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CERTIFIED FOR PUBLICATION

IN THE COURT OF APPEAL OF THE STATE OF CALIFORNIA

SECOND APPELLATE DISTRICT

DIVISION FIVE

THE PEOPLE,

Plaintiff and Respondent,

v.

TERRY SMITH,

Defendant and Appellant.

B153102

(Los Angeles County
Super. Ct. No. TA102226)

APPEAL from a judgment of the Superior Court of Los Angeles County. Dino John Fulgoni and Steven C. Suzukawa, Judges. Affirmed.

Linda Buchser, under appointment by the Court of Appeal, for Defendant and Appellant.

Bill Lockyer, Attorney General, Robert R. Anderson, Chief Assistant Attorney General, Pamela C. Hamanaka, Senior Assistant Attorney General, Mary Sanchez, Supervising Deputy Attorney General, Alene M. Games and Deborah J. Chuang, Deputy Attorneys General, for Plaintiff and Respondent.

I. INTRODUCTION

Defendant, Terry Smith, appeals from his forcible rape conviction. (Pen. Code,[1] § 261, subd. (a)(2).) The trial court also found that defendant had previously been convicted of two serious felonies (§§ 667, subds. (a)(1), (b)–(i), 1170.12.) Defendant's sole argument on appeal is that now retired Judge Dino John Fulgoni improperly ruled at the end of a pretrial motion concerning the admissibility of deoxyribonucleic acid evidence that the process of attributing distinct genetic profiles to multiple contributors of mixed source forensic samples is generally accepted in the relevant scientific community. We reject this contention and affirm the judgment.

II. FACTUAL AND PROCEDURAL BACKGROUND

A. Evidence Presented at Trial

We view the evidence in a light most favorable to the judgment. (*Jackson v. Virginia* (1979) 443 U.S. 307, 319; *People v. Osband* (1996) 13 Cal.4th 622, 690; *Taylor v. Stainer* (9th Cir. 1994) 31 F.3d 907, 908-909.) On November 14, 1999, the 66-year-old victim discovered defendant sitting in her living room. The victim recognized defendant as a neighbor's son. Defendant spoke with her briefly then continued to sit quietly on her couch for approximately 30 minutes. The victim repeatedly stated she was tired. She believed defendant would leave. Defendant suddenly stood up and walked toward the victim. Defendant said, "'I am going to fuck you.'" Defendant pushed the victim down on the love seat where she had been seated. Defendant pulled the victim's pants and underwear down. Defendant unbuckled his own pants. Defendant got on top of the victim. The victim fought

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[1] All further statutory references are to the Penal Code except where otherwise indicated.

with defendant, screaming, "'Get off of me.'" Defendant put his penis in the victim's vagina. The victim continued to yell and attempted to move defendant off her body. Defendant held the victim down in the breast area. Defendant continued to sexually attack the victim for approximately 20 minutes. The victim called out for her neighbor. Defendant got up and left the victim's house. The victim pulled her clothing up. The victim went to a public telephone to call the police.

Los Angeles Police Officer Bradley Smiley arrived at the victim's home. The victim told Officer Smiley that the neighbor's son was the rapist. The victim knew defendant through previous contacts. Two officers transported the victim to the hospital for a medical examination. The victim suffered pain in her lower abdomen and back, genitalia, and chest as a result of the attack. The medical examination revealed that the victim had an abrasion, bruising, bleeding, and secretion to her vaginal area consistent with forcible trauma. The victim had not had consensual sexual intercourse for over a month prior to defendant's attack. Semen is only viable for 72 hours.

Blood samples were taken from both the victim and defendant. Samples from the sexual assault kit collected at the time of the victim's medical examination revealed sperm on the cervical and genital swabs and the vaginal lavage. Those samples, along with the victim's and defendant's blood samples, were forwarded to Cellmark Diagnostics for deoxyribonucleic acid analysis.

Deoxyribonucleic acid is material present in each cell of the human body that determines an individual's characteristics. Virtually all deoxyribonucleic acid is the same from one human to another. However, a small percentage of the deoxyribonucleic acid is different in each individual. Cellmark Diagnostics tests deoxyribonucleic acid by comparing an unknown sample from a crime scene to that from known individuals. The tests serve to either include or exclude an individual as a possible source of the biological sample. As will be explained in more detail below, the polymerase chain reaction is a technique that has been used in the field of molecular biology since the 1980's to copy small specific regions of deoxyribonucleic acid. The deoxyribonucleic acid is isolated into a form that can be copied. Then copies of that deoxyribonucleic acid sequence are copied. Finally,

the actual deoxyribonucleic acid types are examined and compared to other samples to determine whether they could be included or excluded as a donor source for the sample.

In this case, Cellmark Diagnostics, employing proper procedures, tested the three samples provided by the Los Angeles Police Department using the polymerase chain reaction technique and a Profiler Plus testing kit. Dr. Charlotte Word, deputy director for the forensics laboratory at Cellmark Diagnostics, explained during the trial that in the testing of the external genital swab, two separate tubes of deoxyribonucleic acid were obtained by separating the sperm cells from any others present in the sample. The Profiler Plus test looks at nine regions of the deoxyribonucleic acid that have been demonstrated to differ in the human population as well as a tenth region that types the sample by gender. Cellmark Diagnostics follows a strict protocol, which includes: changing gloves; processing one sample at a time; transfer and isolation of the deoxyribonucleic acid of the unknown sample first; one-way flow through the laboratory; restriction of equipment to specific regions to prevent contamination; and retesting of scientists at least twice annually to insure reliability of procedures.

The results demonstrated that the non-sperm fraction had a primary source that was female and was consistent with the profile from the victim. The deoxyribonucleic acid from the sperm fraction was determined to be from a male. The deoxyribonucleic acid from the sperm fraction matched that from defendant. Dr. Word's testimony included a detailed description of how the conclusions were drawn from the various consistencies and inconsistencies in the samples tested. Statistical frequency based on the types obtained in this case for primary donor using population databases were determined to be approximately 1 to 460 billion unrelated individuals in the Caucasian database and 1.15 trillion unrelated individuals in the African-American database. A more conservative "mixture" calculation for the determination of a primary donor in this case revealed 1.1 million unrelated Caucasian individuals from one database and 1.3 trillion from another source of data. For the African-American database, the results were 1 in 580,000 unrelated individuals. In a Hispanic database, the results were 1.2 million unrelated individuals. Based upon

Dr. Word's training and experience, the more appropriate statistics to utilize in this case to determine the primary source of the sperm would be the first two statistical calculations.

B. *Kelly* Hearing

Prior to trial in this case, defendant stipulated to the consolidation of his case with three unrelated cases for purposes of a discovery motion and *Kelly* hearing. (*People v. Kelly* (1976) 17 Cal.3d 24, 30-41; see *People v. Roybal* (1998) 19 Cal.4th 481, 505.) Now retired Judge Fulgoni presided over a hearing pursuant to Evidence Code section 402 to determine whether deoxyribonucleic acid evidence was admissible pursuant to *Kelly*. The hearing involved 19 days of testimony and argument on whether the mixed source sampling of deoxyribonucleic acid testing had gained general acceptance in its field pursuant to prong one of *Kelly*. Thereafter, Judge Fulgoni reached the conclusion that the evidence was generally accepted in the scientific community.

