STATE OF VERMONT
GRAND ISLE COUNTY, ss.

VERMONT DISTRICT COURT
DOCKET NO. 57-4-96 GiCr

STATE OF VERMONT)
)
v.)
)
MICHAEL PFENNING)

DECISION AND ORDER REGARDING
DEFENDANT'S MOTION IN LTMTNE TO EXCLUDE RESULTS OF DNA TESTING

I. Introduction.

Defendant is charged with the second degree murder of Lyda Jameson on March 2, 1976. During the autopsy of the victim's body, "a number of human hairs not matching the victim were collected from Jameson's body."[1] Defendant, (as well as at least 24 other persons), had attended a party near the victim's residence, where the body had been found. According to the affidavit of probable cause, the hairs collected from the deceased's body displayed the same microscopic characteristics as hairs obtained from Defendant.

In March, 1994, samples of hair recovered from the deceased's body were sent to Cellmark Laboratories to determine if DNA could be recovered from the samples and typed. DNA analysis was later performed by Genelex Laboratories as well. Both laboratories have reported DNA typing profiles which are consistent with Defendant's DNA profile. Defendant has filed a motion in limine seeking to exclude the results of DNA analysis on the grounds: (1) DNA analysis utilized by the laboratories does not comply with minimum standards enunciated in Daubert v. Merrell Dow Pharmaceuticals, Inc., 509 U.S. 579 (1993) and State v. Streich, 163 Vt. 33 I (1995); (2) Deficient laboratory methodology makes the testing results

[1] Affidavit of probable cause dated April 15, 1996.

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unreliable; and (3), the prejudicial effect of admitting the evidence outweighs whatever probative value it may have.

The admissibility of DNA test results for inclusion based on PCR techniques has not yet been reviewed by the Vermont Supreme Court. This Court conducted evidentiary hearings concerning admissibility of the DNA test results at the Costello Courthouse in Burlington on December 6-10, 1999, December 17, 1999, and February 17, 2000, taking testimony from six prosecution experts and three defense experts. The transcript from the hearings numbers over 1000 pages and the record contains over 100 exhibits.

II. The Legal Standard.

In State v. Streich, 163 Vt. 331 (1995), the Vermont Supreme Court adopted the standard enunciated by its federal counterpart in Daubert v. Merrell-Dow Pharmaceuticals, Inc., 509 U.S. 579 (1993) to test the admissibility of novel scientific evidence in Vermont courts. Streich, 163 Vt. at 342. The Daubert decision replaced the then-widely accepted "Frye[2] 'general acceptance' requirement with a flexible standard governed by two principles: reliability and relevance." Streich 163 Vt. at 342, citing Daubert, 509 U.S. at 595.

> Reliability is assured if the expert testimony is supported by "scientific knowledge," defined as information that is more than a subjective belief or unsupported speculation, and that is grounded in the methods and procedures of science.. . . Science represents a "'process for proposing and refining theoretical explanations about the world that are subject to further testing and refinement.'"

Streich, 163 Vt. at 343, quoting Daubert, 509 U.S. at 590 (emphasis in original).

The Vermont Supreme Court proceeded to adopt the "four non-exclusive factors

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[2] See Frye v. United States, 293 F. 1013 (D.C. Cir.1923).

designed to assist a trial judge how to determine whether expert testimony was sufficiently rooted in 'scientific knowledge' to be admissible:" Id. at 343.

> (1) Whether the theory or technique involved is capable of being tested;
> (2) whether the theory or technique has been subjected to peer review and publication;
> (3) the known or potential rate of error associated with the scientific technique; and
> (4) whether the theory or technique has been generally accepted in the scientific community.

Id. at 343 (citations to Daubert omitted).

As in the Streich case, the relevancy component of the analysis is not at issue. Here, as in Streich, the identity of the perpetrator of the offense is a key factual issue. i s shows that the DNA profile of the hairs found at the crime scene'matches Defendant's DNA profile, such evidence is clearly relevant. Id. It is the purpose of this decision to apply the Streich/Daubert standards to the credible evidence.

III. The State's Witnesses

A. Dr. Robin Cotton.

Dr. Robin Cotton is the forensic laboratory. director at Cellmark Diagnostics, a privately-owned laboratory engaged primarily -in forensic testing, in Germantown, Maryland. She has a bachelor of science degree and a master's degree, both in biology, and both from Southern Methodist University in Dallas, Texas. She also has a Ph.D. in molecular biology and biochemistry from the University of California at Irvine. After receiving her Ph.D., Dr. Cotton was employed at the University of Iowa for three years as a post-doctoral fellow in the Department of Biochemistry. She subsequently worked as a staff fellow for five years at the National Institutes of Health, and in 1988 left NIH to work at Cellmark. Since obtaining her

Ph.D., she has engaged in continuing education, including several professional meetings each year. She has published five or six peer-reviewed articles, as well as other articles which are not peer-reviewed. Since. 1988 she has given presentations al scientific conferences relating to the use of DNA typing on biological evidence. In her current position at Cellmark, she is responsible for overall supervision of the forensic laboratory, doing technical review, along with two other Ph.D. level scientists, of cases tested in the laboratory, and testifying in court when necessary. She has supervised approximately 500 cases each year since 1990, and has done a technical review of approximately 'a quarter of those. She has previously testified as an expert on the use of DNA technology to identify genotypes in biological evidence and to compare those to known individuals. She has testified about 150 times in about 35 states. The Court finds that Dr. Cotton is qualified as an expert in molecular biology and DNA identification methods. (Tr. 12/6/99 at 4-9).

B. Anjali Swienton.

Anjali Swienton (known as Anjali Ranadive at the time of the testing she conducted in connection with this matter), is currently employed by ACS Defense, an on-site federal contract& of the National Institute of Justice, the research branch of the United States Department of Justice. Her current work involves administering grants through the Office of Science and Technology in the Investigative and Forensic Sciences Division of NIJ, the bulk of which are concerned with DNA improvement capabilities and capacities. She is also a 'second-year student at the American University Law School in Washington, D.C. She was employed by Cellmark Diagnostics from June, 1991 through March, 1998, first as a laboratory assistant, then as an analyst in the Paternity Division, and later as an analyst in the Forensic

Division. She worked on paternity cases for about a year, using DNA technology, before spending about four and a half years in the Forensic Division. She holds a bachelor's degree in biology from Johns Hopkins University in Baltimore, Maryland, and a master's degree in forensic science from George Washington University in Washington, D.C. Throughout her tenure at Cellmark, Ms. Swienton was given standard training for each of the different DNA procedures for which she did casework. These usually involved several months of training using mock samples obtained from the quality control manager. She was required to demonstrate proficiency with the mock samples, then was given a proficiency test. After completing this training, she would use that particular technique in casework. She estimated that she had done several hundred cases involving the PCR technique, with each case involving one to dozens of samples. The majority of those cases involved the Polymarker/DQAlpha system. She estimated she had also done about two hundred cases involving the CTT STR system, as well as about a hundred additional cases using a gel-based system other than the CTT STR system. She was also involved in RFLP testing, a non-PCR, gel-based system, in the Paternity Division, as well as in typing convicted sex offenders under Cellmark contracts with two states, also using RFLP technology. While employed at Cellmark, she was required to undergo a minimum of two proficiency tests per year for each' type of system in which she conducted casework. To the best of her knowledge, she passed every proficiency test that she took. While employed at Cellmark, she was also involved in continuing education, including both in-house training and national forensic meetings. While employed at the Justice Department, she has been involved in organizing conferences involving forensic DNA testing, and has attended several national and local and FBI

sponsored meetings as well. She is a member of the American Academy of Forensic Sciences and the Mid-Atlantic Association of Forensic Sciences. The Court finds that Ms. Swienton is qualified as an expert in the laboratory analysis of DNA using PCR, reverse dot blot and gel electrophoresis systems. (Tr. 12/1 7/99 at 6-14).

C. Juliet Harris.

Juliet Harris is employed as a staff DNA analyst at Cellmark Diagnostics. Her duties involve taking custody of forensic evidence and conducting DNA testing on that evidence. She has been employed in that position since May, 1999. She has a bachelor of science degree in biology from George Washington University in Washington, D.C., and a masters degree in criminal justice from the University of Colorado. Before working at Cellmark, Ms. Harris conducted RFLP DNA typing at the Fairfax Identity Laboratories in Fairfax, Virginia. She also worked for the American Red Cross in Baltimore, Maryland, in their histocompatibility laboratory, which does DNA typing relating to matching up transplant donors and patients. She was also employed at the Colorado Bureau of Investigation for about eight months, working in the crime laboratory, DNA and serology sections. She made solutions relating to DNA typing, poured gels, and conducted similar duties. She has received specialized training in PCR techniques, including attending an STR workshop at the South Carolina Law Enforcement Division in June, 1999, as well as training at Cellmark. The South Carolina training also included capillary electrophoresis. She has conducted a few hundred PCR tests, incorporating a few thousand samples. She has conducted approximately one hundred DNA tests using capillary electrophoresis. While at Cellmark, she has undergone one proficiency test, utilizing the PCR and capillary electrophoresis systems, and obtained the

expected results. Ms. Harris has not contributed to any scientific publications. The Court finds that Ms. Harris is qualified as an expert in the laboratory analysis of DNA using PCR and capillary electrophoresis. (Tr. 12/8/99 at 83-87).

D. Dr. George Riley

Dr. George Riley is a consulting forensic scientist, prior to which he was the scientific director of Genelex, a small DNA testing company located in Seattle, Washington. He was employed at Genelex for about four and a half years, leaving shortly before testifying in this case. He holds a bachelor of science degree in biology from Dickinson College, and a Ph.D. in biology from Georgetown University. His post-doctorate employment included a research position in the Genetics Department of the University of Washington, and a research position at the Seattle Biomedical Research Institute. Since obtaining his Ph.D., Dr. George Riley has engaged in'both genetics training and molecular biology training. He also engaged in continuing education as a part of his employment at Genelex. He has published a number of papers, the majority of which have involved methods used in DNA testing, although not specifically related to forensic DNA testing. He has also made a number of presentations at scientific conferences, the majority of them concerning forensic science. His duties at Genelex included supervising the paternity and forensic laboratories, as well as the convicted offender data bank testing laboratory. He reviewed work done by others as well as conducting some of the analytical work himself. He conducted the scientific management of the laboratory and Conducted validation studies, among other duties. He has conducted approximately 1,500 DNA tests himself, reviewed approximately 10,000 additional DNA tests, and supervised approximately 20,000 DNA tests. He has testified on about sixteen occasions

as an expert in DNA testing, eleven times for the prosecution, and 4 times for the defense, in about thirteen jurisdictions. The Court finds that Dr. George Riley is qualified as an expert in molecular biology and DNA identification techniques. (Tr. 12/7/99 at 66-72).

E. Piper Schwenke.

Piper Schwenke is currently employed at Cwiklik and Associates, in Seattle, Washington, and is also self-employed as a DNA consultant. Cwiklik and Associates is a forensic science firm, and Ms. Schwenke provides forensic support. Before beginning her employment there approximately a month before the hearing in this matter, she was employed at Genelex Corporation, where she worked for about three years. At Genelex she was employed as a forensic scientist, and her duties involved DNA analysis in criminal and civil cases. As such, she examined evidence, extracted DNA, and performed PCR typing using STR and Polymarker/DQAlpha systems, as well as RFLP analysis. She has a bachelor's degree in 'biology and psychology from Nebraska Wesleyan University, and has also taken graduate courses in immunology and genetics at the University of Nebraska in Lincoln. She also has an associate's degree in biotechnology from Seattle Central Community College: At Genelex, Ms. Schwenke was trained to do DNA extractions using various extraction techniques on varying cellular material and substrates. She was also trained to do DNA quantitation, RFLP testing, fluorescent STR testing, and Polymarker/DQAlpha testing. She has conducted approximately 100 tests involving the PCR technique. She underwent approximately six proficiency tests while at Genelex, and the results were correct in each case. She is a member of the Northwest Association of Forensic Science and the Puget Sound Forensic Science Association. The Court finds that Ms. Schwenke is qualified as an expert in

the laboratory analysis of DNA. (Tr. 12/8/99 at 3-8).

