

STATE OF MINNESOTA

DISTRICT COURT

COUNTY OF HENNEPIN

FOURTH JUDICIAL DISTRICT

State of Minnesota,

ORDER AND MEMORANDUM

Plaintiff,

vs.

Brian Ladell Dishmon,
James Leroy Bozeman,
Rodney R. Derby,

File Number: 99047345
99069306
99079650

Defendants.

The above-entitled matter came on for hearing before the Honorable Thor Anderson, one of the Judges of the above-named Court, during the months of January and February, 2000.

STEVE REDDING, ESQ., Assistant Hennepin County Attorney, appeared as counsel for and on behalf of the State.

PATRICK SULLIVAN, ESQ., Assistant Hennepin County Public Defender, appeared as counsel for and on behalf of the Defendants.

Based upon the file, the record and proceedings herein,

IT IS HEREBY ORDERED:

1. That the DNA matches found by the Minnesota BCA in these cases are admissible and can be described to the jury as set forth in this memorandum.
2. That the attached memorandum be incorporated herein.

BY THE COURT:

THORWALD H. ANDERSON

Thor Anderson
Judge of District Court

Dated: March 3, 2000

MEMORANDUM

In this consolidated pretrial motion the defendants, and each of them, move to suppress evidence obtained by the Minnesota Bureau of Criminal Apprehension Laboratory using the ABI 310 Genetic Analyzer and the Profiler Plus and Cofiler kits, which evidence shows a "match" with the DNA profile of the defendant with crime scene evidence. The grounds for that motion are the alleged failure by the State to show acceptance in the scientific community of the reliability of the method, the failure to prove acceptable laboratory reliability and a failure to provide needed and required discovery. Should these joint suppression motions be denied the defense further challenges the State's announced intention to offer statistical evidence using the so-called "product" method of computation. Portions of the months of January and February of the year 2000 were occupied in taking evidence on the issue. The matter has been well-tried and well-briefed by the State and the Defendants.

THE DNA TEST ITSELF

As our appellate courts have recognized, and as the testimony at this hearing confirms, DNA is a long double stranded molecule found in chromosomes carried in cell nuclei. It occurs in all cells that have a nucleus. Most

sections of the DNA molecules vary little among individuals within a species but some sections are polymorphic meaning they do vary. If two fragments do not match they could not have a common source but if they do match they might have a common source. The theory underlying the forensic use of DNA profiles is that as the number and variability of the polymorphisms utilized in the typing procedure increases, the odds of two people having the same profile become vanishingly small. See State v. Bloom, -516 N.W.2d 159, 161 (Minn.1994).

Witnesses in this hearing described each full DNA strand as having 3 billion parts (called ^{pairs} baselines). It would be impossible to map all 3 billion baselines in each DNA test, but present biological theory is, our witnesses opine, that if one could do this except for identical twins, no two people would have the same DNA profile. Just as it never can be proven that no two snowflakes are identical (because not all snowflakes have been examined), it is impossible to prove that the full DNA double strand is unique (except for identical twins) because all 3 billion baselines of every human being that has ever existed can never be compared. But if the scientific understanding of human genetics is correct, each full 3 billion baseline DNA strand is unique, except for identical twins.

What was done in the cases at bar, and what is done in

the typing and profiling method used in these cases, 13 locations on the DNA strand are compared and if all are identical it is considered a match. A statistic can be generated, based on the population subset of the defendant, which purports to show the chances of more than one person having the identical match in all 13 locations.

As stated in Bloom, supra, this underlying theory has been accepted by our courts as no longer requiring reproof in each case with the caveat that (a) there are some restrictions on how the statistics are explained to the jury and (b) the lab involved must be shown to follow appropriate established protocols and procedures, and (c) appropriate discovery must be available.

The defendants in our cases at bar do not challenge the concepts so far described, and the Court does not consider their validity or acceptance in the scientific community to be before it.