III. DISCUSSION

A. *Kelly* Determination

Defendant argues that following an extended hearing, Judge Fulgoni improperly found that the technology utilized in deoxyribonucleic acid testing for analysis of mixed source samples was *generally accepted in the scientific community*. Defendant concedes, "It is generally accepted the [polymerase chain reaction and short tandem repeats] can be completely accurate in typing genetic material from single source samples." Defendant argues though, "The question here is whether the test results from the technology can be interpreted in a manner that attributes genetic material from *mixed samples* to specific contributors." (Italics added.) Judge Fulgoni defined the technology in question, "The (new) technology involved in this case is a technology which purports to identify the DNA

at a crime scene compared with samples donated by suspects and victims to see if a match can be declared that incriminates the defendant or not."

1. The *Kelly* Test

Formerly, the federal rule for evaluating the admissibility of new scientific evidence was that specified in *Frye v. United States* (D.C. Cir. 1923) 293 F. 1013, 1014. *Frye* was adopted by the California Supreme Court in *People v. Kelly, supra,* 17 Cal.3d at page 32. (See *People v. Venegas* (1998) 18 Cal.4th 47, 76; *People v. Leahy* (1994) 8 Cal.4th 587, 594.) In *Daubert v. Merrell Dow Pharmaceuticals, Inc.* (1993) 509 U.S. 579, 585-589, the United States Supreme Court held that *Frye* had been abrogated by rule 702 of the Federal Rules of Evidence (28 U.S.C.). (See *United States v. Scheffer* (1998) 523 U.S. 303, 311, fn. 7.) After *Daubert* replaced *Frye* as the pertinent federal court test, the California Supreme Court held, "[W]e conclude that the *Kelly/Frye* formulation (or now more accurately, the *Kelly* formulation) should remain a prerequisite to the admission of expert testimony regarding new scientific methodology in this state." (*People v. Leahy, supra,* 8 Cal.4th at p. 591; see *People v. Venegas, supra,* 18 Cal.4th at p. 76, fn. 30.) In *Kelly*, the California Supreme Court set forth the following "general principles of admissibility" for opinion testimony based on new scientific techniques: "(1) [T]he *reliability of the method* must be established, usually by expert testimony, and (2) the witness furnishing such testimony must be properly *qualified as an expert to give an opinion* on the subject. [Citations.] Additionally, the proponent of the evidence must demonstrate that correct scientific procedures were used in the particular case. [Citations.]" (*People v. Kelly, supra,* 17 Cal.3d at p. 30, original italics; see also *People v. Diaz* (1992) 3 Cal.4th 495, 526.) In *People v. Soto* (1999) 21 Cal.4th 512, 519, the California Supreme Court held: "However, *Kelly* 'does not demand that the court decide whether the procedure is reliable as a matter of scientific fact: the court merely determines from the professional literature and expert testimony whether or not the new scientific technique is accepted as reliable in the relevant scientific community and whether "'scientists significant either in number or expertise

publicly oppose [a technique] as unreliable.'" [Citations.]' (*People v. Axell* (1991) 235 Cal.App.3d 836, 854 [] . . . .) '"General acceptance" under *Kelly* means a consensus drawn from a typical cross-section of the relevant, qualified scientific community.' (*People v. Leahy, supra,* 8 Cal.4th at p. 612.)" Moreover, the California Supreme Court has held: "[T]he trial courts, in determining the general acceptance issue, must consider the quality, as well as quantity, of the evidence supporting or opposing a new scientific technique. Mere numerical majority support or opposition by persons minimally qualified to state an authoritative opinion is of little value . . . ." (*People v. Leahy, supra,* 8 Cal.4th at p. 612; accord, *People v. Venegas, supra,* 18 Cal.4th at p. 85.) Defendant's challenge relates only to the first prong of the *Kelly* test—whether the mixed samples testing that occurred in the present case meets the *Kelly* reliability test.

2. Description of deoxyribonucleic acid

In the recent case of *U.S. v. Trala* (D. Del. 2001) 162 F.Supp.2d 336, 339-340, the District Court of Delaware explained the basic principles pertaining to deoxyribonucleic acid: "Each human body contains a large number of cells, each of which descends from successive divisions of the fertilized egg that was its origin. Virtually all non-reproductive cells in the body contain identical copies of a complex structure called deoxyribonucleic acid or, DNA. This structure represents the genetic code for that individual. The DNA is in the form of microscopic chromosomes, which are located in the nucleus of a cell. A chromosome is a thread of DNA surrounded by other materials, mainly protein. A fertilized egg contains 23 chromosomes, with one member of each pair being contributed by the mother and father, respectively. Each cell contains identical, duplicates of the 46 cells from the fertilized parent cell. Therefore, each cell in the human body has the same DNA. [¶] The structure of DNA consists of two strands, coiled in the form of a double helix (i.e., a twisted ladder). Each strand is composed of a string or a sequence of nucleotide bases held together by a sugar-phosphate backbone. To use the ladder metaphor, running between the sugar-phosphate strands (the side rails of the ladder) are billions of rungs, each of which is

composed of two bases. There are only four possible types of bases—A, T, G, C. ‘A, T, G, C’ represent adenine, thymine, guanine, and cytosine, respectively. The order in which the base pairs appear on the DNA ladder constitutes an individual’s genetic code. [¶] A gene is a particular DNA sequence located along a chromosome, ranging from a few thousand to tens of thousands of base pairs, that produces a specific product in the body. In other words, a gene is a site (a sequence of letters) on the DNA that encodes for a protein. A marker is a site on the DNA that does not code for proteins; the marker is also known as the locus (or location). [] In essence, the specific base sequence on the gene acts as an encoded message to the body to produce certain amino acids, which ultimately combine to form a protein. The function of a given gene is determined by the order of bases in the gene. The position that gene occupies along the DNA thread is known as its locus. [¶] Human beings share more biological similarities than differences. Thus, over 99% of human DNA does not vary from person to person. Each person’s DNA, however, has certain regions where the rungs of the ladder will be different. This area where a locus is different is polymorphic. The possible arrangements of base pairs that could occur in one of these polymorphic areas (i.e., the alternative forms of a gene that an individual could possess) are known as alleles. These alleles can result from differences in single base pairs, differences in multiple base pairs, or differences in the number of base pairs found in a given region. The individual genetic makeup described by the alleles is known as the genotype. In forensic analysis, the genotype for a group of analyzed loci is called the DNA profile. When a sample of DNA is typed, the lab examiner looks at predetermined polymorphic loci, identifies the alleles that make up the DNA sequence at those polymorphic loci, and then determines how likely it is for this sequence to appear in a given population.” (See also Nat. Research Council, *The Evaluation of Forensic DNA Evidence* (1996) pp. 12-14, and glossary, pp. 214-218.)

