A They do have meetings, they have many committees, but
15 and as I said, they have branches like the National
16 Research Council which puts together committees to
17 consider important scientific issues, although I should
18 mention the members of the National Research Council
19 that wrote that report, actually one is, but are not
20 members of the National Academy of Sciences. They were
21 chosen because of their knowledge, not because they were
22 members. So being a member isn't a prerequisite to
23 being on the National Research Council.

24 Q But the National Academy is going to collect those
25 individuals, those people that they deem to be

LAURENCE D. MUELLER

739

1 appropriate for these various committees, isn't that
2 right?

3 A Well again, it's not even the National Academy. There
4 was basically two people from the National Academy of
5 Sciences in charge of putting that committee together,
6 and again, these were professional employees of the
7 National Academy, they weren't members of the National
8 Academy, and they can certainly consult with those
9 people but --

10 Q The NRC-2 recommendations are the currently accepted
11 methods in the scientific community, is that correct?

12 A I wouldn't say that. I mean they are the set of
13 recommendations which some people agree with, some
14 people don't. I already mentioned that there's in fact
15 been a fair amount of criticism of their recommendations
16 on lab errors. So I don't consider their recommendation
17 there to be -- to be generally accepted at all.

18 Q Their recommendation as to the use of the product rule
19 is generally accepted in the scientific community, is
20 that a fair statement?

21 A There's still some disagreement about it. I would
22 certainly have to say, though, it's clearly the
23 predominant method that's being used today but there is

24 still some concerns about some of those issues that I
25 mentioned today.

LAURENCE D. MUELLER

740

1 Q And you're one individual that has concerns about the
2 use of the product rule obviously, is that right?

3 A Sure.

4 Q Who else has concerns about the product rule besides
5 this Mr. Weir?

6 A I'm not sure I want to say Dr. Weir has concerns about
7 it. He developed this statistical test but I'm not
8 going to put him in that category. I mean there are
9 other people in the past that have expressed concerns
10 about these like, you know, Richard Lewenton (ph) at
11 Harvard, Seymour Geiser at the University of Minnesota,
12 some other people whose names I'm forgetting right now.
13 There are other people that have expressed these
14 concerns in the past. I don't keep up to date with all
15 these people and ask them well, last week, do you still
16 have these concerns but certainly there have been a lot
17 of people that have expressed concerns in the past on
18 this issue.

19 Q But currently you don't know of anybody that has
20 expressed concerns about the use of the product rule
21 particularly as it's applied to statistical calculations
22 in DNA typing, is that right?

23 A About the product rule per se?

24 Q Yes, as it's applied to statistical calculations in

25 forensic DNA typing?

LAURENCE D. MUELLER

741

1 A Well again, I'm not going to entirely agree with that.
2 There was actually in fact just a recent series of
3 letters in the Journal of Forensic Science arguing about
4 the way the FBI tested Hardy-Weinberg equilibrium
5 calling it inappropriate. So these issues are still
6 coming up, not as often as they did ten years ago, but
7 these issues are still coming up even today.

8 Q Did the NRC-2 when they were developing their
9 recommendations solicit input from the scientific
10 community as to what should be used for reporting
11 statistics?

12 A Yes.

13 Q And did you offer your input?

14 A Yes.

15 Q And they rejected that, right? Obviously they rejected
16 it?

17 A Their conclusions are clearly different than my own,
18 yes.

19 Q All right. You also, if I understand your testimony,
20 you also don't favor the theta correction as it's
21 applied to the product rule per Dr. Carmody and NRC-2,
22 is that right?

23 A Well I think it's okay for correcting Hardy-Weinberg
24 problems, it's just not appropriate if you believe there

25 are problems with linkage equilibrium.

LAURENCE D. MUELLER

742

1 Q And you believe that there are problems with linkage
2 equilibrium in the BCA's database. That's what you
3 testified to, right?

4 A Well in the two that I mentioned; the Caucasian and
5 Native Americans.

6 Q So just in the Caucasian and Native American
7 populations?

8 A Right.

9 Q No other population that they have in their database?

10 A Not of the BCA's, no.

11 Q All right. So as though those two populations you have
12 expressed concerns about the lack of linkage equilibrium
13 and I think you further testified that you've had these
14 concerns and have been aware of this problem for two
15 years, is that right?

16 A Right.

17 Q And have you ever written a letter and documented your
18 concerns to the BCA in this regard?

19 A I haven't sent them a letter concerning this directly,
20 no.

21 Q Okay. Have you ever -- I mean, that's, I would take it
22 a major, in your view, a major concern as to those two
23 particular populations, is it not?