F. Dr. Frederick Bieber.

Frederick R. Bieber is currently employed as a professor at Harvard Medical School, where he teaches medical and graduate students in genetics and forensic science. He also works at Brigham and Women's Hospital as a medical geneticist. He earned a bachelor's degree in liberal arts, with a concentration in biology, from the State University of New York, and a master's degree in genetics at the University of Rochester School of Medicine, and a Ph.D. in human genetics from the Medical College of Virginia in Richmond. In 1980, he began a three-year post-doctoral fellowship in medical genetics at Harvard Medical School and at the Massachusetts General Hospital. In 1983, he was appointed to the faculty at the Harvard Medical School. He holds certifications from the American Board of Medical Genetics in three areas, medical genetics, clinical cytogenetics, and clinical molecular genetics. He is licensed by the State of New York as a laboratory director in genetic testing and paternity and identity testing. His professional organization memberships include the American Society of Human Genetics, the American Board of Medical Genetids, the American Academy of Forensic Sciences, and the Association for Molecular Pathology. He has published an estimated sixty or seventy articles in the area of molecular biology in peer reviewed journals. He is currently on the editorial board of Clinical Genetics, and served previously on the board of Clinical Dismorphology. He has also given presentations an estimated forty to fifty times to various organizations, including teaching conferences at MIT and at Harvard University, and at crime laboratories around the country, on the topic of forensic uses of DNA. As laboratory director, he supervises the genetic and autopsy studies

on all deceased newborns, stillborn infants, and spontaneously aborted fetuses that may have genetic disorders. He consults with families in the genetics clinic several days a week concerning genetic diseases or abnormal prenatal ultrasounds. He teaches residents about genetic disease, and he is one of the directors of the diagnostic laboratory that serves Brigham and Women's Hospital, Massachusetts General, Children's Hospital, and the Dana Farber Cancer Institute. That laboratory performs genetic studies on blood samples, skin biopsies, tumor cells, and bone marrow samples, and issues laboratory reports on those diagnostic findings. Dr. Bieber is also involved in forensic consulting work, which involves teaching attorneys around the country about genetics, especially forensic genetics and often mathematical genetics as it relates to identity testing and paternity testing. He serves on the Advisory Board of the American, Prosecutors' Research Institute in Alexandria, Virginia, part of which involves putting together three and four-day courses which take place two to four times a year to teach prosecutors and judges about the use of DNA evidence. He is also active with Massachusetts Continuing Legal Education, and is the director of a major course on DNA technology for that group, the participants in which are primarily defense attorneys. He has been hired by lawyers on both sides of criminal cases for review of DNA tests, and is a listed consultant for the Committee for Public Counsel Services, which is an organization of public defenders. He also consults in malpractice cases involving medical genetics. In the course of his work, he frequently uses statistical analysis and population genetics statistical information. He has studied math and statistics throughout his education, in both undergraduate and graduate work, and probability theory statistics, epidemiology; and population genetics, which is a subspecialized branch of genetics. His Ph.D. dissertation

research dealt with the population genetic study of deaf children at the Maryland School for the Deaf. He uses these mathematical approaches to genetics almost on a daily basis, sometimes in the clinic, where he calculates risk estimates for parents whose children may be at risk for problems. Dr. Bieber teaches the undergraduate genetics course at Harvard University, part of which deals with population genetics, and he teaches a graduate level course in forensic science, which covers population genetics. He also lectures on mathematical genetics to post-doctoral research fellows who are part of the American Board of Medical Genetics fellowship training program, and he is one of the directors of this program. He has been qualified to testify as an expert in forensic DNA testing and the statistical analysis of forensic DNA evidence, approximately ten to twelve times, in five or six different states. He was also previously qualified as an expert in a Vermont court. The Court finds that Dr. Bieber is qualified as an expert in the areas of human and medical genetics, forensic DNA identification testing techniques, and the statistical analysis of forensic DNA. (Tr. 1 2/9/99 at 4-14).

IV. Defendant's Witnesses.

A. Dr. Donald Riley.

Dr. Donald Riley is a research associate professor at the University of Washington in Urology and Pathobiology. He is also a consultant in forensic cases, having consulted in over 100 DNA forensic cases, as a result of which he is familiar with the science of DNA typing for identification. He has followed forensic literature since it began appearing, and has performed some forensic type DNA tests, including DQAlpha. He has studied the probes and primers that come with the Polymarker/DQAlpha kit, and published a paper in 1998

concerning the hybridization temperatures for those probes and primers. In 1990 he discovered a short tandem repeat, which he reported in 1991, and his laboratory has typed over 500 people with that locus for medical genetic purposes. Some of that work was published in 1999 in a journal called Molecular Biology Reports. His work in urology relates to prostate cancer, prostatitis, and another prostate disease, known as BPH, and he uses DNA technology to try to find causes for these conditions. Dr. Donald Riley has a bachelor of science degree in chemistry, and a Ph.D. in biochemistry. In the course of developing the short tandem repeat, Dr. Donald Riley designed PCR primers that would be complimentary to the DNA that flanks the repeat, investigated the number of variants and combined them to form a ladder, and designed an amplification procedure taking into account salt and temperature factors. His consulting work typically involves reviewing case report files and any photographic materials, and he has reviewed original data from databases and validation studies. He has also observed the performance of Polymarker/DQAlpha from start to finish in eight or nine cases, at both Cellmark and at Genelex. He has also observed CTT STR testing at Cellmark, and Profiler and Cofiler testing at Cellmark, although not to completion. He is not a member of the American Academy of Forensic Scientists, has attended only one of their meetings, and has never made a presentation to it. He has not attended meetings of, or presented papers at, the International 'Human Identity Symposium or the International Conference of Forensic Statistics. He is not a member of the Scientific Working Group on DNA Analysis. He has used only one DQAlpha test kit, using it to type fifty samples. He has never used the Polymarker kit, or the CTT STR system, the PowerPlex system, or the . ProfilerPlus system, nor has he ever amplified for any of the loci used in the ProfilerPlus

system. He has only conducted two forensic DNA tests himself, in one of which no DNA was located, and in the other of which he only attempted to locate two loci, Dr. Donald Riley was at one point employed by Genelex. He has never testified as an expert for the prosecution in a criminal case, nor been hired by the prosecution to consult in a criminal case. (Tr. 12/9/99 at 114-126). The Court finds that Dr. Donald Riley is qualified as an expert in molecular biology and forensic DNA testing..

B. Dr. Margaret Schwartz.

Dr. Margaret Schwartz is a forensic chemist employed by the Vermont Department of Public Safety Forensic Laboratory. She has been engaged in Polymarker/DQAlpha testing since approximately 1996. She has a Ph.D. in zoology, in the area of genetics. From 1986 to 1991 she worked at the University of Vermont as a research assistant in DNA. Since 1991, she has been employed at the State Forensic Laboratory, during most of that time working in the area of serology or DNA. The Court finds that Dr. Schwartz is qualified as an expert in Polymarker/DQAlpha testing procedures. (Tr. 12/17/99 at 73-75).

C. Dr. William Shields.

Dr. William Shields is a professor of biology at the State University of New York College of Environmental Science and Forestry, in Syracuse, New York, He has a bachelor's degree in biology, and a master's degree and doctorate in zoology from Ohio State University. His Ph.D. dissertation concerned genetic variation and population structure. About half of his professional research has been in the area of population genetics, including population genetic theory, its influence on forensic case work, and the study of population databases. His other research concerns animal behavior and genetics. At SUNY, Dr. Shields has taught in the

areas of biology, zoology, and animal behavior (including humans), evolution, conservation biology, and conservation genetics. Dr. Shields supervises a laboratory at SUNY that is involved with genetic testing as part of various non-human animal studies. His lab does not do any forensic DNA testing. Dr. Shields has published a book and 38 scientific articles. About half of his published work has to do with evolutionary population genetics. Dr. Shields has reviewed databases in raw data form from a number of institutions including the FBI, Cellmark, Life Codes, and from a variety of crime labs. He has consulted with governmental agencies concerning the use of DNA. He has served as a peer reviewer, at the request of the Department of Justice, concerning the use of DNA in Post-Conviction Relief. Dr. Shields has performed analysis on various population databases as part of his own research. He has also analyzed validation studies concerning DNA databases. He was an invited speaker on DNA analysis at an international symposium, and has presented a large number of workshops in several states explaining DNA analysis to lawyers. Dr. Shields has previously testified as an expert witness in a number of states, including as a prosecution witness in a number of cases. He has previously provided testimony in three other Vermont criminal cases involving DNA. The Court finds that Dr. Shields is qualified as an expert in the areas of DNA analysis, population genetics and statistical analysis connected with DNA forensic evidence. (Tr. 2/17/00 at 6-20).

V. The Laboratories.

A. Cellmark.

Cellmark is a privately-owned laboratory engaged primarily in forensic testing, as well as some research-related contractual work. Cellmark is hired by investigators, prosecutors,

defense attorneys, and crime laboratories. It has been in existence since 1987, and i,s accredited by the American Society of Crime Laboratory Directors Laboratory Accreditation' Board (ASCLD LAB). Accreditation involves an on-site inspection as well as a review of documentation, and the purpose is to maintain high standards in laboratories. Cellmark has never been denied accreditation. Cellmark also complies with the DNA Advisory Board laboratory guidelines. As required for accreditation, Cellmark requires its analysts to take two proficiency tests each year. The tests come from an outside vendor, and the results are returned to the vendor and to a proficiency test monitoring board set up by ASCLD LAB. Neither of the analysts involved in this case were ever unsuccessful in completing a proficiency test. However, none of the proficiency tests at Cellmark are true blind proficiency tests, since the employees knew that they were undergoing proficiency testing, rather than performing regular lab work.

Cellmark has reported one incorrect DNA profile, to Dr. Cotton's knowledge. That error occurred in the writing of the report, rather than in the laboratory; that is, the laboratory work in the case was correct, but the results were reported incorrectly. Cellmark's procedures were changed to prevent such an error from happening again. (Tr. 12/6/99 at 9-18).

Cellmark has a review procedure for its DNA testing. All of the results of the testing, including the draft report, are given a technical review by one of the Ph.D. scientists. That review consists of going back through the folder, following how the testing was done, checking each of the steps, and then analyzing the data and ensuring that the analysis and technical review match and are consistent with the report. (Tr. 12/6/99 at 18).

Cellmark also has a standard operating procedure for all of the work that is done in the

laboratory. (Tr. 12/6/99 at 19). Cellmark has reported approximately 1500 DNA profiles per year. (Tr. 12/6/99 at 19). In around 1989, approximately one-third of DNA tests performed in labs around the country, including Cellmark, resulted in an exclusion. (Tr. 12/6/99 at 26).

B. Genelex.

Genelex Corporation conducts paternity testing, forensic testing, and convicted felon data bank testing for the State of Indiana. It is hired by prosecution and police agencies, defense lawyers and defense agencies, and citizens who need paternity or forensic testing done. It has been in existence since 1987, and is accredited by the American Association of Blood Banks for paternity testing, and by the American Society of Crime Laboratory Directors Laboratory Accreditation Board (ASCLD LAB). Genelex has never been denied accreditation. It complies with the guidelines created by the DNA Advisory Board, which is an accreditation requirement. Genelex does routine proficiency testing, as required by both the ASCLD and the DNA Advisory Board. Each analyst is required to take part in a minimum of two external proficiency tests each year. Both the analysts involved in the testing in this case, Dr. George Riley and Piper Schwenke, were subject to proficiency testing, and neither of them ever failed to properly complete a proficiency test. Genelex itself has twice reported incorrect profiles in forensic cases due to typographical errors. In one case, one of the alleles in the profile was mistranscribed and then reported incorrectly. Genelex also reported incorrect profiles in several paternity cases. In each of those cases, the error was due to human error rather than a failure in the DNA typing systems, and Genelex has changed its protocols to ensure that those errors do not occur again. (Tr. 12/7/99 at 72-77).

In every case, Genelex has procedures in place for review of both the DNA testing and

of the resulting reports. Genelex also has standard operating procedures governing all of its procedures. They are written in-house, but are typically adopted from published protocols, from other laboratories, the FBI, and the corporations which make the kits used for doing the testing. In total, Genelex has reported more than approximately 50,000 DNA profiles. Of those, approximately 30,000 to 35,000 were paternity profiles; approximately 22,000 were profiles for the offender data banking; and approximately 2,500 to 3,000 were profiles in the forensic area. For both paternity and forensic testing, typically about 25 to 30 percent of the tests result in exclusions. (Tr. 12/7/99 at 77-79).

VI. The Tests.

A. DNA and Forensic Identification Generally.

1. DNA Generally..

DNA *is* genetic material found in all of our cells, inherited from our parents to produce a unique individual. Half of our DNA is inherited from each of our parents, and therefore we have two versions of every section of DNA. Sections of DNA which have biological meaning, that is, which carry some function, are called genes. There are also many sections of DNA which do not have any known function, but each person has two versions of all of these sections. (Tr. 12/6/99 at 19-20).