3. Deoxyribonucleic acid testing

In *Trala*, the district court described deoxyribonucleic acid testing as follows: “[Polymerase chain reaction (PCR) testing] is used to amplify targeted loci of the sample of

DNA by replicating the process by which DNA duplicates itself naturally. Thus, the lab is able to produce a substantial number of specific, targeted segments of DNA which can then be typed and compared. Short Tandem Repeats, or STR's, are a group of loci which are used to type and compare the DNA. Finally, statistics are used to evaluate how likely it is that a similar match would occur if the DNA sample were drawn randomly from the population. . . . [¶] a. PCR Amplification Process [¶] PCR, a sample preparation technique, is a laboratory process for copying a short segment of DNA millions of times. The PCR process is analogous to the process by which cells replicate their DNA naturally. *See United States v. Gaines* [(S.D. Fla. 1997)] 979 F.Supp. [1429,] 1435. By using this process, a lab can produce a substantial number of specific, targeted segments of DNA which can then be typed and compared. PCR allows the laboratory to amplify only those specific DNA regions which exhibit genetic variations within the population, allowing for DNA typing. Moreover, the PCR process enables the analysis of very tiny amounts of DNA. PCR also permits the analysis of old and/or degraded DNA samples. [¶] The PCR process is comprised of three steps. First, the double-stranded segment of DNA is separated, or denatured, into two strands by heating. This denatured DNA strand forms a template that can allow the manufacture of a new strand that is identical to its former complimentary strand. [¶] Next, each of the single-strand segments are hybridized with primers. Primers are short DNA segments that are designed to bind with the template at particular loci. The primers are designed to compliment a sequence just outside of a target sequence of bases. [¶] Finally, each primer serves as a starting point for the replication of the target sequence. In this third step, a type of enzyme called a polymerase becomes active. In essence, the polymerase facilitates repeated additions of bases to the primer until a new, complimentary strand of the targeted DNA locus is created. [¶] This process is repeated a number of times, creating an exponentially increasing number of copies of the targeted area of the original DNA. Eventually, the PCR amplification process yields a sufficient quantity of the DNA sample to be typed. If the laboratory wants to type the DNA sample at multiple sites, it can add additional primers which will bind simultaneously to their respective target sites. This process is known as multiplexing. According to Dr.

[Bruce] Budowle [Senior Scientist at the Federal Bureau of Investigation Laboratory Division], multiplexing allows the laboratory to minimize the chance of human error and contamination in the PCR process. Using current technology, the [Federal Bureau of Investigation] laboratory can multiplex up to fifteen or sixteen markers with reliable results. [¶] b. Short Tandem Repeats [¶] The PCR process is performed to amplify a targeted locus (or loci) for analysis. These loci are selected because they are polymorphic, thus, making them amenable to typing. One group of such loci involve a class of repeated units, distributed widely throughout the DNA structure, known as short tandem repeats ('STR's'). A tandem repeat involves multiple copies of an identical DNA sequence arranged in direct succession in a particular region of a chromosome. A STR is a tandem repeat in which the core repeat units are just a few base pairs. Loci containing STRs are scattered throughout the chromosomes in enormous numbers. Such loci have a fairly large number of alleles and are usually capable of unique identification. See *Commonwealth v. Rosier* [(Mass. 1997)] [] 685 N.E.2d 739, 742 []. [¶] Once the amount of DNA is amplified by the PCR process[,] the analyst proceeds to identify fragments of different sizes by their migration in an electric field. In order to detect variations, analyst[s] use a process known as electrophoresis. During the PCR amplification of the STR fragments, the primers that are used contain fluorescent tags, which become incorporated into the STR fragments during amplification. During electrophoresis, the amplified fragments will pass through a gel and eventually pass through a detection window at the end of the gel. The fragments can be passed through either a flat slab gel or through a small-diameter capillary that contains a gel or liquid polymer. The difference between these two methods is that the flat gel permits multiple samples to be run at the same time, while capillary electrophoresis only permits one sample to be run at a time. The scientific principles underlying both techniques are the same. [¶] After the fragments pass through the detection window at the end of the gel, a laser fires, striking the fluorescent tags, and causing the tags to emit light. A camera will detect the light and convert it into data. By measuring the amount of time that it takes a particular fragment to reach the laser, the laboratory will be able to determine the size of the fragment and, therefore, it will be able to determine the number of sequence repeats. The faster a

fragment moves through the window, the smaller it is in size and vice versa. [¶] The data generated is analyzed by an accompanying computer software program which determines the size of the alleles based on the rate at which they reach the window." (*U. S. v. Trala, supra,* 162 F.Supp.2d at pp. 341-342, fns. omitted; *United States v. Hicks* (9th Cir. 1996) 103 F.3d 837, 844-845; *United States v. Beasley* (8th Cir. 1996) 102 F.3d 1440, 1445-1446; see also Nat. Research Council, *The Evaluation of Forensic DNA Evidence*, *supra,* pp. 21-23.)

The products used to analyze the deoxyribonucleic acid in all four cases for which the *Kelly* hearing was conducted were manufactured by Perkin-Elmer, which is also known as Applied Biosystems. Utilizing the AmpFLSTR Profiler Plus PCR Amplification Kit, the laboratory is able to amplify nine short tandem repeat loci and amelogenin gender loci. (Exhibit 20, pp. 1-1 – 1-5; see also http://www.appliedbiosystems.com/products/productdetail.cfm?prod_id=100.) In addition, the AmpFLSTR COfiler PCR Amplification Kit amplifies: four short tandem repeats loci; the amelogenin locus; and two of the short tandem repeats loci amplified by Profiler Plus. The Combined DNA Index System (CODIS) was developed by the Federal Bureau of Investigation as a national database containing deoxyribonucleic acid profiles of convicted felons. By using the AmpFLSTR Profiler Plus PCR Amplification Kit and the AmpFLSTR COfiler PCR Amplification Kit, information is generated regarding all 13 core short tandem repeats loci established by the CODIS. (Budowle, *STR Allele Concordance Between Different Primer Sets – A Brief Summary*, 3 Profiles in DNA, No. 3, pp. 1-2; *U.S. v. Trala, supra,* 162 F.Supp.2d at pp. 342-343; see also http://www.appliedbiosystems.com/products/productdetail.cfm?prod_id=97.) The Applied Biosystems Prism 310 genetic analyzer utilizes the Genescan and Genotyper software. This software was described by the district court in *Trala* as follows: "The software detects the light being emitted and converts it into peaks of different sizes. The analyst then compares the configuration of these peaks against known reference standards in order to determine the number of alleles present at the target loci in a given sample." (*U.S. v. Trala, supra,* 162 F.Supp.2d at p. 342; see also *People v. Hill* (2001) 89 Cal.App.4th 48, 57-58; Rosenblum,

Improved Single-Strand DNA Sizing Accuracy in Capillary Electrophoresis (1997) 25 Nucleic Acids Research, No. 19, pp. 3928, 3929; http://www.appliedbiosystems.com/products/productdetail.cfm?prod_id=38.) As our colleagues in the Court of Appeal for the First Appellate District held: "Once the PCR analysis is complete, there may or may not be a need to perform a statistical analysis. If the subject of the investigation is not compatible with the blood evidence, statistics or genetic frequency data is irrelevant. If the person has the same traits as the evidentiary specimen, then the question is how common or rare are those traits, i.e., what percentage of the population are potential donors of such a specimen." (*People v. Morganti* (1996) 43 Cal.App.4th 643, 669.) Where the samples of the evidence and the defendant's deoxyribonucleic acid are found to be sufficiently similar to have originated from the same source, the analyst calculates the profile frequency or the probability that an unrelated person chosen at random from the population would have the same deoxyribonucleic acid profile as the unknown sample. The analyst calculates the statistical frequency by multiplying the frequency of each of the alleles in the profile, then corrects the result to account for inbreeding or substructuring effects in the population. (See *U.S. v. Trala, supra,* 162 F.Supp.2d at p. 343; *People v. Brown* (2001) 91 Cal.App.4th 623, 634 [substructures].)

As Judge Fulgoni explained in his written decision following the *Kelly* hearing: "[D]ifficult problems concern two further situations which do not occur in pristine samples. [¶] The first is mixtures of DNA sources. In cases of rape, epithelial cells from the victim and the assailant can be present in a swab. Other persons who have had intercourse with the victim can deposit sperm. And frequently there is an inability to separate a sperm fraction from a nonsperm fraction of the evidenced DNA. [¶] There is also frequently an inability to separate major from minor contributors to a mixed evidentiary sample. [¶] The second difficulty is stutter. This is a phenomenon that occurs unpredictably and can mask small alleles or actually be an allele that occurs in a stutter position."