The laboratory techniques of profiling the DNA molecule have progressed from one to another and still yet on to another in rapid succession, challenging our legal system's ability to keep up. And it forces the courts to wrestle with the question of what if anything must be relitigated every time a new lab technique appears which at bottom does the same things as the old technique. As will be discussed

later, this Court believes that State v. Jobe, 486 N.W.2d 407 (Minn.1992) answers this question.

Our case involved the so-called PCR-STR typing. In particular, a specific device, the ABI Genetic Analyzer 310 using the Profiler Plus and Cofiler kits were used.

As the Court understands statements by defense counsel during the hearing and as the Court understands defendant's brief the validity of PCR-STR testing (to be briefly discussed below) or its acceptance in the scientific community is not challenged and is not an issue. One defense witness stated he did not believe STR testing to be accepted, but that does not appear to be the essence of the defense position, nor does the witness's assertion seem to be consistent with other evidence.

PCR is an abbreviation of "polymerase chain reaction" which is a methodology of typing DNA samples. It differs from the prior method because the enzyme polymerase causes certain target areas of small DNA fragments to be duplicated many times and enables very small samples to be accurately typed. The PCR method also permits typing in a very short time compared with prior methods (which required the decay of radioactive materials).

This Court finds and believes the defendants concede that the scientific basis and theory of DNA typing using the

PCR methodology is not in dispute and is generally accepted in the scientific community. It is also at present generally accepted for forensic use. A characteristic of PCR typing as presently done is the use of locations on the DNA strand containing short tandem repeats (STRs) of baseline patterns often containing only a few thousand ^{2.} ^{pairs} baselines. Thirteen locations have been selected and are universally accepted for use in looking for a "match". The number of short tandem repeats at these locations tend to vary from person to person and if all 13 locations of the known and questioned sample are identical a "match" is considered to have been made. The Court finds that the STR methodology of PCR typing is generally accepted (and this Court believes the defendant concedes such general acceptance) in the scientific community.

In the cases at bar equipment and chemical compounds are used which are relatively new and differ from prior DNA-PCR-STR typing in that such equipage is a "multiplex" system that can read all 13 locations in one "pass" or procedure. It is to the use of this multiplex system the defendant objects.

The devices used are named the ABI 310 Genetic Analyzer and the Profiler Plus and Cofiler kits used with it. The Court must now ascertain what must be shown by the State to justify admission of DNA matches so obtained.

The defendants, for their part, frame the issue this way: "Is DNA typing using the Profiler Plus and Cofiler kits on the ABI 310 Genetic Analyzer, as performed at the Minnesota Bureau of Criminal Apprehension, accepted in the scientific community as trustworthy and reliable?" (See page 12, Defendant's Written Closing Argument.)

The State, for its part argues that once the PCR-STR system of testing is accepted in the scientific community (and the Court finds and understands the defendant to concede that it is) the only issue is whether the procedures followed in the lab (including, of course among other things, the validation in the lab of the ABI 310 and kit procedures) meet accepted and appropriate standards and controls.

The State relies on State v. Schwartz, 447 N.W.2d 422 (Minn.1989) and State v. Jobe, 486 N.W.2d 407 (Minn.1992) arguing that such is the ruling in those cases with reference to the old RFLP typing method which had then, as the PCR-STR typing method does now, met the Frye/Schwartz scientific acceptance theory.

This Court concludes, relying on Schwartz and Jobe, supra, that because PCR-STR typing meets the Frye/Schwartz test, it is not required that the use of the 310 Genetic Analyzer and associated kits or their use by the BCA lab be found "generally acceptable in the scientific community" but

only that the lab meet accepted and appropriate standards and controls.

Should this Court be mistaken and the use of ABI 310 and its kits must be accepted in the scientific community the best view of the evidence is that they are. Scientific articles and testimony of prosecution witnesses convinces the Court that there is such acceptance. In particular the testimony of Dr. Eisenberg, Dr. Budowle, Ann Gross and Pat Wojtówicz are to this effect, which then brings the Court to the next issue, to wit: What are those standards and controls and does the evidence show the lab has met them?