DNA is organized into 23 pairs of chromosomes. Each chromosome is a long, thin strand of DNA. One of each pair of chromosomes is inherited from each parent. The chromosomes have been numbered, and can be identified individually under a microscope as a result of their different size and shape. DNA controls essentially all of our biochemical functioning. (Tr. 12/6/99 at 20-21).

Although most of the DNA is the same between different individuals, there are some sections that differ. In these sections the differences are either differences in the sequence of the DNA, or they are differences in length. Both kinds of differences can be used to distinguish individuals at a molecular level. (Tr. 12/6/99 at 21).

DNA has a structure that is similar to a ladder. The components of the DNA form the rungs of that ladder. There are only four components, and they are abbreviated A, T, G and C. These components are paired up in a specific way. There are only A-T pairs and G-C pairs, sometimes referred to as "base pairs". A's'will only pair with T's, and G's will only pair with C's. It is possible, using techniques of molecular biology, to determine the sequence of these components along a length of DNA. An example of a sequence difference would be a location on a chromosome with the sequence AGAA, compared with the same location on the same chromosome of another individual, with the sequence AAAA. This sort of sequence difference is used in forensic testing in the test called Polymarker/DQAlpha. The sequence difference may be at a single base pair, or it may be at multiple places. (Tr. 12/6/99 at 21-24).

The other type of difference is the length difference. A location on a chromosome may have the sequence CATCATCAT, whereas the same location on the same chromosome on a different person will have the sequence CATCATCATCATCAT. Both chromosomes have the same sequence (here, CAT), but it is repeated a different number of times. The forensic testing which exploits these length differences is called short tandem repeat testing, or STR testing. (Tr. 12/6/99 at 24-25).

Many scientific uses exist for identifying sites on the DNA, other than for forensic

identification purposes, including identification of genes which cause disease, genetic screening, identification of viral sequences, such as HIV, and monitoring successive bone marrow transplants. (Tr. 12/6/99 at 25-26).

2. The PCR Technique.

Polymerase chain reaction (PCR) is a technique used in the STR and Polymarker/DQAlpha tests, as well as in research laboratories all over the country for a wide variety of purposes. The technique permits the copying of a very small sample of DNA in order to produce a larger sample for testing purposes At a molecular level, the PCR technique makes copies of specified sections of DNA. The sections are specified by using "primer" DNA, a short piece about 20 to 30 base pairs in length, which identifies each end of the segment to be copied. The primers bind to the ends of each section of interest; those sections are then copied using the same molecular machinery that copies DNA when cells divide. The primer is placed in the tube, along with the enzyme which does the copying, called polymerase, and with individual nucleotide triphosphates (the A's, T's, G's and C's). The copying, referred to as amplification, is exponential, doubling with each step of the process. At each step of the process, the DNA molecule is split down the middle, and the primer attaches along the length of each side of the molecule. The entire strip of DNA is not duplicated, just the area of interest: (Tr. 12/6/99 at 26-32).

Multiplexing is the process of using PCR to duplicate more than one area of interest at a time. A different set of primers is used for each DNA segment to be duplicated. Multiplexing is used in many applications other than forensic and paternity testing, such as testing parents to determine if they are carriers of cystic fibrosis. Different segments of DNA

have different optimal temperatures for the PCR process, in part because the bonds between A's and T's are weaker than the bonds between G's and C's. Hybridization consists of repeated chemical reactions in which the strands of DNA bind together and come apart, and is controlled by salt concentrations and temperatures. Depending upon the proportions of A-T bonds and G-C bonds in the area of interest, different sequences will have different optimal temperatures. The temperatures used in multiplexing systems are compromises made in order to make copying of all of the segments work. The companies which develop the test kits conduct research and development to devise systems which work together. (Tr. 12/6/99 at 32-38).

Contamination is a concern when using PCR to amplify DNA, because- the PCR method works with such small amounts of DNA, as few as 150 cells. Cellmark has taken a number of steps to reduce. or eliminate possible contamination. In order to reduce the risk of contamination from another source, Cellmark extracts its DNA from the evidence at a different time for each sample within a given case. That eliminates the possibility of contaminating a crime scene sample with DNA from a known sample submitted in connection with the same case. Beginning with the process whereby DNA is extracted from a sample, a second tube is maintained, called a reagent blank. Everything (except the sample) that is added to the evidence sample is added to the reagent blank. At the end of the test, the reagent blank is processed, and it should return no result at all, (since no DNA was placed in the tube). That ensures that no extraneous DNA was present in any material added to the evidence sample. In order to eliminate contamination by amplified product, preparation for the amplification step is conducted at a different location in the laboratory than the extraction

step, and the amplification step itself is conducted at a third location in the laboratory. I ho amplified DNA is taken backwards from that location. In addition, only one tube or evidence envelope is open at a time, and gloves are changed in between handling of each item. (Tr. 12/6/99 at 38-41; Tr. 12/17/99 at 17).

At Cellmark, when DNA is transferred from one tube to another, a second scientist looks at the transfer tube to ensure that the labeling is correct. The tubes themselves (which are about an inch and a half tall) have a snap cap on them. (Tr. 12/6/99 at 41).

In addition to these precautions, positive and negative controls are run during the amplification step. The positive control is a known type that should give a certain known DNA profile. The negative control is another blank tube, and should give no result Finally, Cellmark personnel are trained in sterile technique. (Tr. 12/6/99 at 41-42).

Genelex also takes precautions to avoid contamination. Genelex personnel are trained in laboratory technique. They wear lab coats and gloves. Extraction of DNA from samples in the same case is done at different times; the amplification step takes place in a separate area; filtered pipette tips are used; the tools are routinely decontaminated before and after use; other materials are sterilized and autoclaved before use; and the amplification tools are UV irradiated to destroy DNA. No amplified DNA product or anything that has come into contact with such product leaves the amplification room except when bagged up to be incinerated. (Tr. 12/7/99 at 79-81; Tr. 12/8/99 at 10-12).

Genelex also requires that tubes remain sealed except when a transfer takes place at which time no more than two tubes are opened. Every sample bears' a unique identifier and every tube to which the samples are transferred bear that unique number. Once a transfer has

taken place, the order of the tubes is checked by a second person or rechecked by the same analyst to ensure that the transfers have been correct. Finally, Genelex runs positive and negative controls, and reagent blank controls, to ensure that any contamination will be observed. (Tr. 12/7/99 at 81-82; Tr. 12/8/99 at 10-12).

B. Polymarker/DQAlpha Testing.

1. The Polymarker/DQAlpha System.

The Polymarker/DQAlpha test comes in a kit, manufactured by Perkin Elmer. The original kit tested for the DQAlpha site only, and underwent a significant amount of validation testing. A validation study is designed to test the system to ensure that it reacts in the way that is expected, so that the results are accurate, reliable, and reproducible, both within the laboratory and from laboratory to laboratory. To that end, studies are done of reproducibility, sensitivity, and precision Typically, the company which manufactures the kit does this type of testing as well. Numerous papers were published in connection with the validation testing for this kit. Cellmark itself conducted validation testing on the DQAlpha system. When the system was combined with the Polymarker system, additional validation testing was done at a number of laboratories, including Cellmark. (Tr. 12/6/90 at 50-51; Tr. 12/7/99 at 86-88).

Validation testing typically involves testing for sensitivity at different dilutions of DNA; detection of mixtures of DNA from two individuals, including lop-sided dilutions with, for example, 20 parts of DNA from one person, and one part from another person; testing of mock forensic samples, including stains, swabs, cigarette butts, bones, and other materials that might be encountered in casework; and variation of the chemistry and temperatures. Several

laboratories also conducted studies using degraded DNA. Cellmark's validation testing, as well as that of some other laboratories, included some DNA from hairs, but there is nothing unusual about DNA from hairs. (Tr. 12/6/99 at 52, 63).

Although Dr. Donald Riley testified that these systems, as well as the other systems used for DNA testing in this case, have not necessarily been subjected to validation testing with the exact type of biological samples involved in this case, i.e., hairs stored on a slide for twenty years, (Tr. 12/10/99 at 18-21), the Court finds that such specificity is not necessary in order to allow the use of testing in such cases. The concern about DNA from hairs rather than body tissues goes to the weight of the evidence, and not its admissibility. Dr. Donald Riley, also testified that Cellmark documents indicated an experiment had been conducted in which DNA from hairs which had been amplified for DQAlpha were re-amplified for Polymarker, and that three alleles were obtained at some loci as a result. (Tr. 12/10/99 at 22-23). Since this was an experiment using a technique not used in this case, the Court finds this study irrelevant to the admissibility of this evidence. Dr. Donald Riley is unaware of any articles or abstracts dealing with false positives with the Polymarker system. (Tr. 12/10/99 at 94).

Genelex also conducts Polymarker/DQAlpha testing, for which it conducted validation studies. Genelex's validation studies for the Polymarker system included tests on DNA from hair and on small amounts of DNA. Genelex's validation studies indicated that the Polymarker and DQAlpha systems were reliable, accurate, and reproducible. In Dr. George Riley's opinion, these systems are generally accepted in the scientific community, and in fact are probably the most widely used forensic testing in the United States. (Tr. 12/7/99 at 86-

88).

When conducting a test using the Polymarker/DQAlpha system, the first step is to extract the DNA from the evidence and from the known samples. The DNA is then amplified using the reaction components that come with the kit, which include the enzyme and the primers. These amplified products are then applied to a nylon strip that has probes bound to it for the various alleles. A color reaction is done, which produces a blue dot where the amplified DNA was bound to the probes. (Tr. 12/6/99 at 53).

The nylon strip is about a quarter inch high and about five inches long, and is divided. into five different designated areas, and an area that is marked by an S. The designated areas are LDLR, which is a gene that is being tested for; GYPA, which is a gene that is being tested for, and so forth, for five genetic locations. Each area has a circle for each allele which exists for that genetic location. For example, the LDLR gene has two alleles, which differ in their sequence from each other. One allele is arbitrarily called an A, and the other is arbitrarily called a B. Any given person will have two versions of this gene, one inherited from each parent. If they have inherited an A from both parents, their DNA will bind only to the circle where the A probe is bound. If the person inherits an A' from one parent, and a B from the other, then the DNA will bind to both circles. If they have inherited a B from both parents, then the DNA would only bind to the probe in the B circle. In each case, the circle where the DNA binds to the probe will turn blue, as a result of a chemical reaction. If there are two alleles for a particular gene, there are three possible types (AA, BB, and AB); if there are three alleles for a gene, there are six possible genotypes. The strips used to test the negative control and the reaction blank should not have any reaction, and should not light up

at all. (Tr. 12/6/99 at 58-61).

During the hybridization process, the strips are submerged in solution in slots on trays. Dr. Schwartz testified that in one case in which she conducted a test in the Vermont State Forensic Laboratory (not a test in connection with this case), solution sloshed from one slot to another, and as a result a faint dot appeared on a strip which was caused by the sloshing. Dr. Schwartz had observed the sloshing when it occurred, and generally an analyst would notice such an occurrence. (Tr. 12/17/99 at 82-83).

Immediately after the test is done, the analyst reads the results and records them on paper. A second analyst may also read the results and record them, and a photograph is taken. The most reliable record is the recording of the results, and the second most reliable record is the photograph. The color on the strips themselves fades with time. (Tr. 12/6/99 at 61-62).

Between 50 and 100 laboratories in the United States use this system for genetic testing purposes, and it has been in use since about 1991. The system is generally accepted in the scientific community. In Dr. Cotton's opinion, the Polymarker/DQAlpha system is a reliable way to determine a genetic profile. (Tr. 12/6/99 at 63-64; Tr. 12/9/99 at 22).

2. Applying _Streich_ to the Polymarker/DQAlpha System.

Defendant does not contest that PCR analysis is generally accepted in the scientific community. He does question whether the specific tests utilized in connection with this case are generally reliable, whether they are reliable when used to analyze small quantities of degraded DNA, whether the laboratories followed established protocols, and whether the

individual tests were free of contamination.

Polymarker/DQAlpha testing has been employed by laboratories since about 199 1. The technique is capable of being tested, and has been the subject of multiple scientific studies which have been published in peer-reviewed journals.[3]

Defendant claims that the guidelines established by the Technical Working Group for DNA Analysis Methods, (hereafter referenced as TWGDAM), require that primer sequences used in PCR techniques be published.’ The purpose of publication is to allow scientists to examine the primers in order to determine if they are working the way their manufacturers claim. TWGDAM guidelines were in effect when Cellmark utilized Polymarker/DQAlpha in this case.