4. Evidence presented

a. prosecution evidence

Rhonda Roby, the senior forensic specialist for Applied Biosystems, testified as part of the prosecution case. Ms. Roby testified regarding various reports and Applied Biosystems procedures related to AmpFLSTR Profiler Plus and COfiler kits.

Dr. Bruce McCord, associate professor of analytical and forensic chemistry at Ohio University, also testified for the prosecution. In that capacity, Dr. McCord taught classes in deoxyribonucleic acid typing and instrumental analyses. He also did research in the areas of deoxyribonucleic acid analysis. Dr. McCord was previously employed by the Federal Bureau of Investigation, where he taught courses in forensic chromatography and polymerase chain reaction testing using capillary electrophoresis. Dr. McCord published approximately 30 articles. Dr. McCord was also on the editorial boards of the Journals of Electrophoresis and Capillary Electrophoresis. He attended and made presentations at numerous conferences each year related to capillary electrophoresis and human identification.

Dr. McCord conducted tests to check the accuracy of the Applied Biosystems Prism 310 genetic analyzer as compared to those of other manufacturers. Dr. McCord ran approximately 100 to 200 samples that had been initially analyzed by the Applied Biosystems Prism 310 genetic analyzer and compared the results with the Molecular Dynamics prototype system. With one exception, all of the genotypes were exactly the same. The exception was made by the Molecular Dynamics system. Based on his experiments, Dr. McCord concluded that capillary electrophoresis is an effective and efficient technique for use in the genetic typing of polymerase chain reaction amplified deoxyribonucleic acid. Dr. McCord further deduced the results demonstrated the capability of capillary electrophoresis to rapidly and precisely type deoxyribonucleic acid.

Dr. McCord relied in part on an article entitled, "*Validation of STR Typing by Capillary Electrophoresis*." The article was the result of a Federal Bureau of Investigation

validation paper on capillary electrophoresis utilizing the Applied Biosystems Prism 310 genetic analyzer as well as Profiler Plus and COfiler typing kits. The article concluded, "The results support the reliability of 310 for the electrophoresis and detection of DNA samples amplified using Profiler Plus and COfiler and of genescan and genotyper software for sizing and designating alleles." (Moretti, *Validation of STR Typing by Capillary Electrophoresis* (Federal Bureau of Investigation, 1999) pp. 25-26.) Based on his education, professional experience with the Applied Biosystems Prism 310 genetic analyzer, review of peer review literature and papers he had written, attendance at conferences where electrophoresis results were presented, and discussions with other scientists, Dr. McCord believed that capillary electrophoresis and specifically the Applied Biosystems Prism 310 genetic analyzer are accepted in the scientific community for the analysis of short tandem repeats loci used in criminal cases. Dr. McCord believed the Applied Biosystems Prism 310 genetic analyzer provides precise data regarding fragments analyzed in short tandem repeats loci utilizing AmpFLSTR Profiler Plus and COfiler kits. Dr. McCord testified he wrote an article entitled, *The Application of Capillary Electrophoresis in the Analysis of PCR Products Used in Forensic DNA Typing*. In that article, Dr. McCord explained that when analyzing a mixed sample using the Applied Biosystems Prism 310, a competent analyst can determine more precisely which individual is the major contributor and which one is the minor contributor. Dr. McCord also wrote a chapter related to capillary electrophoresis in forensic biology and deoxyribonucleic acid mixture analysis using the Applied Biosystems Prism 310 in a book written by Eric Buel, a lead scientist from the Vermont state crime laboratory. The chapter describes the quality control factors required to ensure accurate measurement of mixed samples.

Dr. Robin Cotton, forensic laboratory director for Cellmark Diagnostics, testified for the prosecution. Dr. Cotton was responsible for the supervision of all forensic case work conducted at Cellmark Diagnostics, including research and validation. Dr. Cotton was a member of the: American Academy of Forensic Sciences; American Society of Human Genetics; and American Society of Crime Laboratory Directors. Dr. Cotton was also a fellow of the American Academy of Forensic Science. Dr. Cotton attended and made

presentations at professional meetings regarding short tandem repeats forensic case work. Cellmark Diagnostics used the Profiler Plus and COfiler to type both unknown evidence samples and reference samples. Cellmark Diagnostics conducted a series of experiments for purposes of validating the use of the Profiler Plus and COfiler systems on the Applied Biosystems Prism 310 genetic analyzer. Based on those experiments, Cellmark Diagnostics established a stutter value per locus per allele percentage. That data is utilized when examining non-optimal samples. Cellmark Diagnostics conducted similar experiments with mixed sample analysis. Its standard operating procedures were derived from the validation studies conducted on Profiler Plus and COfiler and other deoxyribonucleic acid typing systems.

Dr. Cotton believed the Profiler Plus and COfiler systems were generally accepted within the forensic community for the typing of samples such as in the present case. Dr. Cotton's belief was based upon several factors: the number of actual users of these kits in the forensic community for the same purpose utilized in these cases; numerous papers in the general scientific literature regarding the use of short tandem repeats for genetic mapping; the use of the same detection technology by forensic science groups outside the United States; the wide use of Perkin-Elmer instruments because of their versatility and reliability as supported by a large body of scientific peer review literature; and the use of genescan and genotyper was not unique to forensics. Based on validation experiences in the Cellmark Diagnostics lab as well as those of the peer review community, Dr. Cotton believed the use of these kits to evaluate a sample involving a forensic mixture will give reliable results when used correctly by those with appropriate experience.

Dr. Arthur J. Eisenberg, associate professor in the Department of Pathology and Anatomy at the University of North Texas Health Science Center and director of the DNA Identity Laboratory and Gene Link Repository, testified for the prosecution. Dr. Eisenberg taught medical students in the applications of deoxyribonucleic acid based molecular biological technology. Dr. Eisenberg also taught in a graduate program in forensic molecular genetics. As director of the deoxyribonucleic acid laboratory, Dr. Eisenberg was responsible for the operation of the lab, including techniques used, training of technicians,

and assignment of reports on case work samples processed. Dr. Eisenberg also served as chairperson of the DNA Advisory Board. In addition to other systems, Dr. Eisenberg's laboratory utilized two Applied Biosystems Prism 310 fluorescent detection systems as well as Profiler Plus and COfiler kits.

Dr. Eisenberg previously worked at Life Codes Corporation, where his responsibilities included the development of methodologies, reagents, and materials utilized in the various human identification systems. Dr. Eisenberg was also a member of the: American Association of Blood Banks; American Academy of Forensic Science; Working Group on DNA Analysis Methods; and the Association of Forensic Lab Analysts.
Dr. Eisenberg was involved in the writing of the Technical Working Group on DNA Analysis Methods and DNA Advisory Board guidelines. He also presented numerous papers at professional forensic science meetings. Dr. Eisenberg believed the Profiler Plus and COfiler kits had been properly validated for the use in forensic case work in the United States because they had been "scrutinized by literally hundreds of laboratories throughout the world" subject to the standards specified by the DNA Advisory Board. The systems were examined through concordant studies on a wide variety of adjudicated forensic evidence samples, in terms of dilutions and mixtures, and found to have reliable, accurate typing results.