THE LAB

Schwartz, supra, holds that once the forensic use of DNA methodology is accepted, admissibility of specific test results hinges on the laboratory's compliance with the appropriate standards and controls and availability of their testing data and results (i.e. pretrial discovery).

Jobe, supra, teaches this Court that a Frye hearing is still required but should focus on compliance with the appropriate standards and controls. Reliability of the test, says our Supreme Court, is crucial; and compliance by a lab with appropriate standards and controls is a good indicator of lab test result reliability.

This brings the Court to the question of what the

appropriate standards and controls are. This is a moving target because over the years the source of the guidelines and the guidelines themselves have changed.

Prior to 1994 a Technical Working Group on DNA Analysis Methods (TWGDAM) formulated guidelines for DNA testing labs. Our courts accepted these as appropriate guidelines. Subsequently Congress passed the DNA Identification Act of 1994. This Act authorized the creation of a DNA Advisory Board (DAB) whose duty included developing standards of quality assurance for forensic labs testing DNA samples. Such guidelines were formulated and are in evidence as Exhibit 26. They supercede other guidelines in force previously.

This Court finds that the DAB guidelines as amended from time to time constitute a reasoned, disciplined formulation which serves the same purpose today as the TWGDAM guidelines did when approved by our appellate courts and presently constitute the foundational requirements our appellate courts would require this Court to follow.

The evidence in this case indicates, and the Court finds, full and total compliance with DAB guidelines. There is no credible conflicting evidence. Affidavits of BCA Scientists Gross, Wojtowicz and Bergman detail years of study on STR methodology sometimes in cooperation with other

forensic laboratories. It also details validation studies as required by the DAB guidelines and the typing of DNA samples for the BCA population database.

The validation studies performed by the BCA are particularized in the affidavit of Ann Gross. That affidavit further particularizes the compliance with each standard of the DAB guidelines.

The BCA lab also passed its second American Society of Crime Laboratory Directors (ASCLD-LAB) inspection which substantially tracks DAB standards.

Two issues raised during the hearing deserve comment at this point. Firstly, the BCA lab, of course is not an error-free lab. Everyone agrees that no lab can be. But at least the discovered errors are few in number: On one occasion a report was mistyped and the error was found and corrected after the report was mailed out. On another occasion samples were switched and at another time period difficulty was experienced in properly sanitizing certain lab equipment (a "slot ^{block} block") thus creating contamination. Each of these errors were internally discovered and corrected and in each case procedures were adopted to minimize the chance for recurrence. The important thing, however, is that even if these errors did not occur it is a conclusive, almost irrebuttable presumption that at some point a mistake or

mistakes will be made.

This Court believed, however, that the teaching of Schwartz is not that a mistake-free lab is required. The requirement is that the lab meet acceptable standards and the BCA lab does. Compliance has been shown with DAB guidelines and the lab has passed ASCLD-LAB outside inspections.¹ The ABI 310 and its associated kits have been verified and the lab is run in accordance with acceptable procedures. That is the test. The lab passes it.

A second issue is appropriate for discussion here and will fit in later with the question of informing the jury of a lab error possibility statistic. It should be noted that separate from all discussion of lab reliability our legal system affords a proven method of testing the accuracy of the particular test sought to be introduced. And of course, it is this accuracy which is really the issue in the case. First of all the witness can be cross-examined and the witness's lab reports are available to assist in this endeavor. Secondly, the defense may send a representative to watch the test and thirdly, samples are available for retest. Defendant argues these last two items should be ignored in

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It appeared from the answers to defense counsel's questions that proficiency tests were given to teams, rather than individuals. Follow-up testimony by Ann Gross indicated this is not true.

this Court's consideration of the matter because they shift the burden of proof. They do not do so, any more than the right of cross-examination shifts the burden of proof. Cross-examination and discovery are simply instruments provided to a defendant to test the truth of the prosecution witness. This has nothing to do with the burden of proof. So, with respect to the use of the ABI 310 and its kits and the procedure for the DNA test this Court finds the BCA lab meets accepted standards of procedure and performance.