Defendant claims that it is particularly important that primer sequences be known because Polymarker/DQAlpha, (like the other kits used by the two laboratories in this case), is a multiplex testing kit. The kit analyzes six genetic loci simultaneously. (Other kits analyze various numbers of loci). Each locus has an optimal temperature and an optimal mixture of chemicals for successful amplification. The kit and corresponding protocol represents a “compromise” of the various optimal temperatures and chemical additives which enables the kit to process the various loci simultaneously. Thus, even if amplification of each individual locus was well established, before the Court accepts analysis of the kit, the package

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[3] Although the State’s experts stated that validation testing had been performed, no articles on validation testing were provided to the Court. However, we note that there are a number of published articles in scientific journals validating the Polymarker/DQAlpha kit. See State v. Batchelder, No. 1127-B-95, slip op. at 29-30 (Wind.Dist.Ct. Aug. 7, 1997) (Grussing, J.). This opinion is on file with the Court.

[4] See Defense Exhibit # 180, § 4.1.4.

"compromise" processes should be validated.

The State's experts never explained why the TWGDAM guideline was not followed.[5] Current guidelines, issued by the DNA Advisory Board, no longer require publication of primer sequences. Again, no explanation of the modification was offered; the Court infers it was done in order to bring the guideline into compliance with practice.

Whether or not current guidelines require such publication, the Court is troubled by the lack of publication of the primer sequences. Propiietary information or not, the lack of transparency is disturbing. Nevertheless, with respect to Polymarker/DQAlpha, the Court is satisfied that there has been sufficient validation testing over a period of several years to enable the Court to conclude that Polymarker/DQAlpha constitutes a valid and reliable analytical technique when properly employed. See Daubert, 509 U.S. at 594 ("submission to the scrutiny of the scientific community is a component of 'good science,' in part because it increases the likelihood that substantive flaws in methodology will be detected"). If the thermal and chemical compromises created by the manufacturer did not function properly, this fact would have been exposed long ago. Polymarker/DQAlpha is utilized in 50-100 laboratories in the United States, and is widely accepted in the scientific and forensic communities.

Defendant claims that Polymarker/DQAlpha has not been validated for use on

[5] The State's witnesses did testify that the manufacturers considered the primer sequences to be proprietary information and so did not publish them. However, they failed to explain how and why the scientific community was able to tolerate non-compliance.

degraded samples[6] of DNA derived from hair roots. Evidence from the State on this issue was general, but was unimpeached and was btherwise credible.[7] The Court concludes that Polymarker/DQAlpha has been validated for use with degraded DNA.

Numerous courts have reviewed the issue of admissibility of results from Polymarker and DQAlpha testing. The district court for the Southern District of Florida performed a thorough Daubert analysis, reviewing genetic testing of the Polymarker and DQA1 loci. United States v. Gaines, 979 F. Supp. 1429 (S.D. Fla. 1997). The court held that "the PCR method of analysis for these genetic markers has been tested extensively, and, when the FBI Protocol is followed, the analysis consistently generates true results." Id. at 1435. The court noted that these genetic markers have been the subject of numerous published articles which confirm the validity of their use for this purpose. Id. at 1436. The court further held that the PCR method of analysis has an acceptable rate of error and there are standards which control the technique's operation. Id. Finally, the court held that the PCR techniques used were "generally accepted within the scientific community of forensic geneticists." Id. at 1437.

After an evidentiary hearing , the federal district court for the District of Massachusetts ruled that the PCR methodology passed Daubert muster with respect to the Polymarker loci. United States v. Lowe, 954 F. Supp. 401, 418 (D. Mass. 1996) (validity of DQA1 testing not challenged). The district court for the District of New Hampshire followed suit, holding that

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[6] As noted above, the crime scene samples were recovered at the time of the homicide in 1976. All the expert witnesses assumed, expressly or implicitly, that any DNA derived from these samples had degraded to some extent over time.

[7] Dr. Cotton testified, "Several labs have also done studies on looking at degraded DNA with this system, ... [O]ur validation included some DNA from hairs.. . . There's nothing unusual about DNA from hairs. It works.. . ." (Tr. 12/6/99 at 63).

"the tests used to type each of the 7 sites examined in this case were validated in a carefully constructed series of experiments and the results were later published in peer-reviewed publications." United States v. Shea, 957 F. Supp. 331, 339 (D. N.H. 1997) (reviewing DQA1, Polymarker loci, and D1S180), citing C. Comey and B. Budowle, Validation Studies on the Analysis of HLA DQAlpha Locus Using the Polymerase Chain Reaction, 36 Journal of Forensic Sciences 1633 (1991) and B. Budowle, et. al., Validation and Population Studies of the Loci LDLR, GYPA, HBGG, D7S8 and Gc (PM Loci) and HLA-DQAlpha Using a Multiplex Amplification and Typing Procedure, 40 Journal of Forensic Sciences 45 (1995).

In the first federal appellate decision reviewing DQAlpha and Polymarker test kits, the Eighth Circuit Court of Appeals concluded that the "reliability of the PCR method of DNA analysis is sufficiently well established to permit courts of this circuit to take judicial notice of it in future cases." United States v. Beasley, 102 F.3d 1440, 1448 (8th Cir. 1996). Beasley relied in part on the large number of state appellate decisions sustaining the admission of DNA evidence derived from the PCR method. Id. at 1447 n.4.

A large number of state appellate courts have approved the admissibility of evidence from Polymarker and DQAlpha testing under either Daubert or Frye. See Fugate v. Commonwealth, 993 S.W.2d 931 (Ken. 1999) (PCR DNA evidence is per se admissible, without Daubert hearing); People v. Allen, 72 Cal.App.4th 1093 (Cal. Ct. App. 1999); Ledesma v. State, 993 S.W.2d 361 (Tex, Ct. App. 1999); People v. Rozo, 708 N.E.2d 1229 (Ill. Ct. App. 1999) (results admissible); State v. Carter, 586 N.W.2d 818 (Neb. 1998); Smith v. State, 702 N.E.2d 668 (Ind. 1998) (evidence admissible); People v. Wright, 62 Cal.App.4th 31 (Cal. Ct. App. 1998); Commonwealth v. Sok, 683 N.E.2d 671 (Mass. 1997) (Polymarker

testing is scientifically valid and properly conducted tests are admissible); State v. Harvey, 699 A.2d 596 (N.J. 1997) (Polymarker evidence admissible); Keen v. Commonwealth, 485 S.E.2d 6.53 (Va. Ct. App. 1997); Brodine v. State, 936 P.2d 545 (Alaska Ct. App. 1997); People v. Pope, 672 N.E.2d 1321 (Ill. Ct. App. 1996); and People v. Morales, 643 N.Y.S.2d 217 (N.Y. App. Div. 1996) (Polymarker evidence admissible).

The Polymarker/DQAlpha system has been subjected to validation testing, publication, and peer review. The potential for error in this case has been addressed, as discussed below. The Polymarker/DQAlpha system has been generally accepted in the scientific community, and the results of such testing have been deemed admissible by numerous state and federal courts. The Court finds that the Polymarker/DQAlpha system passes muster under Streich.

3. The **Polymarker/DQAlpha** testing at Cellmark.

a. **Cellmark: Polymarker/DQAlpha:** Crime Scene Hair.

The first DNA test undertaken in connection with this case was done by Cellmark, using the Polymarker/DQAlpha system, on a hair discovered at the crime scene. Anjali Swienton performed the testing. The evidence received consisted of a sealed slide carrier, inside of which were two 'different slides, each labeled separately. One slide contained two mounted hairs, and the second slide contained one mounted hair. The hairs were sealed onto the slides, with glass cover slips on top of them. Ms. Swienton removed the cover slip from the slide containing two hairs. She cleaned the hairs of mounting substance, then cut a portion of the root end of the hair with a sterile scalpel and transfened it to a test tube. She also removed a portion of the hair shaft to use as a control. The samples were given the

labels 01 and 01S. She also started a reagent blank, and added chemicals which would extract the DNA from the hair root cells. She then conducted a slot blot test to determine if any usable human DNA had been extracted from the sample, and determined that none had been. She amplified the sample anyway, following which she conducted a product gel test to determine if any DNA product from the amplification were present. That test indicated that there was no DNA present, (Tr. 12/6/99 at 80; Tr. 12/17/99 at 14, 18-23).

Ms. Swienton then extracted DNA from the second hair on the slide, labeling it Sample 02. She amplified the extracted DNA, then ran another product gel. Running a product gel involves taking a tenth of the amplified sample, and putting it on a small agerose gel, applying an electrical current, and staining the gel. This test indicates whether the amplification step was successful. The product gel for Sample 02 was run on March 25, 1994, and was a normal product gel. The gel shows six bands, for the six loci which were amplified. There is also a fainter, less distinct band at the bottom of those six, for Sample 02, and also for four other samples from other casework that were run on the same gel.

The seventh band does not indicate the possibility of cross-contamination, but is most likely what is called non-specific product or a "primer-dimer." The protocol created by the manufacturer of the kit, Perkin Elmer, anticipates that these bands will sometimes appear. Non-specific product results when the primers bind to genes other than those of interest, during the amplification process. The likelihood of non-specific product resulting in an incorrect profile is very small. The Polymarker validation studies include instances in which the band is present, and instances in-which it was not, and there was no indication that the presence or absence of the band ever made any difference. (Tr. 12/6/99 at 80-83; Tr.

12/17/99 at 23-26).

Dr. Bieber was shown a photo on page 87 of the Cellmark case file, which corresponds to Defense Exhibit # 102. This is a photograph of the March 25, 1984, product gel. Dr. Bieber testified that he faintly saw a so-called "seventh band" which could be the result of a number of artifacts of the PCR process, such as a "primer-dimer." This can occur when a primer dimerizes, or binds with and labels itself. Such an occurrence is neither unusual nor surprising in a sample that contains a large amount of DNA, which' was the case here. Under such circumstances, the presence of a so-called "seventh band" on the product gel does not call into question the validity of the test result. (Tr. 12/9/99 at 45-47).

Although Dr. Donald Riley expressed concerns about the seventh band, (Tr. 12/9/99 at 172), he agreed that a seventh band is not unusual in this type of test, that he does not know whether the seventh band had any effect on the outcome of the test, and that he is not aware of any non-specific PCR reactions that will inappropriately light up a dot on the strip, other than the DQAlpha. Although the DQAlpha is known to light up the 1.1 dot, the 1.1 dot was not lit up on the strip in this case. (Tr. 12/10/99 at 67-69).

The upper two bands in the gel for Sample 02 are lighter than the lower four, which is typical of a sample that has some degradation. One would expect to see differences in the larger bands before seeing differences with the smaller bands. The upper band is the DQAlpha band, which is the largest gene in this system. (Tr. 12/6/99 at 83-84).

Dr. Donald Riley testified that the fifth band on the product gel for Sample 02 appeared to be weak and blurry, indicating the possibility of a missed allele. However, he also testified that the fifth band corresponded to the LDLR location, and that the testing

indicated that the sample was heterozygous at that location. When a location is heterozygous, there is no possibility of a dropped allele. (Tr. 12/10/99 at 66-67). Therefore, Dr. Donald Riley's concern about the fifth-band is of no relevance to the testing in this case.

The next step in this test was to hybridize the amplified product to the strips. Also on the strips are a C dot and an S dot, which are controls. They are designed to give a blue color, but a lighter blue color than any of the other dots on the strip. If a dot is lighter than the control dot, caution must be used in making an interpretation of the test results. The reason for that is, if the dot for a locus is lighter than the control dot, that would indicate that there was only a small amount of DNA for that locus, and an allele might not have been detected. It does not mean that the type that is seen is unreliable, but it means that other types might be missing. In this case, the C dot is faint, but is not too faint to provide a valid reading for the rest of the strip. (Tr. 12/6/99 at 84-87). Ail the controls functioned properly for this test. (Tr. 12/6/99 at 93; Tr. 12/17/99 at 24-25).

In addition, Ceiimark tested an extract from the hair shaft, which gave no results, as expected. (Tr. 12/6/99 at 98; Tr. 12/17/99 at 29-31). Although the hair shaft extract was amplified and tested at a different time than the 02 sample, (Tr. 12/9/99 at 169), the Court finds that this point is not relevant to the validity of the results.