Dr. Eisenberg participated in the audits of crime scene forensic laboratories throughout the country. Dr. Eisenberg was familiar with people's exhibit No. 40, a paper prepared by the Federal Bureau of Investigation, which detailed the validation studies related to commercial kits for short tandem repeats multiplexing, including Profiler Plus and COfiler kits. (Moretti, *Validation of Short Tandem Repeats (STRs) for Forensic Usage: Performance Testing of Fluorescent Multiplex STR Systems and Analysis of Authentic and Simulated Forensic Samples* (Federal Bureau of Investigation 1999).) Dr. Eisenberg agreed with the conclusions that the procedures used in those commercial kits were robust and reliable. Dr. Eisenberg also believed the criteria for evaluating a forensic mixture as set forth in the Federal Bureau of Investigation paper were adequately understood and discussed within the literature and the scientific community. Dr. Eisenberg believed that primer

binding mutation may occur in the analysis of a sample. But Dr. Eisenberg believed primer binding imitation was of no consequence in the interpretation of the results because what affects the known sample will also affect the evidentiary sample. Dr. Eisenberg believed Cellmark Diagnostics was "a very competent, thorough testing laboratory" that "strive[s] to do the best possible job they can and in general produce very good, quality results."

The prosecution's final witness was Dr. Frederick Robert Beiber, associate professor of pathology at Harvard Medical School. Dr. Beiber taught medical and graduate students on subjects related to genetics, pathology, and forensic science. Dr. Beiber was also a medical geneticist at the Brigham and Women's Hospital in Boston. Further, Dr. Beiber was a member of the: DNA Advisory Board; Technical Working Group on DNA Analysis Methods; American Society of Human Genetics, the American Board of American Genetics; American Academy and Forensic Science; and American Prosecutors Research Institute. He also served as a consultant to the Connecticut State Police forensic science laboratory. In addition, Dr. Beiber attended annual forensic meetings and authored publications in peer review journals and books. In the year 2000, Dr. Beiber authored a paper entitled, "Combined Probability of Exclusion Estimates, Their Use in Forensic Analysis of Complex DNA Mixtures."

Dr. Beiber believed: the Profiler Plus and COfiler kits had been widely used in 70 to 80 percent of the crime labs in North America and other parts of the world; the reliability of these kits had been validated by the various labs ; the Profiler Plus and COfiler kits rendered reliable results when used properly and correctly ; and that primer binding site mutations had no effect in any particular individual case because "samples from known individuals and samples from evidentiary exhibits would be typed or profiled using the same reagent . . . or the same kit, using the same primers." As a result, if the deoxyribonucleic acid sample comes from a single individual, it would be the same. Dr. Beiber concluded, "[T]he net effect of the presence of these variations would be negligible on the determination of allele or genotype or profile frequencies, virtually no effect." With respect to mixed forensic samples, Dr. Beiber testified: "[I]n the context of sexual assaults, when intimate samples are taken, mixtures tend to be often the rule rather than the exception . . . [O]nce the

electropherograms are obtained from the various samples and the known individuals, it's often possible to quite clearly identify a so-called major contributor and a so-called minor contributor through the DNA mixture from the evidence." Dr. Beiber further related that the calculation for a mixed sample is essentially the same calculation made in single source samples.

The prosecution also introduced as exhibits: various manuscripts; validation studies; operating procedures utilized by Cellmark Diagnostics; publications; professional manuscripts and presentations attributable to professional scientific conferences; and related court decisions. The substance of some of these exhibits will be discussed later.

b. defense evidence

The defense called Marc Taylor, a forensic scientist and owner of a laboratory known as Technical Associates Incorporated. In the course of his business, Mr. Taylor reviewed forensic casework involving deoxyribonucleic acid evidence. These cases utilized the Applied Biosystems Prism 310 genetic analyzer as well as Profiler Plus and Cofiler kits, and genescan and genotyper programs. Mr. Taylor reviewed the validation studies filed under protective order in this case by Perkin-Elmer (Applied Biosystems). Mr. Taylor testified that the articles did not appear to be a complete validation in the context of the Technical Working Group on DNA Analysis Methods guidelines. Mr. Taylor's comparison of Federal Bureau of Investigation validation studies on Profiler Plus and COfiler with Perkin-Elmer's data demonstrated different percentages of stutter occurrence as well as different peak-height ratios at one locus. Mr. Taylor acknowledged that there were over a hundred validation studies on the loci that are used in the Profiler Plus and COfiler. Mr. Taylor also agreed that much of the data already in the public domain of the scientific community applied to some extent to Profiler Plus and COfiler kits.

Dr. Laurence Mueller, a professor at the University of California at Irvine, testified for the defense. Dr. Mueller did research related to population genetics and evolutionary biology. Dr. Mueller was an editor of a journal entitled "'Researches on Population

Ecology.'" He also studied forensic issues regarding population studies related to deoxyribonucleic acid evidence, lectured on the subject, published papers, and reviewed databases and casework from forensic laboratories. Dr. Mueller explained the "Hardy-Weinberg law" as follows: "[It involves an estimation of] how likely it would be to find a person in the population that has [a] particular combination of copies of [a] gene that you observe in the evidence. . . . If a person has two similar copies of a gene then that individual's called a homozygote, and the frequency of that pattern is given by the Hardy-Weinberg law simply by taking the frequency of that genetic variant or allele and squaring it or multiplying it by itself. [¶] If the individual has two different forms of the particular gene, the individual is called a heterozygote. And the Hardy-Weinberg law states that the frequency of people that will be heterozygote for that particular combination of alleles is given by twice the product of the constituent allele frequency." Dr. Mueller believed that if a particular allele was not properly amplified in the polymerase chain reaction so that only one of the two copies of that individual's gene was amplified, the individual may be a heterozygote but appear to be a homozygote, thereby causing a departure from the Hardy-Weinberg law.

Dr. Mueller's review of the Federal Bureau of Investigation population databases for Caucasian and African-American groups revealed a 13 to 14 percent departure from linkage equilibrium. That signaled a potential problem with the assumption of linkage equilibrium for the Caucasian population that is correctable. There were no significant departures of linkage equilibrium for the African-American population. Also, the 13 to 14 percent departure presented a fundamental problem with a technique based on multiplication across loci. Dr. Mueller also reviewed reports related to the Perkin-Elmer databases for the 13 CODIS loci contained within Profiler Plus and COfiler. Dr. Mueller testified he needed further data regarding the complete multi-locus genotypes for each of the samples used to fully analyze the database utilized by Perkin-Elmer. Dr. Mueller acknowledged that scientists who prepare peer review articles normally present data by providing the allele frequencies rather than the genotype profiles for each person in the database.

Dr. William Shields, a professor at the State University of New York, College of Environmental Science and Forestry, also testified for the defense. Dr. Shields taught and did research in population genetics and behavior of birds and mammals. Dr. Shields performed deoxyribonucleic acid typing in his work. Dr. Shields did not personally perform forensic deoxyribonucleic acid testing but had reviewed the literature on the procedures. Dr. Shields supervised deoxyribonucleic acid testing at the university to determine maternity and paternity in swallows, beavers, and giraffes as well as to examine genetic verification in rare or endangered species. Dr. Shields previously testified on the issue of validation sufficiency as it relates to Profiler Plus and COfiler as related to population genetic issues. Dr. Shields had modified protocols designed by others, but had not designed one himself.

Dr. Shields had never worked with capillary electrophoresis or done any criminal forensic case work. Dr. Shields had studied literature regarding validation studies and testified about the specific kits. Dr. Shields reviewed the Perkin-Elmer documents in people's exhibit Nos. 14 through 17 related to the validation of Profiler Plus and COfiler. Dr. Shields found the manuscripts lacking in data. Dr. Shields believed the validation report, people's exhibit No. 16, was inadequate because the sample sizes were too small to determine the error rate. When comparing the Perkin-Elmer data to that developed by the Federal Bureau of Investigation, Dr. Shields found "hard-to-explain" differences between the two. Dr. Shields testified he would like to see all laboratories have sufficient data to remove as much subjectivity from the testing process as possible.