THE DEFENSE SUBPOENA TO PE BIOSYSTEMS

In a timely fashion the defendants herein requested this Court to sign the required paperwork to institute a subpoena to PE Biosystems to produce extensive records including manufacturer's validation studies and other material. PE Biosystems is headquartered in California and the subpoena was certified to the California court under the appropriate interstate compact. A hearing is set for March 8, 2000 and PE Biosystems aggressively opposes the subpoena as they have in other cases, with mixed results. The prosecution here has done nothing to frustrate the subpoena and does not oppose it. This Court has seen an affidavit filed in this action by a PE Biosystem employee and PE Biosystems claims trade secrets, overwhelming expense and effort and reading between the lines claims that the material is not needed here.

While there is an important issue here, it is not a discovery issue. PE Biosystems did not perform any tests offered in evidence here. (In Schwartz, Cellmark, whose data was not disclosed, had performed the tests). It is also important to note that in a Minnesota criminal case discovery is an obligation of one party toward the other. PE Biosystems is not a party and they have no discovery obligations. Their obligations arise from and only from the obligations imposed on them by the subpoena. The prosecution is obligated to provide discoverable material it possesses or, possibly, material it can obtain. But the State is not obligated to supply material it does not have and to which it does not have access. The Rules cannot be read to require the impossible.

What the issue really comes down to is: Can the State meet its burden of showing the admissibility of the tests run on the PE Biosystem's equipment without the defense subpoenaed material? And even if the State can, is the unavailability of this material, even if the unavailability is not the State's doing, of such a nature that defendants cannot get a fair trial under the due process clause without it?

It should first be noted that this issue is technically not ripe because it is possible the California court will

enforce the subpoena. So far that Court has not ruled. This Court feels uncomfortable, however, delaying its decision pending that leisurely proceeding. Certainly should documents or useful live testimony become available this matter could be reopened before this Court or the trial judge by either party.

This Court concludes, however, that the State has made the required showing of admissibility without the use of the material (interestingly, the State never asked for it) and the defense suffers no known harm by not having it. The reason in layman's terms is that the BCA lab has validated the system as have other labs. The system simply has been shown to work, time after time, by lab after lab, with or without studies from PE Biosystems. The system is like a Model A Ford. Thousands of owners can tell us it works even if Henry Ford can't or won't explain it. The customers have thoroughly and scientifically validated this system. And because the BCA's validation is in evidence here and is subject to impeachment here and before the jury, no due process violation or unfairness befalls the defendant.

POPULATION GENETICS AND THE ISSUE OF
HOW BEST TO DESCRIBE THE SIGNIFICANCE OF
A DNA MATCH TO THE JURY

Having decided that evidence of a "match" of the DNA of defendants and DNA at the crime scene, obtained by the BCA lab with the ABI 310 and its kits, the Court must address the question of how best to describe the significance of the match to the jury. The answer to this issue is rooted in the science of population genetics.

The parties treated the Court to a tutorial on the arcane world of population genetics. This issue of how best to describe the significance of a match has troubled our courts for years, starting with the Kim trilogy which held that statistical probability could not be presented to the jury to show likelihood of evidentiary certainty. State v. Kim, 398 N.W.2d 544 (Minn.1987).

The latest word on the subject is State v. Bloom, 516 N.W.2d 159 (Minn.1994) and Bloom II, the appeal to the Court of Appeals of the subsequent trial itself. State v. Bloom, (in Court of Appeals C8-95-218). Bloom justified its conclusion on statistical probability evidence on the National Research Council's 1992 report's (NRCI) adoption of a so-called conservative "interim ceiling method" for probability computation. The NDA testing method was the old

RFLP testing method.

The State now argues that a further report by a new National Research Council (NRC II) renounces the "interim ceiling method" and recommends the product rule (NRC II Recommendation 4.1).