24 A Well, I mean there's -- the BCA is just one of many
25 labs. There are concerns across multiple laboratories

1 or about this issue in general. In fact in 1999 I did
2 publish a paper expressing these concerns for DQalpha
3 and Polymarker and also for a number of labs doing four
4 short tandem repeat loci. So that my general level of
5 concern about this problem in US forensic databases has
6 in fact been expressed publicly and published in a
7 peer-reviewed venue.

8 Q Which paper is that?

9 A On my CV it would be number 57.

10 Q And again, does that paper reflect your specific
11 concerns with -- well it probably wouldn't, that was
12 written in '99. That wouldn't reflect your specific
13 concerns about the BCA's database?

14 A Not about their STR database, although it did include an
15 analysis of their DQalpha and Polymarker database.

16 Q Have you ever voiced your concerns about BCA's database
17 in any other forum or any other manner, Dr. Mueller?
18 You indicated you haven't written a letter to them
19 expressing your concerns. Have you every expressed your
20 concerns about their database in any other formalized
21 fashion other than testifying in court?

22 A Yah. Not about their STR database. I mean I haven't --
23 I don't have a formal publication on that particular
24 issue.

25 Q So the only forum in which you expressed these concerns

1 is when you come into court and testify about it, is
2 that right?

3 A No, that's not right. As I said, the issues that I
4 actually outlined in the paper in 1999 are issues that
5 carry over even to the STR database. For instance, the
6 reasons for seeing the departures I did in STR and some
7 of the DQalpha Polymarker systems are things that would
8 be of concerns for these. So the nonrandom sampling,
9 the mixture of ethnic subgroups, those are issues which
10 in fact one would believe if they're causing the
11 problems in those genetic systems they might very likely
12 be problems for STR.

13 So now saying it over again, I'm sure it
14 wouldn't hurt, but really the major issues that I'm
15 addressing here in terms of population genetic and
16 database sort of security and soundness are things that
17 I have made previously in published papers.

18 Q One published paper in 1999, right?

19 A Well no, in fact some of the issues about database
20 samples and the problems with databases was made in an
21 earlier paper in 1993 where I analyzed some of the
22 problems with the FBI's database, including duplicate
23 samples and in fact mistyping of samples. So I talked
24 about those issues. Those issues. Those included RFLP
25 databases, even earlier than that '99 paper.

1 And then let me just, now that we're getting
2 into this, there is yet another paper which came out,
3 let me make sure, paper number 53 was also a publication
4 pointing out problems with the way the FBI processed the
5 data that they used to support their contention of
6 independence. Now in that particular letter there was a
7 very specific issue that was addressed, but it goes to
8 your question about have I ever talked about these
9 things before and the answer is yes and in the published
10 literature I've done it.

11 Q Item 53 is in fact not a published article, it's a
12 letter to the editor, is that right?

13 A Right, but it was reviewed by other scientists prior to
14 its publication.

15 Q And did it make it to publication?

16 A Yes, it did.

17 Q You talked about laboratory error rates and you think
18 it's important that laboratory error rates be included
19 in any reporting statistics concerning analysis of
20 forensic DNA samples is that right?

21 A Yes.

22 Q Have you come up with an error rate for your own
23 laboratory?

24 A For my laboratory?

25 Q Yes.

1 A On certain analyses we do in fact we do have rough
2 estimates of how often people screw thing up, like
3 counting out eggs for instance. We're not a lab that
4 does the same procedure over and over again like the
5 forensic testing lab, but on some things we do we do
6 test people and see how well they do.

7 Q Forensic labs test people and see how well they do, too,
8 don't they?

9 A Most of them do do proficiency tests, that's correct.

10 Q Are you aware of anyone else who's reviewed the BCA
11 database that concluded that two particular populations
12 are not in linkage equilibrium other than yourself?

13 MS. FUNK: Your Honor, I'm going to object to
14 this consistent practice of asking my witnesses to name
15 individuals by name. I don't know if the prosecution is
16 planning on engaging in some counting method where we
17 weigh the number of scientists on one side against the
18 number of scientists on the other. If the Court's going
19 to allow it I'd ask for some notice so I can sit down
20 with my scientists and have them really think and write
21 down the names of each individual they've ever
22 encountered who may have expressed a similar opinion and
23 perhaps my scientists should be given time to call each
24 one of those people so that they can assure themselves
25 that they would be providing accurate testimony on the

1 date that they testify.

2 I don't see a point to it. I think it's not
3 only counterproductive but I don't know that it's
4 relevant. If he wants to know if there's published
5 papers that agree with him, I'm fine with that. Asking
6 my client to -- or my witnesses to name individuals by
7 name I think goes beyond what is appropriate for this
8 hearing.