The genotypes which Ceiimark obtained for Sample 02 were as follows: DQAlpha: 1.2; LDLR: AB; GYPA: A; HBGG: A; D7S8: AB; GC: A. (Tr. 12/6/99 at 91).

b. Celtmark: Polymarker/DQAlpha: Known Sample.

The next test which Cellmark undertook in this case was testing a known sample from Defendant, using the Polymarker/DQAlpha system. That sample, consisting of a cotton swab,

was received in the laboratory on December 15, 1994. The Polymarker/DQAlpha testing on the crime scene hair was reported on September 13, 1994, and therefore at the time the work was done on the known sample, the work on the crime scene hair had been completed for. months, and the hairs themselves were not even in the laboratory, having been returned on October 3, 1994. (Tr. 12/6/99 at 9 I-92; Tr. 12/1 7/99 at 3 1-32).

Dr. Donald Riley conceded that the long period of time between the extraction and typing of these samples served to allay to some extent his concerns about contamination. He also agreed that the risk of contamination of a hair mounted on a slide is less than for other forms of storage, unless the mounting medium has dried out and exposed the hair to some air. (Tr. 12/10/99 at 60-61).

This sample was labeled 03. All of the controls ran properly for the 03 sample, and the C and the S dots were dark enough to validate the test results. Although Dr. Donald Riley testified that the C dot was not visible on the positive control, he was referring to a photograph of the strip, and he also testified that the photograph of the strip may miss a control dot. (Tr. 12/1 0/99 at 4, 96). Since the analyst viewed the original strip at the time of the test, and testified that the C dot was present, the court credits her testimony. The test results, reported on January 1 I, 1995, were as follows: DQAlpha: 1.2; LDLR: AB. GYPA: A. HBGG: A. D7S8: AB. GC: A. This profile is the same as that obtained from the test conducted *on* the crime scene sample. (Tr. 12/6/99 at 92-96; Tr. 12/17/99 at 32).

4. Applying Streich to Cellmark Polymarker/DQAlpha Testing.

Since the Court has concluded that the Polymarker/DQAlpha system complies with the minimum standards adopted in Streich, the Court now turns to examine whether Cellmark's

use of the test sufficiently followed validated procedures for the Cellmark testing to he considered reliable and therefore admissible.

Defendant asserts that the hair shaft control, which was extracted and amplified at the same time as the hair root sample, was not hybridized until several months after the hair root sample. The Court finds no difficulty with the later hybridization of the hair shaft control, and Defendant has not specifically identified any problem, except to suggest, without foundation, some nefarious purpose.

Defendant also contends that the results are not reliable because the State cannot show that the lab's thermocycler which was utilized in the amplification process functioned properly. The thermocycler is programmed to go through a series of some 32 cycles of heating and cooling in order to amplify the original extracted DNA. For the most part, the machine operates during the night when'the lab is closed. On at least one occasion, unrelated to the samples in this case, the thermocycler malfunctioned. The Court is not convinced that thermocycler malfunction is a problem in this case. The positive control, which was processed with the crime scene sample, produced the expected result, suggesting that the thermocycler performed properly. (Defense Exhibit # 105 at 156).

Similarly, Defendant's contention that undetected contamination somehow affected the test result is not convincing. Neither the negative control nor the reagent blank showed any evidence of contamination, nor did the laboratory analyst observe any evidence of contamination. Although Defendant has suggested that airborne contamination might have affected the sample without affecting the controls, (since each tube was un-stoppered separately), Defendant has presented no credible evidence that airborne contamination was a

realistic threat.

Defendant suggests that the result is not valid because the product gel, which is supposed to show six clear bands, produced only four.[8] There was no credible evidence that two bands were absent. Admittedly, the two upper bands were weaker than the other four. Credible evidence indicated this was most likely caused by degradation of the DNA.

Similarly, Defendant claims that the presence of a mysterious seventh band on the product gel is evidence of some sort of contamination. However, the manufacturer's protocol acknowledges that a seventh band may sometimes appear. Although it offers no explanation of the phenomenon, the protocol states that it does not affect the validity of the test result.”

Defendant also claims that there might have been spillage in the hybridization tray between the 02 sample lane and one of the adjacent lanes which may have contained high quality DNA from another source. The analyst observed no spillage. Furthermore, if there had been spillage, one would expect to see typing dots from both the 02 sample and the adjacent lane, (which did not occur), since the product gel indicated that there was typable DNA in the 02 sample. (Tr. 12/7/99 at 10-12).

Evidence regarding the third Streich factor, the known or potential error rate, was not presented in this case. The State's experts claim that the error rate cannot be measured

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[8] Defendant's requests, ¶ 28 claims the absence of product on two bands.

[9] The protocol was admitted into evidence as Defense Exhibit # 140. Section 7.9 reads in pertinent part:

> Primer-dimer bands and unincorporated primers may appear as broad bands near the bottom of the gel in the region of lower molecular weight. Occasionally, non-specific bands or smearing can be observed above and/or below the six specific bands, but they do not compromise the typing results on the . . . Probe Strips.

because as soon as an error is discovered, corrective measures are implemented to insure that the error does not recur. The State's witnesses are not entirely accurate. The National Research Council Committee on DNA Forensic Science suggested that laboratory error rates can be estimated through blind proficiency testing." Howkver, NRC II recognizes the practical difficulty in implementing such a program."

The Court recognizes that true blind proficiency testing would be difficult to attain in forensic laboratories, at least on a regular, on-going basis. Most courts do not require such proficiency testing as a condition of admissibility. See 1 D. Faigman, Modern Scientific Evidence § 15-4.4, at 644 (1997).

NRC II recommends that duplicate tests be performed as an alternative to eliminate or reduce the possibility of error.

> Recommendation 3.3: Whenever feasible, forensic samples should be divided into two or more parts at the earliest practicable stage and the unused parts retained to permit additional tests. The used and saved portions should be stored and handled separately. Any additional tests should be performed independently of the first by personnel not involved in the first test and preferably in a different laboratory.

NRC II, sum-a, at 88.

In this case the State has substantially complied defacto with Recommendation 3.3. As a practical matter, the forensic sample was divided and was sent to different laboratories. For the reasons stated below, the Court concludes that the Polymarker/DQAlpha results of the

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[10] "[L]aboratory error rates must be continually estimated in blind proficiency testing." See 1 D. Faigman, Modem Scientific Evidence § 15-4.4, at 644 n.26 (1997), quoting National Research Council, DNA Technology in Forensic Science 89 (1992) ("NRC I").

[11] See National Research Council, The Evaluation of Forensic DNA Evidence 24, 86 (1996) ("NRC II").

sample sent to Genelex are not reliable enough to be admitted into evidence... However, for loci where results were obtained by Genelex, they confirm the Polymarker/DQAlpha results obtained by Cellmark.

The duplicate Polymarker/DQAlpha test performed at Genelex serves to reduce the possibilily of error in the Cellmark Polymarker/DQAlpha results. While the Genelex results are not admissible at trial in the State's case in chief, for the purposes of deciding the instant motion they provide assurance that the risk of error in the Cellmark Polymarker/DQAlpha testing has been properly addressed."

The testimony concerning Cellmark's protocols for this test and its adherence to its protocols was subjected to lengthy and searching cross-examination. Based on the detailed testimony adduced at the hearing, the Court concludes that Cellmark substantially complied with the manufacture's protocols as well as the laboratory's own protocols. Since the Court has already found that the Polymarker/DQAlpha system has been scientifically validated, and the Court further finds that Cellmark performed the tests according to the procedures for which the test has been validated, the Court concludes that the Cellmark Polymarker/DQAlpha test results are reliable scientific evidence which may be admitted at trial for consideration by the jury.

5. **Polymarker/DQAlpha** Testing at Genelex.

a. Genelex **Polymarker/DQAlpha** Test: Second Crime Scene Sample.

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[12] As held, see <u>infra</u>, pp. 40-42, the State will not be permitted to introduce the Genelex results in their case in chief. However, should Defendant attempt to suggest that Cellmark results are invalid, the Stale may be permitted to introduce Genelex results by way of rehabilitation.

Piper Schwenke conducted a Polymarker/DQAlpha test at Genelex using DNA which had been isolated earlier from the crime scene hair root. This DNA was amplified for the Polymarker/DQAlpha loci. After the amplification, Ms. Schwenke ran a product gel. The product gel indicated that there were weak bands present for all of the genes tested. The shorter genes had amplified more efficiently than the larger genes, and so the bands for these genes were somewhat stronger. This result is typical of partial degradation of the DNA. The controls which were run on the product gel gave the expected results. (Tr. 12/7/99 at 107-109; Tr. 12/8/99 at 24-26). Dr. Donald Riley testified that the fifth and sixth bands could not be distinguished clearly, indicating very little DNA, which potentially affected the results of the test. (Tr. 12/9/99 at 159). However, Dr. Bieber was asked to examine Defense Exhibit # 162, which is a copy of the loading sheet and product gel photo for the Polymarker/ DQAlpha test done at Genelex. He testified that he saw 6 bands (the expected number) in both lane 1, which contained the case sample, and lane 3, which contained a control. According to Dr. Bieber, these results indicated that there was enough DNA present to go on to the next step in the testing process. The Court credits Dr. Bieber's testimony on this point. (Tr. 12/9/99 at 43-44).

The next step taken by Ms. Schwenke was to hybridize the DNA product to nylon strips. The controls were hybridized as well as the samples, and the controls returned the expected results. As discussed above, additional controls are present on the strips themselves, called the control dots. For sample DNA to be valid, the dots should be brighter than the control dot. In this case, Genelex obtained signals for all of the loci on the strips except for the C and S dots. (Tr. 12/7/99 at 109-1 12; Tr. 12/8/99 at 26-28; Tr. 12/1 7/99 at 27-28). The

results from Genelex's Polymarker/DQAlpha testing were as follows: DQAlpha: 1.2; LDLR: A, B; GYPA: A; HBGG: A; D7SA: A, B; GC: A. These results were all returned with the notation, "interpret with caution." (Tr. 12/7/99 at 115-1 16).

The Genelex laboratory protocol states that results such as thkse may be interpreted with caution if, in the analyst's judgment, the results are strong enough to report. In this case, the analyst believed that the results were intense enough to be interpreted, and were also consistent with degradation of the DNA, and therefore Genelex did interpret them with caution, and reported the results with that notation. (Tr. 12/7/99 at 112-1 13).

6. Applying Streich to Genelex **Polymarker/DQAlpha** Testing.

,The Court must determine whether Genelex' usage of the Polymarker/DQAlpha system followed validated protocols sufficiently closely for the Genelex test results to be deemed reliable enough to admit at trial.

The 1994 protocol of Polymarker/DQAlpha manufacturer Perkin Elmer Corporation states that laboratories may wish to interpret test results without C and S dots with caution. However, the present protocol recommends "that a DNA probe strip with no visible "S" dot not be typed for any locus."[13] Similarly, the protocol states, "If the "C" dot is absent, an accurate determination of the type cannot be made."[14] The protocol of the Vermont State Laboratory, operated by the Vermont Department of Public Safety, contains analogous

[13] Exhibit #140, § 12.1.

[14] Exhibit #140, § 12.2.

language. [15]

The State's experts witnesses uniformly testified that even though the Genelex Polymarker/DQAlpha test results were not reliable as independent tests, they nevertheless had value in that they provided corroboration for the results provided by Cellmark. Though these results do provide evidence that no significant laboratory errors were made by Cellmark, they do not independently meet the standards of scientific validity and reliability established by Daubert and Streich.

The Polymarker/DQAlpha test kit is validated for use when all the controls are working, including the C dot and the S dot. Under the Perkin Elmer protocols, the test is not valid when the dots are not present. The Court finds there is no evidence that the Polymarker/DQAlpha test kit has been validated for use without the C dot and S dot controls. In light of the manufacturer's protocol, the naked assertions of the State's witnesses are insufficient to sustain their burden of proving that the testing is reliable under these conditions. Because neither the C dot nor the S dot are visible on the typing strips produced by Genelex testing, the results cannot be deemed to be reliable. For a contrary determination, the State would have had to produce expert testimony showing that the Polymarker/DQAlpha test kit has been scientifically validated to produce reliable results even in the absence of the C and S dots required by the manufacture's protocols.

> A control dot, marked "C" on the DQA1 test strips, and "S" on the PM test strips, is used as a standard to determine if sufficient quantities of DNA were present to enable: a reliable match to be declared. A match cannot be declared unless there is a visible control dot, and the intensity of the dot is equal to or

[15] See Exhibits #193 and #194.

greater than the intensity of the control dot.