Before going further it should be said that two holdings of Bloom, in this Court's opinion, persist even with the PCR-STR multiplex testing and should govern the trials in these consolidated cases. The first rule is that a witness may not testify that a DNA strand is "unique" if tested by the PCR STR method. It simply may not be. In fact, even the use of the product rule would imply it is not unique. It cannot be said to be unique because only 13 locations of 3 billion have been tested.

The second rule that persists, in this Court's view, and is still appropriate with the PCR-STR method is that a properly qualified expert, assuming adequate foundation, is allowed to express an opinion that to a reasonable degree of scientific certainty the defendant is or is not the source.

Focusing on the term "adequate foundation" it should be pointed out that such a foundation includes a valid population data base to use as a foundation for any conclusion testified to, whether it be non-statistical ("to a reasonable degree of scientific certainty the defendant is or

is not the source") or statistical by the product rule or even the most conservative counting method. So the Court must examine whether or not the BCAS has valid population data bases.

A primary area of concern during the evidentiary phase of the hearing was whether the BCA population data bases can be used to calculate a statistical frequency for evidence profiles. Dr. Carmody's letter of 12/21/98 to the BCA contains the results of his statistical analysis of 12 of the loci in the four Minnesota data bases. The loci were examined for evidence of deviations from Hardy-Weinberg and linkage equilibrium using three separate computer programs. Dr. Carmody finds the BCA population data bases usable to calculate a statistical frequency. Defense witness Dr. Mueller finds two of the data bases out of linkage equilibrium, but he did not apply a correction (known as the Bonferroni correction) which was used, and the Court finds was appropriate to use, by Dr. Carmody. This Court finds that the BCA data bases are suitable for use and Dr. Mueller's testimony would go only to the weight of the evidence.

The last issue turns on how, if at all, statistical probabilities of a match can be presented to the jury. In Bloom, our Supreme Court permitted the interim ceiling method

described in NRC I. This ceiling method was described for VNTR DNA fragments. The issue is whether that "interim ceiling method" computation is stare decisis as to DNA fragments such as STRs; and if not, is the interim ceiling method appropriate anyway, and in any event what method is appropriate?

A new National Research Council was created after NRC I and issued a report known as NRC II in 1996. While that report is not, of course, binding on our Minnesota Judiciary, it represents, and this Court finds that it represents the best scientific thinking of the scientific community on the subject. It would meet the Frye test as clarified by Schwartz. That report concludes that the "interim ceiling method" has no legitimate application or scientific bases in DNA-STR testing and concludes the so-called "product rule" as scientifically described in Recommendation 4.1. of NRC II (which is in evidence in this case). Therefore, this Court concludes that the "interim ceiling method" has no application to DNA STR testing and therefore the requirement of its use set forth in Bloom is not stare decisis in the case at bar. This Court finds the "product" method as computed by the formula described in 4.1 of NRC II is admissible.

A further remark is in order. Often the product method

results in a statistic of one in so many billions or quadrillions that the denominator is larger than the present earth's population. The figure is ridiculed for that reason. That fact neither impeaches the statistic's validity nor does it justify a conclusion that the 13 loci match is unique. There still may be within the present population an identical match and may be among persons born and died in the past or yet to be born in the future.

Attached hereto in Exhibit A is a list of facts found by this Court which are supplemental to the fact finding alluded to in this Memorandum and said Appendix is included herein and adopted as in part hereof.

A P P E N D I X A
S U P P L E M E N T A L F I N D I N G S O F F A C T

1. That the State seeks to admit evidence of DNA testing performed by the Minnesota Bureau of Criminal Apprehension (BCA) in each of the above-entitled cases.
2. That the testing was performed at the BCA using a methodology known as PCR STR typing.
3. That the admissibility of DNA typing employing this methodology has apparently not been decided by any trial or appellate court in Minnesota.
4. That prior Minnesota case law has developed what can be termed a two-prong test for the admissibility of DNA typing.
5. That the first prong is governed by the case of Frye v. United States, 293 F. 1013 (D.C. Circ. 1923), and requires that the test must be generally accepted in the scientific community.
6. That the second prong is that the admissibility of test results in a particular case "hinges on the laboratory's compliance with appropriate standards and controls, and the availability of their testing data and results." State v. Schwartz, 447 N.W.2d 442, 428 (Minn.1989).

