

NOT TO BE PUBLISHED IN OFFICIAL REPORTS

California Rules of Court, rule 977(a), prohibits courts and parties from citing or relying on opinions not certified for publication or ordered published, except as specified by rule 977(b). This opinion has not been certified for publication or ordered published for purposes of rule 977.

IN THE COURT OF APPEAL OF THE STATE OF CALIFORNIA

FIRST APPELLATE DISTRICT

DIVISION TWO

THE PEOPLE,

Plaintiff and Respondent,

v.

DAVID SILVA,

Defendant and Appellant.

A102007

(San Francisco County
Super. Ct. No. 180945)

Appellant David Silva was convicted, following a jury trial, of the rape and murder of an 86-year-old woman. On appeal, he contends the trial court erred in (1) failing to hold an evidentiary hearing, pursuant to *People v. Kelly* (1976) 17 Cal.3d 24 (*Kelly*), to determine whether subsequent scientific developments had undermined the general acceptance of deoxyribo-nucleic acid (DNA) typing of the kind used in this case (i.e., polymerase chain reaction (PCR)-based DNA typing involving short tandem repeats (STRs)), and (2) refusing a special defense instruction regarding the jury's consideration of DNA typing evidence and that evidence's relationship to reasonable doubt. We shall affirm the judgment.

PROCEDURAL BACKGROUND

Appellant was charged by information with murder (Pen. Code, § 187—count one),¹ and rape (§ 261, subd. (a)(2)—count two). The information also alleged that both

¹ All further statutory references are to the Penal Code unless otherwise indicated.

counts were committed against a person who was 60 years of age or older (§ 1203.09, subd. (b)(1)), that the murder was committed while appellant was engaged in the commission of rape, a special circumstance (§ 190.2, subd. (a)(17)(c)), and, with respect to the rape, appellant committed great bodily injury on a person who was 70 years of age or older (§ 12022.7, subd. (c)).

Following a trial, the jury found appellant guilty as charged, and found all of the allegations true.

On February 28, 2003, the trial court sentenced appellant to a term of life in prison without the possibility of parole.

Although appellant initially stated that he did not want to appeal, counsel filed a notice of appeal on his behalf on March 13, 2003.

FACTUAL BACKGROUND

General Evidence

In March 1999, Velma S. was 86 years old. She lived alone on Norton Street in San Francisco, where she had resided since the 1960's. She walked with a cane, but otherwise was in good health. On the afternoon of Tuesday, March 9, 1999, after a friend expressed concern about being unable to reach her the previous evening, Velma S.'s niece, Shirley Hack, went to her house and found Velma S.'s body in her bedroom, lying on her back on the bed. There was a pillow over her face, her night dress was pulled up around her upper thighs, and her underwear were on the floor. Her nightstand was at an angle and some things had been knocked over. There was no paper money in her purse, though she usually carried \$20 to \$40, and an empty coin purse that was normally in her purse was on the floor. Also in the bedroom there were broken pieces of a necklace Velma S. always wore. Hack left the room and called 911.

Velma S. had previously told Hack that appellant did odd jobs for her and had introduced Hack to appellant three times in the neighborhood. Hack gave appellant's name to the police the night she found Velma S.'s body. When Hack was later cleaning out her aunt's house, she found four oil paintings in the basement that Velma S. had said she was letting appellant store there.

James Spes, who lived near to Velma S. and knew her for about 30 years, took care of her cat when she was out of town, including a Wednesday to Sunday trip she had taken a few days before her death. Spes knew appellant, whom he had seen in the neighborhood many times in the four or five years before Velma S.'s death, in front of a local church, where appellant panhandled; in a parking lot at the end of Norton; and riding his bicycle around the neighborhood. On the Friday evening before her death, when Spes was leaving Velma S.'s house, appellant approached him and asked if Velma S. was home. When Spes said she was not, appellant urgently asked if he could get into the garage because he needed to get some artwork out, and Spes told appellant he had no access to the garage. Appellant then turned around and walked away without another word.

Michella Griffin, who lived across the street from Velma S., saw appellant around the neighborhood at least every week, usually in a nearby parking lot, where he would ask for money to watch people's cars. She also saw him go to Velma S.'s house once or twice a week; Velma S. would let him into the garage, and sometimes he would take out her garbage can. The night Velma S.'s body was found, Griffin told police they needed to investigate appellant.

Arlyn Dumlao lived three houses down from Velma S. She saw appellant in the parking lot on Norton almost every day and occasionally gave him money. The evening before Velma S.'s body was found, appellant knocked on Dumlao's living room window and asked if she could give him money for a prescription. When she told him she did not have any money, he was persistent and asked her if she was sure.