United States v. Gaines, 979 F. Supp. 1429, 1438 (S.D. Fla. 1997).

The Court concludes that the absence of the C and S dots on the Genelex typing strips renders the results from the Genelex Polymarker/DQAlpha test unreliable and therefore are not independently admissible.[16] Thus, it is unnecessary for the Court to analyze the other *issues* raised by Defendant concerning this test.

C. STR CTT Testing.

1. The STR CTT System.

The STR CTT system, provided in kit form by the Promega Corporation, tests for length differences at three loci, labeled CSF1PO, TPOX, and THO1. The first step is the same as with Polymarker/DQAlpha, beginning with the extraction of the DNA from the evidence or known sample, followed by an amplification step. The amplification step amplifies the three locations, abbreviated C, T, and T. Unlike the Polymarker/DQAlpha system, there is no hybridization step, and no strip is used. Instead, the fragments of DNA which are obtained at the amplification step are separated by size on an acrylamide gel. The DNA is inserted into a well at one end of the gel. An electric current is then applied to the gel, which draws the fragments through the gel. Since the longer fragments move more slowly than the smaller fragments, the result is a separation of the fragments by length.. The gel is then stained to make the DNA visible in the form of bands, and the length of the DNA fragments is determined. DNA from different sources is run in different lanes on the same gel. One of

[16] See, however, footnote 12 and accompanying text.

the lanes contains an allelic ladder, a known standard which consists of all of the alleles that are generally seen in a population for a particular gene. The bands from the evidence and known samples can be compared to the allelic ladder to determine their length. All three loci are separated on the same gel. The CSF fragments wind up at the top of the gel, the TPOX fragments in the middle, and the THO1 fragments on the bottom. Each is read by comparing their position to the position of the bands in the allelic ladder. (Tr. 12/6/99 at 66-71).

2. Applying Streich to the STR CTT System.

The CTT STR system has undergone peer review, and the same sorts of studies were conducted as for the Polymarker/DQAlpha system.[17] The system has been in use by Cellmark since 1994, but was available and in use before that time. Like the Polymarker/DQAlpha system, the CTT system uses a reagent blank and positive and negative controls. The system is generally accepted in the scientific community. In Dr. Cotton's opinion, the CTT STR system is a reliable way to determine a genetic profile. (Tr. 12/6/99 at 70-71; Tr. 12/9/99 at 20).

CTT testing has been held to be valid and reliable by courts of other jurisdictions. The Massachusetts Supreme Judicial Court held that Cellmark's STR CTT test was scientifically valid under Daubert. See Commonwealth v. Rosier, 685 N.E.2d 739 (Mass. 1997). The Court noted that Cellmark had conducted extensive validation tests to evaluate the reliability and sensitivity of STR testing. Id. at 813 n. 10. The Court relied in part on a

[17] No articles on validation testing were provided by the State to the Court. However, the Vermont trial courts have previously relied on published articles in scientific journals validating the STR Triplex (CTT) test kit. See State v. Batchelder, No. 1127-g-95, slip op. at 30-31. (Wind.Dist.Ct. Aug. 7, 1997) (Grussing, J.).

pubiished validation study. Id. at 814 n.11, citing Micka, Validation of Multiplex Polymorphic STR Amplification Sets Developed for Personal Identification Applications, 41 J. Forensic Sci. 582, 589 (1996) (validating combined STR testing at CSF1PO, TPOX, and TH01, through GenePrint STR Systems; testing found "sensitive and robust" and "highly reliable").

CTT has also been accepted under the more restrictive Frye test. See, People v. Allen, 85 Cal.Rptr.2d 655 (Cal. Ct. App. 1999) (Ceilmark's STR test on three loci is generally accepted, based on endorsement of the technique by the Massachusetts and Nebraska Supreme Courts). The Nebraska Supreme Court has approved the use of STR testing, concluding that STR tests are generally accepted in the scientific community under the Frye test. See State v. Jackson, 582 N.W.2d 317 (Neb. 1998).

STR testing has also been admissible in two other cases, where it was not challenged., See Watts v. State, 733 So.2d 214 (Miss. 1999) (STR Triplex testing) and United States v. Beeler, 62 F. Supp.2d 136 (D. Maine 1999) (Cellmark STR analysis).

The Court finds that thk CTT STR system has been subjected to validation testing, publication and peer review. The Court further finds that it is generally accepted in the scientific community, and the results of such testing have been deemed admissible in a number of state courts, including a trial court in Vermont. The Court concludes that the CTT STR system is a reliable scientific technique under Streich.

3. STR CTT Testing'at Cellmark.

a. Cellmark CTT STR Test: Crime Scene Hair and Known Sample.

Anjali Swienton also conducted tests utilizing the CTT STR system, using both the

crime scene hair DNA sample and the known sample from Defendant. The DNA used for these tests was obtained from the DNA extracted originally from the crime scene hair and from the known sample. It was amplified for the CTT loci, and a product gel was run. The product gel indicated that no product had been obtained for Sample 02. Double the amount of extracted DNA from Sample 02 was then amplified, and the product gel for that amplification indicated that product had been obtained. The known and unknown samples were amplified at the same time. Although the protocols do not permit extraction from known and unknown samples to occur at the same time, concurrent amplification is permitted, and this practice does not create an unacceptable risk of contamination. As with all such tests, reagent blanks and positive and negative controls were run. (Tr. 12/6/99 at 97-102; Tr. 12/17/99 at 33-34).

After the second amplification, the product for both the known and unknown samples were run on a gel, and the results were analyzed. The profile for the crime scene hair was as follows: CSF: 11, 12; TPOX: 8, 11; THO1: 7, 9.3. These results reflect the number of repeats found, i.e., the CSF loci consisted of two alleles, one eleven repeats long, and the other 12 repeats long. The 9.3 allele for THO1 indicates nine repeats plus three more base pairs, (The repeated segment itself is four base pairs long). The results for Sample 03, the known sample, were as follows: CSF: 11, 12; TPOX: 8, 11; THO1: 7, 9.3. The two profiles are the same. (Tr. 12/6/99 at 102-104; Tr. 12/17/99 at 34-36).

At no time during the testing in this case did Ms. Swienton see any evidence of contamination. At no time did she observe anything that would cast doubt about the reliability of the tests. It is her opinion that the profiles reported for Samples 02 and 03

accurately represent the actual profile for those samples. (Tr. 12/17/99 at 36-37).

4. Applying Streich to the CTT STR testing at Cellmark.

The CTT system, like Polymarker/DQAlpha, has *been* in use for a number of years. It, too, has been the subject of many studies which have been published in peer-reviewed journals.

Again, the Court is concerned that the manufacturer of the test kit has elected not to publish the primer sequences. Despite this deficiency,-because of the length of time this kit has been in operation, the number of laboratories utilizing it (at least 20) and the number of validation studies conducted (the lack of primer sequences notwithstanding), the Court is comfortable in concluding that the CTT system constitutes a valid and reliable technique when properly employed. The CTT system is generally accepted in the scientific and forensic communities.

The Court received credible testimony that the CTT test had been validated. There was no specific evidence offered that it had been validated for use on degraded DNA samples. However, the Court' notes that throughout the testing process, none of the controls indicated a problem. The Court concludes that any DNA degradation did not interfere with the CTT process. Defendant has failed to demonstrate why, under these circumstances, the results should not be accepted as trustworthy.

Similarly, Defendant asserts that laboratory contamination may have somehow affected the results. Specifically, Defendant points out that the Cellmark laboratory was closed for a period of time in April, 1995, and suggests that the interruption was caused by the need for

the lab to cleanse itself of some unspecified, generalized contamination, While it is true that Cellmark employees are not now able to explain the hiatus, the Court concludes that since the controls in this case indicated no malfunction, the results here were not affected by whatever else might have been occurring in the lab. There is simply no evidence that contamination affected the results in this case.

As noted above, both the amplified product for the known and unknown samples were run on the same gel for electrophoresis. Defendant suggests that contamination might have occurred during this part of the process, but has presented no evidence that this is a practical concern or that there was actual contamination.

The Court concludes that CTT STR testing performed by Cellmark substantially followed the procedures for which the test was validated. Therefore, the evidence'is scientifically reliable and thus is admissible evidence which may be considered by the jury.

D. **Profiler** Plus Testing.

1. The Profiler Plus System.

Cellmark also used a STR testing system called Profiler Plus. The Profiler Plus system, available in a kit from Perkin Elmer, also involves DNA extraction, followed by amplification, followed by an electrophoresis step. The system tests for a group of STR's, just as the CTT system does. However, it targets nine STR's rather than only three. The electrophoresis is done through a capillary, instead of a gel. The visualization of the DNA is done using fluorescent tagged primers. As the DNA passes through the capillary, in order of size, it passes a window through which a laser is directed. The laser excites the fluorescent

tag, which gives off light at a particular wavelength, which in turn is detected by the machine, called a 3 10 Genetic Analyzer. (Tr. 12/6/99 at 71-72).

The fluorescence passing by the window creates a profile of peaks, measured in fluorescent units. Two peaks will appear for each locus, one peak for each allele. Through a series of comparisons with controls that are also run on the capillary, one can translate the peaks into the number of repeats, just as with the CTT system. The controls include both an allelic ladder and an internal standard that runs with each sample. In addition, reagent blanks, and positive and negative controls are also run on this system. (Tr. 12/6/99 at 74-75).

Capillary electrophoresis is used for research purposes, for gene mapping, for location of disease genes, and for anything that has to do with locating a specific gene on a specific part of a chromosome or associating it with another gene physically on the chromosome. The use of fluorescent primers and the generalized use of STR's has been in place for some time, as early as 1990. The specific group of nine STR's used in Profiler Plus has been in existence for a couple of years and a few papers have been published to date. The multiplex itself is relatively new, but the technology and the use of fluorescent tagged primers and the use of STR's is not new. The nine foci used, plus four others, have been designated as the 13 loci that will be used in the combined DNA index system for profiling convicted offenders around the country. Therefore, almost every laboratory in this field has either implemented this system, or is in the process of doing so. That group of 13 loci was validated in a study sponsored by the FBI that included twenty laboratories across the country. Although there is no publication of the results of this study, a large amount of information has been presented in meetings on these particular group of loci. According'to Dr. Cotton, Profiler Plus is

generally accepted in the forensic community. (Tr. 12/6/99 at 75-78).

2. **Applying Streich** to Profiler **Plus** System.

The Profiler Plus system which Cellmark used on a known sample from Defendant, has only been in use for a couple of years. As indicated, the basic technologies incorporated in Profiler Plus have been utilized as independent entities for longer periods of time, and are generally recognized as valid scientific techniques.

As explained above, the Profiler Plus system is greater than the sum of its parts. Because of the compromises made in creating multiplex systems, it is necessary that the entire system, as a package, be examined and validated. In the case of Profiler Plus this simply has not been accomplished. When the testimony of the State's witnesses is examined, none of them pretend that it has been.

As the Court has noted twice above, the failure of the manufacturers of DNA testing systems to disclose the primer sequences they have created to permit amplification of DNA is problematic from the perspective of scientific knowledge and, consequently, validation. It is more than problematic, it is anti-scientific in that it inhibits the ability of scientists in the field (including defense experts) to test the manufacturers' claims. Although the Court understands that the manufacturers believe they need to maintain as confidential what they consider to be proprietary information, in the case of new technology, it delays acceptance by the courts. In view of the mandate of Streich -- particularly the first and second factors -- the results of the Profiler Plus tests cannot be admitted.

Profiler Plus has not been subject to scrutiny through articles in peer-reviewed

journals. There have been no independent validation studies of Profiler Plus. There is no published validation of the Profiler Plus as a multiplex system. According to its own scientists, Cellmark has not yet completed its own validation work on Profiler Plus.

Furthermore, computer-assisted legal research has not disclosed any appellate court in the country -- or even a trial court -- which has held that Profiler Plus is valid and reliable. Counsel have failed to cite any such authority. Evidence from a similar system, using a Perkin Elmer Genetic Analyzer 310 capillary electrophoresis instrument, was held to be inadmissible. See People v. Bokin, No. SCN: 168461 (Cal. Super. Ct. May 6, 1999).[18] As that court observes: "It is not enough that the particular laboratory which developed a procedure which is marketed engage in their own internal validation." Id. at 5. The court concluded that DNA evidence obtained from these tests was not admissible because it was not scientifically validated. Id.