7. That the DNA typing at issue in Schwartz was performed by the methodology known as restriction fragment length polymorphism (RFLP) typing.
8. That since the time of the Frye hearing in Schwartz, the BCA, other forensic labs, and many DNA labs engaged in the research and medical diagnostics have begun using the methodology known as polymerase chain reaction (PCR) to type DNA samples.
9. That the scientific basis and theory of DNA typing using the PCR methodology is not in dispute and is generally accepted in the scientific community.
10. That while some years ago a dispute existed in the scientific community about whether or not PCR typing was generally accepted for forensic use, that dispute has been resolved in favor of general acceptance.
11. That while RFLP and PCR typing are different methods of typing DNA, each employs a number of steps in its procedure which are very similar to each other.
12. That the one additional step in PCR typing not found in RFLP typing is that PCR utilizes a process to amplify or reproduce certain "target" areas of small amounts of DNA. This process results in millions of copies of those "target" areas being made so that there is then a sufficient amount of DNA that can be typed. RFLP

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testing requires a larger amount of existing DNA, and if the initial sample is too small, no typing result will be obtained.

13. That the defendants through their counsel have conceded this, and in fact have conceded that PCR STR typing is generally accepted.
14. That the defendants have focused their dispute on whether or not the particular kits and instruments used in PCR STR typing are generally accepted and whether or not the manufacturer of these items must provide discovery of studies done by the manufacturer on these kits and instruments, and what is known as the "primer sequence" for some of the components of these kits.
15. That the Court has determined that the State must demonstrate general acceptance in the scientific community of the underlying method and theory behind PCR STR typing, but that the particular machine and kits only need to be shown to have been used in accordance with appropriate and accepted standards, including verification by the BCA lab and demonstrated lab proficiency.
16. That PCR STR typing involves the generally accepted procedures entailed with PCR using a number of loci known as short tandem repeats (STRs).

17. That STRs are repeating units of DNA similar to the variable number of tandem repeats (VNTRs) used in RFLP typing.
18. That STRs are very common and scattered throughout the human genome in large numbers.
19. That STRs have come into increasing use in DNA research, medical diagnosis and forensics over the past few years, and that there is a huge body of scientific literature pertaining to STRs.
20. That pertaining to the methodology of PCR STR typing used by the Minnesota BCA, the State called Ms. Ann Gross of the BCA; Ms. Patricia Wojtowicz of the BCA; Mr. Dan Bergman of the BCA; Dr. Bruce Budowle, Chief of the Forensic Science Research Unit at the FBI; Dr. Arthur Eisenberg, Associate Professor in the Department of Pathology, Director of the DNA/Identity Lab at the University of North Texas, and Chairman of the United States DNA Advisory Board; and Dr. P. Michael Conneally, Distinguished Professor of Medical Genetics at Indiana University.
21. That beginning as early as 1993 the FBI and BCA began studying the feasibility of using STRs in forensic typing employing the PCR methodology.

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22. That in 1996 the FBI sponsored a project entitled the "STR Standardization Project," and that the BCA was one of the more than 20 laboratories who participated in this study.
 23. That the project focused on identifying and validating methods and procedures for a set of up to 15 loci to be used by federal, state, and local forensic laboratories in DNA casework.
 24. That the goal was to develop a system which would also be used in CODIS (Combined DNA Index System). CODIS is the computerized database of DNA profiles which allows comparisons to be made between DNA profiles obtained from casework specimens and the DNA profiles obtained from the known samples of convicted offenders.
 25. That an additional objective of the STR Standardization Project was that all STR systems were to be validated for use with automated detection equipment.
 26. That the project was divided into three phases, the goal of the first phase being to examine a number of STR loci to determine and identify which if any of the large number of STRs might be suitable for forensic testing, especially using these STRs in multiplexes, or many STR genes in one reaction.