The defense also called Dr. Donald Riley, Associate Professor of Urology and Pathobiology at the University of Washington. Dr. Riley conducted research related to prostate diseases, including deoxyribonucleic acid testing. The testing was performed to detect bacterial and viral deoxyribonucleic acid sequencing as well as genetic difference in various individuals. Dr. Riley also served as a reviewer of manuscripts submitted by other scientists to determine whether the paper is worthy of publication in a journal. Dr. Riley authored an article describing optimal hybridization temperatures for another type of deoxyribonucleic acid testing. Dr. Riley testified concerning polymerase chain reaction based testing approximately 50 times. Dr. Riley visited crime laboratories, including

Cellmark Diagnostics, where he observed forensic testing. Dr. Riley did not conduct multiplex polymerase chain reaction testing.

Dr. Riley reviewed people's exhibit No. 20, the Profiler Plus polymerase chain reaction amplification kit user's manual. Dr. Riley believed the denaturing temperature at which the COfiler and Profiler Plus operated did not support the user's manual's representation that they were optimized to give reliable performance. However, Dr. Riley acknowledged that other articles supported the user's manual's claims. Dr. Riley did not believe that Perkin-Elmer provided adequate data regarding degraded deoxyribonucleic acid in the user's manual or in the relevant professional literature. Dr. Riley also believed the mixed specimen studies outlined in the user's manual did not indicate that the limitations of the system had been thoroughly reviewed. Nor did Dr. Riley believe the article written by Dr. Clyde Holt, people's exhibit No. 41, gave members of the scientific community adequate data to determine whether the manufacturer's claims were accurate. Dr. Riley was concerned with contamination, degradation and accuracy with the Profiler Plus, COfiler systems and Applied Biosystems Prism 310 genetic analyzer. Dr. Riley believed that the Profiler Plus and COfiler systems and Applied Biosystems Prism 310 genetic analyzer were not generally accepted for testing mixed forensic samples.

Dr. Kenneth Berger, Vice President of regulatory affairs at Lifepoint, Incorporated, testified for the defense. Dr. Berger's work experience involved the development of systems for quality assurance and product validation. At the time of his testimony, Dr. Berger was involved with the validation of saliva-based test kits for use with drugs and alcohol. Most of Dr. Berger's work related to validations by the Food and Drug Administration. Dr. Berger reviewed people's exhibit Nos. 15, 16, and 17 as well as the Perkin-Elmer user's manuals as well as other articles on the subject of short tandem repeats and capillary electrophoresis. Dr. Berger acknowledged that these documents contained the results of some validation studies. However, he did not believe any of those articles were complete validations. Dr. Berger was unaware how Profiler Plus and COfiler were used. Dr. Berger had never run a capillary electrophoresis platform or the Applied Biosystems

Prism 310 genetic analyzer. Judge Fulgoni determined that Dr. Berger was not qualified to testify regarding capillary electrophoresis and limited his testimony to validation.

5. Prior validation and acceptance of mixed sample analysis

We agree with the Attorney General that the use of polymerase chain reaction and short tandem repeats technology to analyze a mixed-source forensic sample is neither a new or novel technique or methodology. As the Attorney General points out, several published rape cases involve mixed source samples that were analyzed by polymerase chain reaction or short tandem repeats. In *People v. Hill, supra,* 89 Cal.App.4th at pages 52-53, the victim was raped and sodomized by an intruder in her home. Vaginal and anal swabs were submitted for deoxyribonucleic acid testing. The forensic lab utilized a DQ-Alpha Polymarker test and a Profiler Plus test. The Profiler Plus test indicated the sperm's deoxyribonucleic acid and the defendant's deoxyribonucleic acid "had a unique genetic profile occurring in only one of 5.89 trillion African-Americans." (*Id.* at p. 53.) The other test found the defendant could not be excluded as a source of the sperm deoxyribonucleic acid. (*Ibid.*) In finding the Profiler Plus test kit did not embrace new scientific techniques, our colleagues in Division Six of this appellate district found: "California courts have recognized that two methodologies are widely used in forensic DNA testing: restriction fragment length polymorphism (RFLP) and PCR. (*People v. Venegas*[, *supra,*] 18 Cal.4th [at pp.] 57-58 & fn. 6 [].) There are three subtypes of PCR testing: DQ-Alpha, which tests a single genetic marker; Polymarker, which tests five genetic markers; and the STR, which tests three or more genetic markers. (*People v. Allen* [(1999)] 72 Cal.App.4th [1093,] 1097.) The RFLP and PCR methodologies, including the PCR subtypes, have acquired general acceptance in the scientific community. (*People v. Venegas, supra,* 18 Cal.4th at p. 79 [RFLP]; *People v. Wright* (1998) 62 Cal.App.4th 31, 34 [] [PCR/Polymarker]; *People v. Morganti, supra,* 43 Cal.App.4th at p. 666 [PCR/DQ-Alpha]; *People v. Allen, supra,* 72 Cal.App.4th at p. 1100 [PCR/STR].)" (*People v. Hill, supra,* 89 Cal.App.4th at p. 57.)

In *People v. Wright, supra,* 62 Cal.App.4th at pages 35-36, the defendant repeatedly raped a young girl and forced her to orally copulate him. Oral and vaginal swabs were submitted for forensic testing. The trial court and our colleagues in the Court of Appeal for the First Appellate District found that the polymerase chain reaction testing method utilized in that case was generally accepted as reliable and valid in the scientific community. (*Id.* at pp. 38-41.) As the *Wright* court pointed out: "'[C]ase-by-case adjudication as to the "general acceptance" prong of the *Kelly* test is *not* required once the scientific technique in question has been endorsed in a published appellate opinion. ([*People v. Barney*] [(1992)] 8 Cal.App.4th [798,] 824-825.)' (*Morganti, supra,* 43 Cal.App.4th at p. 658, italics added.)" (*People v. Wright, supra,* 62 Cal.App.4th at p. 42, fn. 2.)

More recently, in *U.S. v. Trala, supra,* 162 F.Supp.2d at page 349, the defendant, as does defendant here, specifically challenged the reliability of a *mixed* deoxyribonucleic acid sample utilizing the Profiler Plus and COfiler materials kits in combination with Genoscan and Genotyper software. The defendant in *Trala* claimed the systems had allelic drop out, stutter and differential amplification and problems that would "have to 'be explained away through numbers set by laboratories to obtain a profile.'" (*U.S. v. Trala, supra,* 162 F.Supp.2d at p. 349.) After extensive testimony by competent professionals and the introduction of laboratory protocol evidence, the district court, after applying the standards of *Daubert v. Merrell Dow Pharmaceuticals Inc., supra,* 509 U.S. at pages 589-590, held, "In light of the controls to reduce the effects of inherent flaws such as stutter or allelic drop out, the court finds that the defendant's challenges are directed to the weight of the evidence and not its admissibility." (*U.S. v. Trala, supra,* 162 F.Supp.2d at p. 349.)