San Francisco Police Officer William Braconi interviewed neighbors in the area on March 10, 1999, the day after Velma S.'s body was discovered, and, based on information that appellant lived in the area and did work for Velma S., began a search for appellant. Braconi learned that appellant lived nearby, beneath the outside staircase to a home, where there was a small storage room. Braconi arrested appellant on an outstanding drug warrant. On the way to the police station, appellant said he had just

returned from a trip to Reno. When Braconi asked if he was going to go back to Reno, appellant said, “ ‘No. I’m tired now. I’m ready to die.’ ”²

Oral and penile swabs were collected from appellant on the night of March 10, 1999; the penile swab was for trace evidence and the oral swab was for DNA.

Dr. Boyd Stephens, Chief Medical Examiner for the City and County of San Francisco, collected specimens from three areas of Velma S.’s genitalia, each of which revealed the presence of sperm, and also conducted an autopsy on her body. Velma S. had suffered numerous lacerations, abrasions, and contusions in the vaginal area, indicating a “forceful entry” into the vagina. There were many lacerations and abrasions on her face, which was very swollen. A chain link necklace found at the scene could have caused a pattern injury to her neck. Blunt trauma had caused numerous injuries to Velma S.’s body, including her chest, arms, and legs. Internal injuries included a fracture at the base of the skull, five fractured ribs, a fractured hyoid bone in the front of the neck, and a large amount of hemorrhaging in the neck, the base of the brain, and both kidneys. Some of the injuries were consistent with asphyxia. The cause of death was listed as multiple traumatic injuries. The evidence reinforced Dr. Stephens’s opinion that Velma S. “was sexually assaulted near the end of the process of dying.”

Photographs taken of appellant on the night of March 10, 1999 showed abrasions to his chin and neck that were about one to two days old, as well as many small injuries to his shoulder, arm, torso, legs, and buttocks that were all recent.

Shortly before trial, on November 7, 2002, Police Inspector Armand Gordon reviewed the evidence in the case with the district attorney. When he emptied items that had been removed from appellant’s pants pockets at the time of his arrest onto a table, he saw a small, round piece of white metal that had not been noticed previously. On the day Velma S.’s body was discovered, Gordon had seen pieces of a chain link necklace and numerous loose links on her bed and around the bedroom, which were taken from the

² Appellant was 46 years old at the time of his arrest.

home. Gordon did not mix the contents of appellant's pants pockets with the contents of the envelope containing the necklace and links found in Velma S.'s bedroom.³

A criminalist specializing in tool mark analysis compared the link found in appellant's pants pocket with a link found on Velma S.'s bed and concluded they were sufficiently similar that they could have come from the same necklace. Another criminalist found that "the two loops were cut or made by the same kind of tool process, possibly by the same kind of tool or the same tool."

DNA Evidence

Forensic criminalist Alan Keel worked at Forensic Science Associates in Richmond, where he specialized in forensic serology, including DNA analysis. Keel had previously supervised the forensic biology section of the San Francisco Police Department Crime Laboratory.

In March 1999, while still working at the San Francisco Police Department Crime Laboratory, Keel and his staff performed DNA testing on a reference blood sample and the contents of a vaginal wash from Velma S., and an oral swab sample from appellant.⁴ Keel used the PCR method to amplify a series of 16 different genes from the samples tested. Six of the genes were a suite called DQ-Alpha and polymarker; the remaining 10 genes, which included gender, were a suite of STR genes. The lab amplified and tested the genes using two commercial kits containing the reagents necessary to accomplish PCR; one was the DQ-Alpha polymarker kit and one was the Profiler Plus kit.

The vaginal wash specimen contained Velma S.'s epithelial cells and many thousands of sperm cells, which were isolated from nonsperm cells. The specimen

³ A law clerk for defense counsel testified that she reviewed the evidence in appellant's case on October 5, 2000 and did not see the single white metal link when she examined the contents from appellant's pockets.

⁴ The laboratory also examined a penile swab from appellant, and found several hundred sperm, but no epithelial (female) cells; the swab was not subjected to any DNA testing.

contained DNA from only two people. The sperm cells were compatible with originating from appellant and the epithelial cells were compatible with originating from Velma S. Had there been a discrepancy at any of the genes, appellant would have been eliminated as a potential donor. The genetic profile from the sperm cells was unique, meaning that “no more than one person who has ever lived would have that profile.” The cumulative frequency of the profile was one in 12 trillion Caucasians, one in 287 trillion Blacks, and one in 25 trillion Mexican-Americans. It is estimated that approximately eight billion people have lived on the planet during the course of human evolution.