27. The advantages of multiplexes are that by doing many genes at once, there is a considerable time saving as opposed to testing genes individually, and testing a large number of genes at once reduces the chances of human error because the samples are handled fewer times.
28. That the second phase of the project was designed to more closely study such things as quantity of DNA to be input, the appropriate number of amplification cycles to be run, the performance of various enzymes, the optimal DNA extraction methods, etc.
29. That the third phase was to consist of population studies performed on a large number of samples by a number of labs so that frequency estimates could be established.
30. That the project selected 13 core genetic loci which were found to be suitable for use by forensic laboratories participating in CODIS.
31. That multiplex kits were to be designed to incorporate at least two (2) overlapping loci as a quality assurance feature.
32. That multiplex kits and instruments designed to automate significant portions of the process were developed by a number of manufacturers, including PE Applied Biosystems, Promega, and Hitachi.

33. That the BCA, FBI and a number of other DNA labs chose kits and instruments developed and sold by PE Applied Biosystems for use in their laboratories.
34. That the kits developed by PE Applied Biosystems to meet the requirements of the STR Standardization Project are the Profiler Plus and Cofiler kits.
35. That the instruments developed by PE Applied Biosystems are the 310 and the 377.
36. That these kits and instruments have come into wide use in forensic labs around the USA as well as the world.
37. That prior to actually beginning testing of actual evidence samples from law enforcement agencies, the FBI and BCA each performed a number of studies designed to determine whether or not these kits and instruments are capable of producing accurate and reliable DNA typing results.
38. That the conclusion drawn by the FBI, BCA, and a number of other labs who participated in similar studies to validate these kits is that, when used according to the procedures developed for their use by the laboratory, do produce accurate and reliable typing results.
39. That there exist in the scientific community a set of guidelines or standards designed to govern the testing of evidence samples in forensic DNA testing labs, and

that these guidelines are known as the DAB (DNA Advisory Board) guidelines. The complete title is Quality Assurance Standards for Forensic DNA Testing Laboratories.

40. That these guidelines were promulgated by the DNA Advisory Board and took effect on October 1, 1998, and that they succeed guidelines formerly in effect known as the TWGDAM (Technical Working Group on DNA Analysis Methods) guidelines.
41. That State v. Schwartz, supra, referred to the TWGDAM guidelines as the proper "standards and controls" with which laboratories must demonstrate compliance.
42. That the affidavit submitted by Ann Gross details these guidelines and that the BCA does in fact comply with each section of the DAB guidelines.
43. That the affidavit submitted by Dan Bergman indicates that the BCA has been fully accredited by ASCLD-LAB.
44. That the supplementary affidavit of Dan Bergman further details that a significant portion of the ASCLD-LAB standards and criteria for accreditation directly track the DAB standards, thus providing further documentation and demonstration that the BCA complies with the DAB guidelines.

45. That there appears to be no evidence to indicate anything but full compliance by the BCA with the DAB guidelines, therefore indicating that PCR STR typing as performed by the BCA complies with the second prong of Schwartz.
46. That although the argument has been advanced that the State must demonstrate general acceptance down to the level of the particular kits and instruments used by the BCA, the Court has determined that the general acceptance standard must be applied to PCR STR methodology, and that methodology is clearly accepted within the scientific community.
47. That the Court has found no support for applying the general acceptance standard down to that level, either in Minnesota law or the law of any other jurisdiction.
48. That the Schwartz prong two requirement that the laboratory demonstrate that it complies with the applicable standards and controls is a proper and legal requirement to ensure that labs produce accurate and reliable forensic testing results.
49. That the reliability of these kits and instruments has been demonstrated through the studies done by the BCA, which have been made completely available to the