9 THE COURT: Well, there maybe some overlap.
10 I'll overrule the objection. He may know some who
11 disagree with other people or agree with him based on
12 what he reads, I don't know. Go ahead.

13 BY MR. FRISTIK:

14 Q Are you aware of anyone else whose reviewed the BCA's
15 databases as to those two populations that you referred
16 and concluded that they are not in linkage equilibrium?

17 A No, I don't know anyone else that's reviewed them and
18 made those conclusions, no.

19 Q You indicated that in your opinion the general
20 scientific community favors the reporting of error rates
21 and my question is, do you know whether or not the
22 forensic scientific community favors the reporting of
23 error rates?

24 A I mean I don't have a good separation of where those two
25 communities start so I'm just basing my opinion on, as I

1 said, the published literature and published literature
2 is fairly one sided in stating that this is an important
3 issue. And that would include published literature by
4 forensic scientists.

5 Q And what forensic scientists are you referring to who
6 favor reporting of error rates?

7 A Well they haven't published papers on this issue. I
8 mean they don't go out and do studies and conclude based
9 on those studies, hey, errors rates aren't an issue or
10 they're unimportant. No forensic scientist that I know
11 of has done a study which has presented data that
12 supports that. So I'm saying they're not out there.
13 The papers that are out there have been fairly strongly
14 in favor of using this statistic in the presentation of
15 this kind of evidence.

16 Q You testified in a case in Washington, State of
17 Washington versus Gore, in 1996, did you not?

18 A Yes.

19 Q Do you happen to recall whether or not you ever looked
20 at the judge's findings and her decision in that case
21 where she made comments about your testimony?

22 MS. FUNK: Objection, Your Honor. Relevance.

23 MR. FRISTIK: I'm asking if he --

24 MS. FUNK: I'm going to say I know where he's
25 going. Any comments any judge made in a case six years

LAURENCE D. MUELLER

1 ago not in this state without providing also a hundred
2 other details, it's not relevant. It's certainly not
3 relevant, as Mr. Fristik is so fond of pointing out, to
4 the issues of prong one in this case.

5 MR. FRISTIK: It's relevant to his credibility.

6 MS. FUNK: What a judge thought six years ago
7 in a case where we don't have any additional
8 information?

9 THE COURT: Let's get it in the record. I'll
10 decide if it's relevant or not.

11 MS. FUNK: Excuse me. It can come in the
12 record if Dr. Mueller is aware of it, is that right?

13 THE COURT: He can answer the question. That's
14 the first threshold here.

15 BY MR. FRISTIK:

16 Q Do you recall the comments the judge made in that record
17 about your testimony in that case? I guess the first
18 question is did you read the comments?

19 A The answer is no, I've never read that judge's decision
20 or opinion.

21 Q You haven't? Did you ever read the comments in the
22 decision made by the presiding judge in California
23 versus Howard, in a case from 1990, about your
24 testimony? Do you recall reading that portion of that
25 judge's opinion about your testimony?

LAURENCE D. MUELLER

1 A The Howard decision, yes, I have actually read that
2 page. That was was from 1990, I believe or '91.

3 Q That's right. And do you recall the judge saying about
4 your testimony in that case that your financial interest
5 and the shifty nature of your criticism gave the judge
6 considerable pause that has caused that judge to
7 conclude that you seem to fit in with a description of
8 the creation of a welfare system for academics. Given
9 Dr. Mueller's financial stake it appears --

10 MS. FUNK: I'm going to object to putting this
11 into the record, Your Honor.

12 THE COURT: I'll let him put it in the record
13 for whatever it may be worth, which may or may not be
14 much. But I'll let it go in the record.

15 BY MR. FRISTIK:

16 Q You remember the judge saying that about your testimony?

17 A Well I wasn't there when he said it. I've seen a
18 written transcript of it.

19 MR. FRISTIK: I don't have anything else,
20 Judge.

21 THE COURT: Okay. Any redirect?

22 MS. FUNK: Just a little bit.

23

24 REDIRECT EXAMINATION

25 BY MS. FUNK:

LAURENCE D. MUELLER

1 Q I just wanted to clarify with you, Dr. Mueller, as to

2 the product rule in its purest and most independent
3 form, and specifically I'm talking about taking
4 independent events, looking at their frequencies,
5 multiplying them together, and coming up with a final
6 number, as a population geneticist are you opposed to
7 that theory or that concept?

8 A No. I mean the concept is perfectly straightforward and
9 in certain situations, certainly reasonable thing to do.

10 Q And you accept that it can be an acceptable and valid
11 mathematical equation?

12 A Sure.

13 Q So when the prosecutor was asking you and you were
14 expressing some concerns, that was specifically related
15 to its application in forensic testing particularly
16 using a database that's not in linkage equilibrium, is
17 that fair to say?