On cross-examination, Keel agreed that it was good practice to examine a reference sample from a suspect or victim and an evidence sample “at a different point in either space or time, or even both.” With respect to the samples in this case, Keel examined appellant’s penile and oral swabs on the same date a colleague examined Velma S.’s vaginal wash specimen. He could not recall whether they examined the samples at the same time or in the same room, but, at the least, they would have worked at separate tables.

Following an audit of the San Francisco Police Department Crime Laboratory in December 1998, a report of the audit noted that, while most problems found were of the “I-dotting variety,” the problems included insufficient space, an inadequate number of personnel for caseload, inadequate documentation of technical and administrative reviews, and an inadequate audit trail for instrumentation and material used in testing.⁵

⁵ The audit report further stated: “The analysts are qualified to perform DNA testing. Their work product and the methodologies, reagents and materials used meet the generally accepted standards of the forensic science community. [¶] Numerous deficiencies were noted, especially in documentation, as would be expected with a new and recently implemented quality assurance and quality control system. Almost all of these were of the I-dotting and T-crossing variety and are simply kinks that remain to be ironed out in the system. Incomplete documentation does not mean that the laboratory’s work product is inadequate but only the laboratory in one or more ways lacks documentation with which to support its work.”

Keel also acknowledged that, in this case, there was an “artifact,” i.e., “something within the typing process that’s not intrinsic to the DNA nor the probe strip,” in the reagent blank for the DQ-Alpha typing strip. The artifact did not contain DNA and did not indicate any kind of contamination. In addition, the DQ-Alpha test showed that appellant is a 2 at the allele (i.e., a base-pair variation in sequence at DNA locations) from one parent, and a 4.2 or 4.3 at the allele from the other parent. The DQ-Alpha test cannot distinguish between a genetic type of 4.2 or 4.3. However, while appellant could be 4.2 or 4.3 on one allele, it nonetheless was not possible that appellant and the sperm source did not have the same DQ-Alpha type, based on all of the other genetic typing tests. Finally, Keel stated there was no evidence of contamination in this case.

Lisa Calandro was the DNA laboratory supervisor in the Forensic Science Division at Forensic Analytical, a private forensic and environmental testing and consulting firm in Hayward. She testified as an expert for the prosecution in forensic DNA analysis.

In February 2001, Calandro’s lab received evidence in the Velma S. case for examination. After Calandro separated the epithelial fraction from the sperm fraction of the vaginal wash, distal vaginal wall, and vaginal vault samples, she found a single-source male profile in the sperm fraction of the vaginal wash and distal vaginal wall samples, a single-source female profile in the nonsperm fraction of both samples, a single-source female profile in the nonsperm fraction of the vaginal vault sample, and a mixture of male and female profiles in the sperm fraction of the vaginal vault sample. When separating epithelial cells from sperm cells in a sample, there sometimes is a carryover of female DNA into the sperm fraction when there are a relatively large number of epithelial cells.

Using a Profiler Plus testing kit, Calandro found the female DNA profile in the samples consistent with Velma S.’s DNA profile. The male DNA profile in all three samples was consistent with appellant’s DNA profile. There was no indication of a

second male donor. Blood stains found on appellant's sweatshirt produced a DNA profile consistent with that of appellant. Appellant's DNA profile is found in approximately one in 10 billion African-Americans, one in 20 billion Caucasians, and one in 14 billion Hispanics. The results obtained were consistent with those obtained by the San Francisco Crime Laboratory for the vaginal wash sample (the only sample that both labs tested).

On cross-examination, Calandro agreed that contamination is a big concern in forensic laboratories, where tiny amounts of DNA are amplified millions to billions of times. It was standard practice at her lab to examine and type evidence samples separately from each other and reference samples. However, she believed it was appropriate to have two analysts working in separate areas of the same room on different evidence samples. Calandro saw no evidence of contamination in this case that affected her results.

Calandro further testified about the process of analyzing DNA and about problems that can occur. With the Profiler Plus system, the DNA is amplified as it travels through a very thin capillary, or sieving medium. The DNA pieces are labeled with a fluorescent dye that registers on a camera as a digital image. The amount of that signal is registered as a peak, which is a way to determine the length of the DNA. The raw data in the test is analyzed by a computer program. The parameters controlled by the analyst include the level of relative fluorescence units (RFU), which indicates the intensity of the signal for any particular piece of DNA.