6. The deoxyribonucleic acid evidence, based upon analysis of mixed samples, was properly found to be generally accepted in the scientific community

In any event, even if the acceptance of such analysis was not previously established, the evidence presented at the *Kelly* hearing in this case supports Judge Fulgoni's finding. The trial court may consider the testimony of professionals in the field, decisions from other

jurisdictions, and relevant scientific literature. (*People v. Brown* (1985) 40 Cal.3d 512, 530; *People v. Axell, supra,* 235 Cal.App.3d at p. 854; *People v. Smith* (1989) 215 Cal.App.3d 19, 25; *People v. Reilly* (1987) 196 Cal.App.3d 1127, 1134.) In *People v. Morganti, supra,* 43 Cal.App.4th at page 665, the court noted: "As our Supreme Court has recently confirmed, *Kelly* does not demand an absolute unanimity of views in the scientific community (*People v. Leahy, supra,* 8 Cal.4th at pp. 611-612.) '"[I]f a fair overview of the literature discloses that scientists significant either in number or expertise publicly oppose [the technique] as unreliable, the court may safely conclude there is no such consensus at the present time."' (*Id.* at p. 611, quoting *People v. Shirley* [(1982)] 31 Cal.3d [18,] 56.)" The general acceptance issue is a mixed question of law and fact. (*People v. Reeves* (2001) 91 Cal.App.4th 14, 38; *People v. Hill, supra,* 89 Cal.App.4th at p. 57.) When the trial court concludes that a new scientific technique is generally accepted in the scientific community, we independently review that decision. (*People v. Venegas, supra,* 18 Cal.4th at pp. 84-85; *People v. Ashmus* (1991) 54 Cal.3d 932, 971.)

Judge Fulgoni noted that while all of the defense witnesses were either qualified scientists or had laboratory experience in related forensic technology or validation of new drugs, none had any "appreciable experience in the application or evaluation of capillary electrophoresis in a forensic setting." Judge Fulgoni also noted, "Even more importantly, the defense witnesses do not regularly attend forensic meetings or have much contact with persons who do." On the other hand, Judge Fulgoni stated, "The People's witnesses in contrast, while lacking a great deal of hands-on experience with forensic samples, regularly attend forensic meetings, are conversant with the forensic community doing capillary electrophoresis, and supervise persons who are technicians in the field." Judge Fulgoni emphasized that validation of a new technique, while critical, is not synonymous with general acceptance within the scientific community. Judge Fulgoni noted, "The hearing[] failed to disclose a single article challenging the general acceptance of the technique in forensics." There were excellent results from concordance studies involving comparison of results of the same testing completed by two distinct laboratories. Judge Fulgoni found that the revelation of a laboratory's error rate was inappropriate: "[E]vidence of the error rate,

the causes of errors, their magnitude and even possible causes of errors not detected are all admissible as separate evidentiary categories, and their significance or lack thereof can be argued vigorously by both sides." With respect to this case specifically, Judge Fulgoni noted there were a number of questionable peaks indicating a possible second sperm donor as well as an exceptionally high stutter and unreported peaks. However, Judge Fulgoni held, as the District Court did in *Trala*: "This is not to say that in *Smith* the original calculations are inadmissible. The rather clear separation in peak sizes of what appears to be a single profile within the mixture renders whatever ambiguities that exist, a matter of weight rather than admissibility . . . ."

Judge Fulgoni found, "While validation of a new technique is critical since any technique which is generally accepted without some form of validation would be accepted irrationally, validation and general acceptance are not synonymous." Judge Fulgoni noted that once the four then sealed manuscripts were released by Applied Biosystems (people's exh. Nos. 14-17) their content was extremely helpful. (Budowle, *STR Allele Concordance Between Different Primer Sets – A Brief Summary*, *supra*; Fregeau, *Fingerprint Enhancement Revisited and the Effects of Blood Enhancement Chemicals on Subsequent Profiler Plus™ Fluorescent Short Tandem Repeat DNA Analysis of Fresh and Aged Bloody Fingerprints*, Journal of Forensic Sciences (2000); Moretti, *Validation of STR Typing by Capillary Electrophoresis, supra*; Budowle, *Concordance Study on Population Database Samples Using the PowerPlex™ 16 Kit and AmpFLSTR® Profiler Plus™ Kit and AmpFLSTR® COfiler™ Kit* (Federal Bureau of Investigation 2000); Moretti, *Validation of Short Tandem Repeats (STRs) for Forensic Usage: Performance Testing of Fluorescent Multiplex STR Systems and Analysis of Authentic and Simulated Forensic Samples*, *supra*; and Holt, *Practical Applications of Genotype Surveys for Forensic STR Testing* (2000) 112 Forensic Science International 91.) Judge Fulgoni held: "The requirement that every possibility, real or imagined, that might beset a technology must be addressed in a published article mischaracterizes the nature of both validation and general scientific acceptance. [¶] A technology can be partially validated by recognition of previously demonstrated principles which are obviously applicable to the new technology." Additionally, Judge

Fulgoni relied on a collection of 33 articles from the Journal of Forensic Sciences. In reaching his conclusion, Judge Fulgoni also relied on forensic community meetings: "Furthermore, the exposure of these techniques to the forensic community at meetings devoted largely to this and related technology serves the twin requirements of validation and acceptance. The former is served by discussions, seminars, posters and lectures on the use of the techniques, their problems and how to compensate for and overcome them. The latter is shown by the number of attendees, their exposure to persons who use capillary electrophoresis and their failure to point out any defects of substantial significance." Judge Fulgoni further relied on concordance studies completed by the Federal Bureau of Investigation and the Los Angeles County Sheriff's Department, where in his view, excellent results were obtained. In his decision, Justice Fulgoni explored the various possibilities for error in the analysis of deoxyribonucleic acid by those systems in question. In each instance, he explained that procedures may be put in place to detect and prevent such errors.

Judge Fulgoni's findings were supported by the testimony and documents presented. Dr. McCord's testimony was premised on his education, professional experience with the Applied Biosystems Prism 310 genetic analyzer, review of peer review literature and papers he had written, attendance at conferences where electrophoresis results were presented, and discussions with other scientists. Dr. McCord believed that capillary electrophoresis in general and specifically the Applied Biosystems Prism 310 genetic analyzer are accepted in the scientific community for the analysis of short tandem repeats loci used in criminal cases. Dr. McCord also believed the Applied Biosystems Prism 310 genetic analyzer provides precise data regarding fragments analyzed in short tandem repeats loci utilizing AmpFLSTR Profiler Plus and COfiler kits. Dr. McCord further testified that, as explained in an article he wrote, *The Application of Capillary Electrophoresis in the Analysis of PCR Products Used in Forensic DNA Typing*, he found that when analyzing a mixed sample using the Applied Biosystems Prism 310, the analyst can determine more precisely which individual is the major and which person is the minor contributor.

Dr. Cotton testified that the Cellmark Diagnostics staff conducted experiments with the Profiler Plus and COfiler systems on the genetic analyzer for purposes of validation with both single and mixed samples. Dr. Cotton reported that Cellmark's operating procedures were based on other validation studies conducted on Profiler Plus, COfiler, and other deoxyribonucleic acid typing systems. Dr. Cotton believed the Profiler Plus and COfiler systems were generally accepted within the forensic community based upon: the number of forensic scientists using the systems for the same purpose utilized in these cases; numerous papers published in scientific literature regarding the use of short tandem repeats for genetic mapping; use of the technology outside the United States; and the support of peer review literature. Dr. Eisenberg believed the Profiler Plus and COfiler kits had been properly validated for use in the scientific community because they had been "scrutinized by literally hundreds of laboratories throughout the world" subject to the standards specified by the DNA Advisory Board. Based on their personal experience, review of the extensive literature, studies, presentations at forensic conferences, and laboratory protocols, Dr. Cotton, Dr. Eisenberg, and Dr. Beiber all believed the use of the kits to evaluate mixed forensic samples would give reliable results when used correctly by those with appropriate experience.