18 A Right. Absolutely.

19 Q I'd like to show you Exhibit 6. Do you recognize this?

20 A Yes.

21 Q Did I show it to you this morning?

22 A Yes.

23 Q And does that outline some possible ways to do
24 calculations in forensics?

25 A Yes, it does.

LAURENCE D. MUELLER

752

1 Q Okay. I'd also like to show you Exhibit 5, and I don't

2 know if you've seen this before?

3 A This particular article I have not seen, no.

4 Q Okay. It's previously been admitted. I'd ask you, it's
5 a fairly short article, I would ask you to turn to page
6 two of the article and, as you can see, the title of it,
7 of course, is Interpretation of Complex Forensic DNA
8 Mixtures and the first calculation, sort of type listed
9 in bold, is inferring genotypes of contributors. Could
10 you take a minute to just read that first and second
11 paragraph.

12 A Okay.

13 Q Does that portion of the article talk about using the
14 product rule to obtain a random match frequency?

15 A Okay, well the part that I just read was the two
16 paragraphs entitled inferring genotypes of contributors
17 and no, that part did not talk about the product rule.

18 Q Well, I know it doesn't use the word product rule but
19 where it talks, that first sentence, a second common
20 strategy for mixture interpretation involves deducing
21 the genotypes of the contributors followed by
22 calculating a point estimate of combined match
23 probability for major or minor profile.

24 A Right. And you would presume there that they were
25 thinking of using the product rule. I mean they don't

LAURENCE D. MUELLER

753

1 mention it explicitly.

2 Q Doing that to do a random match calculation?

3 A That's right.

4 Q And looking at that second paragraph that I asked you to
5 read, it outlines some problems that can occur when
6 doing that from a mixed sample, doesn't it?

7 A Sure.

8 Q And it specifically lists potential allele sharing
9 amongst close relatives. Isn't that one of the concerns
10 that you expressed particularly for this database?

11 A It's certainly one way to explain the results that I
12 observed, yes.

13 Q And I know that you didn't observe Dr. Krane's
14 testimony, but you were aware that he had done some work
15 with the Minnesota database as far as combining alleles
16 and in this article it also indicates the possibility of
17 additional contributors with matched alleles could be a
18 concern, isn't that right?

19 A Yes.

20 Q So this is a paper that you were unaware of that
21 expresses concerns in using the random match probability
22 under certain circumstances not unlike the concerns that
23 you expressed, is that fair to say?

24 A It's certainly a different angle but yes, they're
25 talking about a situation where applying that product

LAURENCE D. MUELLER

754

1 rule to a single profile might be questionable.

2 Q Okay, thank you.

3 MS. FUNK: That's all I have, Your Honor.

4 THE COURT: Okay, any re-cross?

5 MR. FRISTIK: A couple questions.

6

7

REXCROSS-EXAMINATION

8 BY MR. FRISTIK:

9 Q Dr. Mueller, do you have any opinion you can offer to
10 the Court about whether or not the PCR-STR method of DNA
11 typing in the forensic community is generally accepted
12 in that forensic scientific community?

13 A Well that, when you talk about the method I think you're
14 now talking about the molecular biology and genetics
15 which is not really an area that I offer opinions about.
16 I mean --

17 Q The answer to my question is no?

18 A Yah.

19 Q Do you have an opinion you can offer to the Court as to
20 whether or not the 310 instrument and the COfiler and
21 Profiler Plus kits are generally accepted for use in the
22 forensic scientific community as giving reliable and
23 valid results?

24 A And the answer would be no, I wouldn't offer an opinion
25 on that.

LAURENCE D. MUELLER

755

1 MR. FRISTIK: No further questions.

2 THE COURT: Okay. Anything else, Ms. Funk?

3 MS. FUNK: Your Honor, I have nothing else for

4 this witness. I have no other witnesses for today.

5 Thank you.

6 THE COURT: Thank you. Thank you.

7 MS. FUNK: I would like to confirm I spoke with
8 Mr. Fristik over a week ago. I will be having a witness
9 go to the BCA to inspect some additional database
10 information that I did just want to confirm that the BCA
11 has been made aware of that and that they are expecting
12 him?

13 MR. FRISTIK: They're aware of that.

14 THE COURT: Okay.

15 MS. FUNK: Thank you.

16 THE COURT: Could somebody help Kerri? I want
17 to make sure we have 27 exhibits here before we leave
18 this afternoon.

19 MR. FRISTIK: Starting at 9:00 Monday?

20 THE COURT: Yes, 9:00 Monday morning.

21 (5:57 p.m.)

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