The Profiler Plus system is capable of being tested in the same way that earlier DNA analysis systems have been tested. However, the Profiler Plus system has not been sufficiently validated. The results of validation testing of Profiler Plus have not been published and subjected to the peer review process. Without the scrutiny of the scientific community, the Court can not establish whether Profiler Plus is a reliable system, or one which is prone to error. Regardless of whether the technique is generally accepted in the commercial forensic community or is widely used in building convicted offender databases, no appellate court has found that this system is validated for use in a criminal proceeding. The Court concludes that the test results from the Profiler Plus system are not admissible in

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18 This opinion is on file with the Court.

this case because Profiler Plus has not yet been scientifically validated.

E. PowerPlex Testing.

1. The PowerPlex System.

Genelex also conducted Short Tandem Repeat (STR) testing in this case. It used a commercial kit from the Prornega Corporation when doing that testing, the name of which is the PowerPlex 1.1 kit. When using this kit, the DNA is first extracted, then amplified at nine different sites, including a gene which tests for sex. The amplified DNA is then run on an electrophoresis gel, which separates out the DNA by size. Once the gel is completed, it is put into a laser scanner, which detects fluorescent molecules which are attached during the copying process. The laser scanner then uses the fluorescence to build an image in the computer, which is analyzed to determine the actual number of repeats at each locus. (Tr. 12/7/99 at 88-90).

As with all of the forensic samples, a positive and negative control. are both used with STR testing, as well as reagent blanks which are generated during the extraction process. The PowerPlex system has undergone peer review through publication of papers in the Journal of Forensic Sciences.

The PowerPlex system has been in use for forensic testing since 1997. Non-fluorescent STR testing was in use for several years before that, and fluorescent testing for systems other than the PowerPlex system was in use before 1997 as well. Genelex conducted validation testing with the PowerPlex system, including testing of reproducibility, accuracy, sensitivity, and other factors, to demonstrate that the system is in fact reliable and

robust and accurate. (Tr. 12/7/99 at 94-96).

Dr. Bieber is familiar with the various forensic DNA testing procedures used in this case including PowerPlex and Profiler Plus. Dr. Bieber holds the opinion that each of these types of tests has been validated within the scientific community, has been subjected to peer review, has been the subject of scientific conferences and seminars, and has been generally accepted as reliable within the scientific community. '(Tr. 12/9/99 at 20-23).

2. Applying Streich to the PowerPlex System.

In June, 1998, Genelex used the PowerPlex system to analyze and type the DNA obtained from a 1976 crime scene hair. The PowerPlex system is quite new, and has only been in use since 1997.. Thus, at the time of analysis, the system had 'been in use for approximately one year. Like the Profiler Plus, the basic technologies comprising the system have been used in previous separate applications and are generally recognized as valid scientific techniques. However, the entire multiplex system, as a package, must be examined and validated.

For the same reasons discussed above with respect to the Profiler Plus, the failure of the manufacturers of PowerPlex to disclose the DNA amplification primer sequences prevents independent scientists from readily validating the PowerPlex system. The manufacturer's proprietary concerns, however, can not trump Defendant's right to a fair trial, which includes the right to have only scientifically validated evidence admitted for the jury to consider in the State's case against him. Especially, with a new test, which has not been validated by long use in a variety of settings with a variety of sample types, it is unacceptable to deny

independent scientists (including defense experts) access to primer sequences, which could allow the scientists to properly investigate the purported reliability and validity of the new technique.

Promega Corporation, the manufacturer of the PowerPlex, has published two papers in the Journal of Forensic Sciences on the PowerPlex System. Only one other validation study by another laboratory has been published.

Moreover, the Court has been unable to discover any appellate decisions in either the state or federal courts which have recognized the PowerPlex system as valid and reliable. Counsel have failed to provide any legal authority on this point.

PowerPlex, like Profiler Plus, was designed and developed to analyze and type DNA samples obtained from convicted felons to enable the various states to build convicted offender DNA databases. The Court infers that the system's manufacturer was principally concerned with developing a system for typing contemporaneously retrieved DNA samples. Thus, the inability of the State to demonstrate successful validation studies on degraded DNA samples is particularly critical.

It is the State's burden to persuade the Court by a preponderance of the evidence that the PowerPlex test results are admissible under *Streich*. The State has not met its burden. The Court concludes that even though the PowerPlex system is capable of being tested, there is no evidence that it has been tested for the use to which it was applied in this case. Although PowerPlex was been subjected to some publication and peer review, publications are not numerous, and more importantly, do not specifically address PowerPlex' ability to reliably

test the type of sample involved in this case. Furthermore, the lack of published sequences does not permit independent scientists to review whether the test functions the way its manufacturer claims. Finally, while PowerPlex may be lauded by the commercial Iaboratories who use it and the crime labs which are pleased to have a tool for efficiently building convicted offender databases, the Court is not convinced that the PowerPlex system has gained general acceptance in the larger scientific community. Like the Profiler Plus, no appellate court has found that PowerPlex is reliable and valid for use in criminal proceedings. The Court concludes that the Profiler Plus is not admissible in this case because it has not yet been scientifically validated as reliable.

VII. Statistical Analysis of Test Results.

A. Population Genetics.

The same basic principles of genetics, such as Mendel's laws of segregation and independent assortment, that are routinely applied in medical research and diagnosis, apply with equal force to forensic uses of DNA. (Tr. 12/9/99 at 16-17).

Population genetics is a subspecialized area of genetics that deals primarily with the genetic diversity that occurs in populations, specifically with regard to the frequency of particular alleles or genotypes in various populations of plants or animals, and it primarily makes use of population sampling. Population sampling is a method used to derive estimates about a large population from sampling a smaller one. Since statistical estimates can be made effectively from smaller populations, it is more efficient and more practical to use sampling theory rather than to attempt to test an entire population. (Tr. 12/9/99 at 23-24).

A database in this context refers to a collection of samples or individuals that are collected and used by population geneticists to make profile tabulations for use in making frequency estimates about a larger population from which that sample is obtained. When creating a database for forensic DNA use, important factors to include in the make up of the database include the size of the database, the exclusion of related individuals (in most cases), and a classification of the database that relates to the estimates to be made. It is common practice to classify humans for forensic purposes into different population groups based upon their so-called race or ethnicity, and sometimes also by religious affiliation,.country of national origin, or linguistic similarities. These factors are relevant because the frequencies of profiles can differ in these different populations. (Tr. 12/9/99 at 14-26).

Databases are created as part of ongoing research into the development of new reagents and genetic loci, to determine whether there is sufficient variation for the loci to be useful. Databases are often gathered and collected by researchers at universities or crime laboratories or commercial companies. In some instances, the databases are collected by law enforcement agencies such as the FBI, or state or local crime laboratories. In some cases, the databases are gathered by the vendors of commercial reagent kits, or by laboratories that perform forensic or paternity testing, so that they can interpret their own laboratory findings.

These databases are collected by scientists who understand the principles behind them, 'and are typically reviewed statistically by scientists either in or outside of their organization. In many instances, the data will be offered for presentation at scientific meetings, such as the Human Identity Symposium, the International Congress on Forensic Statistics, or the American Academy of Forensic Sciences. They are often published in journals, including the

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Journal of Forensic Sciences. However, it is becoming difficult to get this sort of data published, because it is no longer considered new or scientifically interesting. The data has been scrutinized and peer reviewed, but may not have been published for lack of space in the journals, and because the population groups have been thoroughly enough studied that the database would not be donsidered a new and important scientific contribution. (Tr. 12/9/99 at 26-28).

A database with a sample of one hundred, in the context of forensic testing, has been shown to be adequate in detecting alleles as infrequent as one percent, with a high degree of confidence. (Tr. 12/9/99 at 31).

Assuming that a database has been subjected to this kind of peer review, it is reasonable within the scientific community to rely on such a database in performing calculations either in the medical or the forensic context, without personally inspecting the raw data for each of the individuals who gave a sample to that database. It is a common practice to do so in forensics and in every branch of science and the treatment and care of patients. (Tr. 12/9/99 at 28).

B. The Databases.

1. The 1995 Cellmark Database.

Cellmark employees calculated match frequency estimates in this case based on Cellmark population databases. The Cellmark database was originally evaluated in 1995. See B. Weir and J. Buckleton, Tests for Disequilibrium in Cellmark Databases: Polymarker and STR Data (June 1995) (unpublished manuscript). (Defense Exhibit # 172). Dr. Cotton testified

that as a result of scrutiny of the 1995 Cellmark database, a number of samples had to be removed from the Cellmark population database that should not have been there, and other samples were added. (Tr. 12/9/99 at 158, 165). On May 29, 1997 Cellmark modified its 1995 database by removing two individuals from the Caucasian database and replacing 19 individuals with 21 other individuals in the African American databases. See B. Weir, Genotype Frequencies in the Cellmark Databases: PM, DQA1 and STR Data (June 1997) (unpublished manuscript) at 1. (Defense Exhibit # 169). Dr. Cotton acknowledged that the 1995 Cellmark database included incorrect samples. (Tr. 12/9/99 at 166). Dr. Don Riley testified that samples from white employees had ended up in the black database, and in fact had appeared twice each. In addition, at feast ten of the samples included in the African American database were from Hispanic individuals rather than African Americans, and two other samples were from people who resided in Barbados, not the United States. (Tr. 12/10/99 at 14-15).

A June 10,. 1997 Memorandum from the Cellmark senior scientists to Cellmark forensic staff explains the reasons why samples were removed from the 1995 Cellmark database. The reasons for removal were: (1) individuals were included who did not live in the United States, (2) the racial background of the person could not be confirmed or (3) the samples did not come from Cellmark staff or a Cellmark paternity case. (Defense Exhibit # 124). The June 10, 1997 Cellmark Memorandum stated that Dr. Weir had analyzed the updated database and issued a report dated June I, 1997. (Defense Exhibit # 124).

The Court concludes, based on the testimony of Dr. Cotton and Dr. Don Riley, Dr. Weir's June 1, 1997 report, and the June 10, 1997 Cellmark Memorandum, that the 1995

Cellmark database contains a number of errors. No expert witness in this case has testified that the 1995 Cellmark database is currently considered reliable. Therefore, genetic profile frequency calculations based on the 1995 Cellmark database are not admissible at trial.

2. The 1997 Cellmark Database.

Dr. Bieber calculated the frequency of the genetic profilk obtained by Cellmark based on a corrected database constructed by Cellmark, hereinafter, the 1997 Cellmark database. This database has been subjected to validation testing. See B. Weir; Genotype Frequencies in the Cellmark Databases: PM, DQA1 and STR Data (June 1997) (unpublished manuscript). This paper has not been published in a peer review journal. It has, however been widely distributed in the forensic community, and has been presented at scientific meetings. (Tr. 12/9/99 at 50-51). Dr. Bieber testified that the 1997 Cellmark database has been subject to validation by Dr. Weir and is generally accepted as reliable in the scientific community. (Tr. 12/9/99 at 50-51). The Defense has not challenged the validity or reliability of the 1997 Cellmark database.

The Court finds the 1997 Cellmark database is reliable and valid. It has been subjected to a validation study by Dr. Weir, and the results have been made widely available to the scientific community. Dr. Weir's paper reports the frequencies observed in the database itself, so they are available for scrutiny by the scientific community. There is expert testimony that the 1997 database is generally accepted in the scientific community, and there is no contrary evidence. The Court concludes that genetic profile frequency calculations based on the 1997 Cellmark database are admissible, subject to the calculation assumptions which follow.

C. Frequency Calculations.

1. Generally.

Implementation of the product rule consists of the multiplication of probability estimates that are considered independent of one another to produce a combined probability of those two or more separate events. The principle assumption underlying the rule **is** that the occurrence of one of the events does not affect the occurrence of any of the other events, so that the events are independent. (Tr. 12/9/99 at 29).

The Hardy-Weinberg Equilibrium is a condition in which the allele frequencies within a large, random, intra breeding population are unrelated to patterns of mating. In this condition, the occurrence of alleles from each parent will be independent and have a joint frequency estimated by the product rule. 2 D. Faigman, et. al., Modern Scientific Evidence, at 600. The Hardy-Weinberg Equilibrium allows one to predict the frequency of the different categories of individuals, homozygotes (who have two copies of the same allele), and heterozygotes (those who have two different alleles at a particular locus). It allows the prediction of the frequency of each combination of alleles at a certain locus in a sexually reproducing population. (Tr. 12/9/99 at 29-30).