The literature relied on by Judge Fulgoni further supports his findings. In people's exhibit No. 25, the author, Dr. Budowle, of the Federal Bureau of Investigation Scientific Analysis Section, reviewed the short tandem repeats allele concordance between different primer sets, including Profiler Plus and COfiler. Dr. Budowle concluded the Perkin-Elmer kits did not produce significant levels of allele dropout and produced reliable results as long as proper protocols were used. (Budowle, *STR Allele Concordance Between Different Primer Sets – A Brief Summary, supra*, p. 2.) People's exhibit No. 35, an article published in the Journal of Forensic Science in the year 2000, explored the effects of blood enhancement chemicals used for enhancing latent fingerprints from blood on subsequent Profiler Plus deoxyribonucleic acid analysis. The authors concluded none of the chemicals examined had a deleterious effect on the polymerase chain reaction amplification of the nine short tandem repeats systems or the gender marker. (Fregeau, *Fingerprint Enhancement*

Revisited and the Effects of Blood Enhancement Chemicals on Subsequent Profiler Plus™ *Fluorescent Short Tandem Repeat DNA Analysis of Fresh and Aged Bloody Fingerprints, supra*, p. 369.) People's exhibit No. 38, a paper entitled *Validation of STR Typing by Capillary Electrophoresis*, concluded: "In addition to resolving and accurately designating alleles in single-source samples, the analysis of forensic samples may require the identification of components of mixtures of DNA from two or more donors. . . . [T]he analytical parameters used on the [Applied Biosystems]Prism 310 are effective operationally, and comparisons in forensic casework can be reliably made. . . ." (Moretti, *Validation of STR Typing by Capillary Electrophoresis, supra,* p. 19.) These results support the reliability of the Applied Biosystems Prism 310 Genetic Analyzer for the electrophoresis and detection of DNA samples amplified using the AmpFLSTR Profiler Plus and COfiler PCR Amplification kits and of the Genescan and Genotyper software for sizing and designating alleles. (*Id.* at pp. 25-26.) People's exhibit No. 39 was a concordance study on population database samples. Dr. Budowle and Cynthia J. Sprecher, senior scientists at the Federal Bureau of Investigation and Promega Corporation respectively, concluded: "[O]ver 500 samples were typed and allele drop-out was observed rarely using primers from either manufacturer's kit. Although allele drop-out can never be entirely eliminated, the extant data suggest that the primers used in the . . . Profiler Plus™, and COfiler™ kits are reliable for typing reference samples destined for use in CODIS. Furthermore, the data support that the sequences of the primers for STR loci do not need to be known to demonstrate validity." (Budowle, *Concordance Study on Population Database Samples Using the Powerplex*™ *16 Kit and AmpFLSTR® Profiler Plus*™ *Kit and AmpFLSTR® COfiler*™ Kit, *supra*, p. 10.) People's exhibit No. 40 was a validation study on short tandem repeats for forensic usage conducted by the Federal Bureau of Investigation's Forensic Science Research Unit. The study concluded Profiler Plus and COfiler could be used to amplify and type short tandem repeats loci successfully from human biological specimens, including samples that include deoxyribonucleic acid from more than one contributor. (Moretti, *Validation of Short Tandem Repeats (STRs) for Forensic Usage: Performance Testing of Fluorescent Multiplex STR Systems and Analysis of Authentic and Simulated Forensic Samples*, *supra*, pp. 28-29.)

People's exhibit No. 41, an article published in Forensic Science International, concluded that the product rule across the 13 short tandem repeats loci utilized in AmpFLSTR Profiler Plus test kits and the Applied Biosystems Prism 310 Genetic Analyzer is valid for estimation of multilocus genotype frequencies for human identification applications in African-American and Caucasian databases. (Holt, *Practical Applications of Genotype Surveys for Forensic STR Testing*; *supra*; pp. 94, 104-106.) Finally, people's exhibit No. 43, a collection of 33 articles from the Journal of Forensic Sciences (2000), included typing studies by means of short tandem repeats and polymerase chain reaction for world populations as well as the extraction of deoxyribonucleic acid from such diverse sources as stamps, envelope flaps, fingernails, toothbrushes, and fingerprints.

In addition, although Perkin-Elmer validation studies for Profiler Plus and COfiler, introduced at the *Kelly* hearing as people's exhibit Nos. 15-17, were sealed and relied upon by the witnesses subject to a protective order, they were subsequently published. We took judicial notice of these articles as well as two others published subsequent to the hearing, which were filed by the Attorney General and serve to support Judge Fulgoni's finding. (See *People v. Shirley, supra,* 31 Cal.3d at p. 56; *People v. Barney, supra,* 8 Cal.App.4th at p. 810; *People v. Axell, supra,* 235 Cal.App.3d at p. 854.) The three validation studies conclude that the test kits, when used with designated procedures, provide robust, reliable results in mixed deoxyribonucleic acid samples. In an article appearing in the Journal of Forensic Sciences, "*NIST Mixed Stain Studies #1 and #2: Interlaboratory Comparison of DNA Quantification Practice and Short Tandem Repeat Multiplex Performance with Multiple-Source Samples*, two interlaboratory comparison exercises conducted by the National Institute of Standards and Technology concluded: "Given an appropriate total amount of DNA in the reaction mixture, current STR multiplex systems reliably amplify multiple-source DNA." (Duewer, *NIST Mixed Stain Studies #1 and #2: Interlaboratory Comparison of DNA Quantification Practice and Short Tandem Repeat Multiplex Performance With Multiple-Source Samples* (2001) 46 J. Forensic Sci. 1199, 1209.)

Finally, another article in the Journal of Forensic Sciences validated Profiler Plus and COfiler testing as robust and reproducible according to the guidelines provided by The

Working Group on DNA Analysis Methods. The study involved mixed samples. The authors concluded: "The multiplex systems coupled with CE instrumentation, provide sensitive, accurate results even when forensic samples are exposed to extreme conditions. These attributes make the Profiler Plus and COfiler amplification kits powerful, investigative tools for the analysis of forensic samples." (LaFountain, *TWGDAM Validation of the AmpFLSTR Profiler Plus and AmpFLSTR COfiler STR Multiplex Systems Using Capillary Electrophoresis* (2001) 46 J. Forensic Sci. 1197.)

Judge Fulgoni's finding that the mixed sample analysis of deoxyribonucleic acid by means of short tandem repeats utilizing Profiler Plus and COfiler in conjunction with the Applied Biosystems Prism 310 Genetic Analyzer is accepted by the scientific community was well-reasoned, based upon extensive expert testimony, and exhaustive review of the literature and case law. Moreover, any challenges regarding errors in multiple sample deoxyribonucleic acid analysis should be directed to the weight of the evidence and not its admissibility.

B. Harmless Error

We agree with the Attorney General that even if the mixed sample deoxyribonucleic acid evidence was improperly admitted, any resultant error was harmless. It is not reasonably probable that defendant would have had a more favorable verdict absent the error. (*People v. Venegas, supra,* 18 Cal.4th at p. 93; *People v. Watson* (1956) 46 Cal.2d 818, 836.) The victim found defendant sitting in her living room. The victim recognized defendant as a neighbor's son and as an acquaintance of her own children. Defendant remained in the victim's home for over 30 minutes before physically overpowering and raping her for an additional 20 minutes. The victim went to a pay phone as soon after the rape as was possible and telephoned the police. A medical examination revealed forcible trauma to the victim's vaginal area. The victim had not had consensual sex for over a month prior to defendant's rape.

IV. DISPOSITION

The judgment is affirmed.

CERTIFIED FOR PUBLICATION

TURNER, P.J.

We concur:

GRIGNON, J.

ARMSTRONG, J.