- defense, thus validating the ABI 310 and its kits as meant by NRC II and DAB guidelines.
50. That the defense has requested that PE Applied Biosystems provide what is known as the primer sequence for the primers used in the Profiler Plus and Cofiler kits.
 51. That although the exact structure of these primers might be of interest, the defense has not demonstrated any particularized need for this information, nor that there is any indication that knowing this information would enable the defense experts to come to any conclusions about the reliability and accuracy of these kits that could not be reached in other ways.
 52. That the Minnesota BCA has compiled four population databases by obtaining DNA extracts from the Memorial Blood Center of Minneapolis.
 53. That the databases consist of 150 Caucasian, 150 African American, 200 Native American, and 149 Hispanic samples.
 54. That these databases are of sufficient size so that they will provide reliable and accurate estimates of the allele frequencies for the 13 CODIS loci.
 55. That it is necessary and important that when a DNA match has been declared between a known sample and an evidence

sample, that some estimate of that profile frequency be provided to the finder of fact.

56. That all three experts called by the State and the lone expert called by the defense concerning the question of how to present testimony concerning the significance of a DNA match agreed that the statistical frequency should be calculated according to Recommendation 4.1 of NRC II.
57. That this method is generally accepted in the scientific community as a reliable and accurate method of calculating the random match probability, as defined in Bloom.
58. That the method approved for calculating the random match probability in Bloom, known as the ceiling method, is not appropriate to calculate the random match probability for a match developed by BCA DNA STR testing using the CODIS system for two reasons: 1. STRs are discrete alleles as opposed to continuous alleles like the alleles in the VNTR system addressed in Bloom. NRC II specifically declares that the product rule is the appropriate method to calculate frequencies in discrete allele systems. "The ceiling principles were intended for VNTRs with many alleles no one of which has a very high frequency. They are not applicable to PCR-based systems, which ordinarily have few alleles." NRC II, p.

- 158; and 2. "Our view is that sufficient data has been gathered that neither ceiling principle is needed." NRC II, p. 158. "In general, the calculation of a profile frequency should be made with the product rule." NRC II, p. 5. NRC II reflects the opinion of the scientific community that the ceiling methods are no longer generally accepted as accurate and reliable methods of calculating a profile frequency.
59. That statistical analysis performed by Dr. George Carmody, and reviewed by Dr. P. Michael Conneally indicated the databases may be used to calculate a profile frequency, if the recommendations of NRC II, specifically Recommendation 4.1, are followed.
60. That Dr. Carmody testified that he used three separate computer programs to analyze the data bases for deviations from Hardy-Weinberg and linkage equilibrium, and that applying the Bonferroni correction revealed no significant deviation.
61. That defense expert Dr. Mueller indicated that he used one of the programs used by Dr. Carmody and did not apply the Bonferroni correction.
62. That Dr. Mueller opined that he found deviation in the Caucasian and Native American data bases, and that as a result, those data bases should not be used to calculate

- a profile frequency. Dr. Mueller recommended the use of the "counting method" to calculate a frequency from these two data bases. NRC II rejects the "counting method" as a suitable method to present a profile frequency. NRC II, p. 159-160.
63. That this same opinion by Dr. Mueller was presented to the Minnesota Supreme Court in Bloom, and Dr. Mueller's suggestions were rejected. For those same reasons, the suggestion of not using the Caucasian or Native American data bases is inappropriate.
64. That Dr. Mueller's opinion as to the effect of his purported finding of linkage equilibrium is relevant, if at all, to the weight to be given the profile frequency, not to its admissibility.
65. That Dr. Mueller also suggested a method of presenting profile frequency evidence to the jury by combining the calculated profile frequency with a calculation of the "error rate."
66. That this proposal has been rejected by NRC I, State v. Bloom, and that no court decision from any jurisdiction in the United States adopting this method could be found.
67. That combining profile frequency and error rates is not a method generally accepted in the scientific community

to accurately and reliably state the significance of the random match probability.