Linkage equilibrium is a condition in which the occurrence of alleles at different loci are independent, 2 D. Faigman, et al., Modern Scientific Evidence, at 604. Genetic loci that are on separate chromosomes, or are far apart on the same chromosome, typically exhibit linkage equilibrium, in that the segregation of alleles is independent. Genetic loci that are physically very, very close to one another on the same chromosome may not have

independent behavior, and they might be said to be in disequilibrium. (Tr. 12/9/99 at 30).

Any significant and severe departure from either concept could allow the independence of the loci to be questioned, and therefore the product rule might not be applicable. (Tr. 12/9/99 at 30).

When one makes a frequency estimate for a particular genotype, or a set of genotypes in a DNA profile, one is actually presenting what is technically called a point estimate of a combined match probability, also called a match statistic, or a profile frequency estimate. The "confidence interval" is an "estimate expressed as a range, for a quantity in a population. If an estimate from a large sample is unbiased, a 95% 'confidence interval' is the range from about two standard errors below to two standard errors above the estimate. Intervals obtained this way cover the true value about 95% of the time, and 95% is the 'confidence level.'" 2 D. Faigman, et. al., Modern Scientific Evidence, at 588.

A standard accepted confidence interval level within the scientific community for DNA forensic identification testing comparison purposes is 95 percent. This interval is universally used, from psychology to biology to forensics. It is not only common, but also almost universal, for private laboratories to report only the point estimate, and not the confidence limit, because the concept of confidence interval is so well-ingrained and accepted by all people who are familiar with concepts of mathematics and statistics that it is understood that the estimate is a point estimate. (Tr. 12/9/99 at 32-35).

Pbpulation subgroups are defined groups within a large group, based on ethnic or religious or linguistic classifications. The National Research Council, a group appointed by

the National Academy of Sciences to deal with interesting or socially relevant matters involving science and public policy, has produced several important publications that deal with forensics. One of those publications, NRC I[19], recommended a method called the ceiling principle, in order to correct for possible population subgroups. It was a method used to overestimate the true frequency of a particular profile. That report has been superseded by NRC II.[20] NRC II strongly suggests that the ceiling principle be abandoned. See NRC II, supra, at 156-59.ommends the use of a correction factor known as "theta". Theta basically adds a number to the product rule calculation, So that it increases the expected profile frequency. It other words, it results in a more conservative calculation. (Tr. 12/9/99 at 35-37).

2. Application of Streich.

In State v. Streich, 163 Vt. 331 (1995), the Supreme Court acknowledged that there were two distinct, relevant aspects to DNA profiling evidence, laboratory identification of DNA loci and the calculation of probability statistics. As anticipated by the Court in Streich, the "scientific climate is vastly different" today than in 1991, *when* Streich was tried, and 1995, when the Court issued its opinion.

Today, the PCR technique is overtaking the RFLP method used in Streich.. In Streich, the Court categorically rejected the unmodified product method of calculating probability, and endorsed the ceiling principle to account for the vagaries of population substructure "to fully

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19. National Research Council, DNA Technology in Forensic Science (1992) ("NRC I").

20 National Research Council, The Evaluation of Forensic DNA Evidence (1996) ("NRC II").

protect the rights of criminal defendants." Id. at 345. Currently, the experts agree that the ceiling principle has been replaced by a correction factor called "theta."

In the course of testimony taken over seven days, the Court received evidence from both State and Defense experts regarding the proper method for calculating probabilities in connection with the genetic profiles obtained in the instant case. The Streich opinion suggests that it is the duty of this Court to determine which probability statistics will be presented to the jury:

> Thus, we find it wholly impractical to say the dispute over statistical measurement should go before the jury for a clash of experts on the proper probability figures. Such evidence will not assist the jury in understanding the evidence or determining a fact in issue as required by Rule 702. It would threaten to become an evidentiary sideshow raising serious Rule 403 concerns. On the one hand, it may inappropriately undercut the legitimate force of DNA match evidence. On the other hand, it may focus too much attention on the significance of the probability statistics.

Streich, 163 Vt. at 345-46 (emphasis in original).

With all due respect, the import of this passage is not clear. There is no question that statistical analysis is complex and often abstruse. Undoubtedly, the jury will have to struggle to understand and weigh the testimony of the various expert witnesses. However, this Court does not appreciate the qualitative difference between expert statistical testimony and expert testimony in other highly technical fields.

Most troublesome in the context of the instant case is that the Court's language in Streich ignores Defendant's rights under both the Sixth Amendment to the United States Constitution and Chapter I, Article 10 of the Vermont Constitution to confront adverse witnesses and to call witnesses in his favor. A defendant's right to confront and to present his

own evidence might be more theoretical than real when the debate is between minuscule probabilities. Here, the disagreement between the expert opinions results in large and meaningful differences in the calculation of the match probabilities. This Court can find no method of resolving the apparently bona fide -difference of opinion without doing injustice to either the State or Defendant.

This Court concludes that the passage from Streich quoted above is dicta. The holding in Streich is that evidence based on the unmodified product rule does not pass muster under the reliability standai-ds of Daubert, and that admitting the same constitutes error. Id. at 346-47. The language regarding the battle of experts is simply extraneous.

At most, the Court's limitation of expert statistical testimony applies only when the dispute concerns which of two or more minuscule probabilities is more accurate. The undersigned agrees that. it likely would make little difference to a jury "whether the probability of random selection of a person with the same allele is 1 in 100,000 or 1 in 1,000,000." Id. at 345. That is not the case here. Defendant presented evidence that the probability of a random match might be as great as 1 in 2845. The State showed that the probability might be as small as 1 in 17,000,000. Here, the different probabilities are not an "evidentiary sideshow" but a substantial and important issue directly bearing on the State's burden of proving the identity of the perpetrator.

3. The Probability Calculation.

The NRC II Recommendation 4.1 states the following concerning, the use of appropriate databases:

> In general, the calculation of a profile frequency should be made with the product rule. If the race of the person who left the evidence-sample DNA is known, the database for the person's race should be used; if the race is not known, calculations for all racial groups to which possible suspects belong should be made.

Recommendation 4.1, NRC II, supra, at 122.

NRC II Recommendation 4.2 addresses the case where all possible sources of the DNA sample come from the same isolated subgroup:

> If the particular subpopulation from which the evidence sample came is known, the allele frequencies for the specific subgroup should be used as described in Recommendation 4.1. If allele frequencies for the subgroup are no t available, although data for the full population are, then the calculations should use the population-structure Equations 4.10 for each locus, and the resulting values should be multiplied.

Recommendation 4.2, NRC II, supra, at 122.

The State's expert, Dr. Frederick Bieber, calculated profile frequencies based upon Recommendation 4.1. The Defense expert, Dr. William Shields, based his profile frequency calculations on the second sentence of Recommendation 4.2.

Dr. Shields testified that he believed that in all forensic cases, the equations 4.10 incorporated in Recommendation 4.2 should be employed. Recommendation 4.2, by its own terms, is to be used only if the evidence sample comes from a particular subpopulation. The comment to the recommendation indicates that the recommendation should be employed when "the suspect and other possible sources of the sample belong to the same subgroup. That can happen, e.g., if they are all members of an isolated village." NRC II, supra, at 122. Thus, Recommendation 4.2 should be implemented only when (1) the circumstances involve an isolated subgroup, and (2) there is reason to believe that the perpetrator is a member of the

subgroup. As indicated above, this would be an extremely rare situation.

Dr. Shields' approach was considered and rejected by the District Court in United States v. Shea, 957 F. Supp. 331, 343 (D. N.H. 1997). As noted by that court, "The NRC II report considered a similar approach and concluded that it was 'unnecessarily conservative.'" Id. at 343 n.39.

The first option in Recommendation 4.1 is also problematic: In the case of an un-witnessed crime, as here, the race of the perpetrator cannot be "known" prior to the outcome of the trial.[21] Theoretically, all that can be "known" is the race of the suspect.[22]

Since the race of the perpetrator cannot be known, "calculations for all racial groups to which possible suspects belong" must be made, using the second option in Recommendation 4.1. The adjustment equations recommended by NRC Ii "assume that there is undetected substructure in the population and adjusts the product rule accordingly." NRC II, supra, at 28.

The Court concludes that it is appropriate to use the second option set forth in Recommendation 4.1. Recommendation 4.1 should be employed in the probability calculations in this case, using calculations for all racial groups to which all possible suspects

[21] The Court recognizes that even in the event of conviction, the perpetrator is "known" only by proof beyond a reasonable doubt.

[22] The authors of NRC II obviously believed that at least in some cases, the race of the perpetrator could be known. In some instances they use as an example a sexual assault committed by a Caucasian male. See NRC II, supra, at 6. The Court believes that even this form of identification is hazardous in connection with DNA profiling. As NRC II points out, "There is no generally agreed upon vocabulary for treating human diversity.. . . [G]roups are mixed, all classifications are fuzzy at the borders, the criteria for membership are variable." NRC II, supra, at 57. It is very possible, for example, that a perpetrator identified by a victim as Caucasian, may in fact be of Hispanic origin. The Court therefore agrees with Defense expert William Shields that, in the context of a criminal trial, except perhaps in rare instances, the race of the person who left the evidence-sample DNA can never be known.

belong, since the race of the perpetrator is unknown.

All of the equations recommended by NRC II incorporate a "theta" factor. "Theta" is a method of accounting for population substructure through conservative calculation of the probability statistic. It has the effect of increasing the expected profile frequency and so results in a'more conservative calculation, which favors the accused.

NRC II states that "[a] conservative value of theta for the U.S. population is 0.01." However, NRC II explains that a value of 0.03 may be more appropriate for "some small, isolated populations", and that "[a] more conservative value of theta = 0.03 might be chosen for PCR-based systems in view of the greater uncertainty of calculations for such systems because of less extensive and less varied population data than for VNTRs." Id. at 122.[23]

Dr. Bieber used a theta value of 0.03 in his calculations. Dr. Shields testified that a value of 0.05 should be employed to account for sampling error. It appears to the Court that 0.03 is already a very conservative value; it is recommended by NRC II as such. Whilk the evidence did not foreclose Dr. Shields' position, he offered no scientific authority to- support the validity of his approach. Consequently, the Court holds that the theta value of 0.03 is scientifically valid and therefore calculations based on this value are admissible.

Based on the expert testimony and the authorities cited by the experts, the Court concludes that calculations employing part two of NRC II Recommendation 4.1 and a theta value of 0.03 are reliable and therefore admissible under Streich.

[23] NRC IT was published in 1996. Query whether the latter statement would be accurate today.

VIII. Conclusions

1. Admissibility under Streich.

The admissibility or non-admissibility of the State's proposed scientific evidence is summarized in the Order of the Court set forth below.

2. Consideration of V.R.E. 403.

The Court has examined at great length the various testing procedures utilized in connection with this case and has discussed possible problems arising from those procedures. As the Supreme Court recognized in Streich, (with respect to the RFLP technique):

> The process is not error-free, but adherence to accepted procedures and controls minimizes this error.. . . Indeed, we cannot find any recent decision under any standard of admissibility which refuses to admit the DNA match result based on the . . . risk of error of the underlying [RFLP] technology.

Streich, 163 Vt. at 344 (citations omitted). The same may be said of the PCR technology and the tests approved here.

That said, the Court concludes that the probative value of the evidence it is admitting is great and the danger of unfair prejudice small. "[A] claim that scientifically sound methods have been applied improperly ordinarily should be left for the jury to resolve unless the alleged 'error negates the basis for the reliability of the principle itself.'" United States v. Shea, 957 F. Supp. at 337 (citation omitted). The Court has found no such error with respect to the test results approved.

O R D E R

1. The results of Cellmark's Polymarker/DQAlpha testing are admissible.

2. The results of Genelex' Polymarker/DQAlpha testing are not admissible, except as noted in the opinion.

3. The results of Cellmark's CTT STR testing are admissible.

4. The results of Cellmark's Profiler Plus testing are not admissible.

5. The results of Genelex' PowerPlex testing are not admissible.

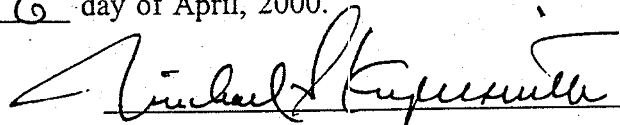
6. Statistical results based on Cellmark's 1995 database are not admissible.

7. Statistical results based on Cellmark's 1997 database are 'admissible.

8. Probability calculations employing the second option set forth in NRC II Recommendation 4.1 are admissible.

9. Probability calculations using a theta value of 0.03 are admissible.

Dated at Burlington, Vermont this 6th day of April, 2000.



Michael S. Kupersmith
District Judge

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