Calandro's laboratory uses 100 RFU as a "normal detection limit," although analysts will go as low as 50 RFU if it is fairly certain there is a peak. It would be necessary to be somewhat cautious about any interpretations below 100 RFU since, the lower the RFU, the greater the possibility of detecting electronic "noise," rather than a true peak. The lower the RFU number, the higher the amount of data that can be

interpreted. But there is also an increased probability of detecting “artifacts,” i.e., not real DNA.

One artifact, called “stutter,” is a byproduct of amplification of DNA. Stutter might be seen as a repeat or a small peak next to a true peak. A software filtering program is used to avoid labeling stutter as a real peak. Calandro did not believe stutter in any way affected the validity of her results in this case. Calandro thought “it would be fairly unlikely that an experienced analyst would call a peak that wasn’t a true peak a true peak.”

Dr. William Shields, a professor of Biology at State University of New York in Syracuse, who testified for the defense as an expert in the area of DNA in a forensic context, testified about the general use of forensic DNA. Dr. Shields opined that a laboratory that did its validation studies on Profiler Plus at 150 RFUs, and later lowered its RFU values to 100 without doing additional validation studies, would not be following proper scientific procedure. The manufacturer of Profiler Plus recommends an RFU cutoff of 150. The FBI laboratory uses a 200 RFU cutoff for inclusionary evidence, and will go down to 50 RFU for exclusionary evidence. A danger in lowering the RFU cutoff is that it becomes difficult to tell the difference between real peaks and false peaks. Analysis at less than 200 RFUs suggests a degradation of or small amounts of the DNA specimen; the results in such a case would not necessarily be reliable.

The use of STR kits in analyzing DNA has “associated with it lots of good things and a few bad things that can make for difficult interpretations.” These “bad things” include the potential to create artifacts, including stutter, which can make interpretation of the data difficult.

Dr. Shields believed separate evidence should be examined in a laboratory at different times and places to lessen the likelihood of contamination. He also believed that one way to test the reliability of an initial analysis was for a second laboratory to conduct an independent retest of the evidence.

Dr. Laurence Mueller, a professor in the Department of Ecology and Evolutionary Biology at University of California at Irvine, testified for the defense as an expert in the area of population genetics as relevant to forensic DNA typing. Dr. Mueller opined that the forensic databases used by DNA laboratories lacked consistency and reliability because they used “convenience” samples, i.e., DNA samples obtained from blood banks, rather than samples chosen at random from the known population.

Dr. Mueller gave several examples of identification of two individuals who shared the same genetic profiles at up to nine loci. Such examples show that the method of statistical analysis used to identify people, called the “product rule,” cannot be thought of as a system of uniquely identifying people. For example, even with a profile “as rare as one in 10 billion, there can actually be a 33 percent chance that someone else on earth would have that profile.”

Dr. Mueller also stated that the FSA DQ-Alpha database, which the San Francisco Police Department Crime Laboratory used in this case, utilized a statistical test called the “chi-square test,” which he did not believe was a very good test. He further stated that error rates can be calculated for forensic DNA-typing laboratories and opined that the industry-wide rate of false matches for PCR-based testing ranged from one in several hundred to one in several thousand. Dr. Mueller believed a laboratory’s error rate was a more important consideration than the random match probability calculated using the product rule.

Dr. Mueller acknowledged on cross-examination that, in 1996, the National Research Council rejected his approach of estimating a laboratory’s error rate and combining it with the random match probability figures as “ ‘ill-advised.’ ” He also acknowledged the National Research Council recommends using the product rule. In addition, every forensic laboratory of which he was aware used the product rule, and his views constituted a minority opinion.

Dr. Mueller also acknowledged that when two laboratories reach the same result following genetic testing, the chance that both laboratories are in error is lower than the chance would be if only one lab had done the testing. Finally, Dr. Mueller had never heard of a case in which there was a genetic match between two individuals across 15 genetic loci during DNA testing.

DISCUSSION

I. The Trial Court's Refusal to Hold a "Prong One" Kelly Hearing

Appellant contends the trial court erred when it refused to hold a "prong one" hearing, pursuant to *Kelly, supra*, 17 Cal.3d 24, regarding the DNA evidence admitted in this case. According to appellant, he presented a sufficient offer of proof to entitle him to an evidentiary hearing regarding whether there have been recent scientific developments showing that PCR/STR typing of the sort done in this case is no longer generally accepted by the relevant scientific community.

A. Admissibility of Scientific Evidence under Kelly

In *Kelly*, the California Supreme Court held the admissibility of expert testimony based on a new scientific technique requires proof of its reliability. (*Kelly, supra*, 17 Cal.3d at p. 30.) The purpose of the rule is "to protect the jury from techniques which, though 'new,' novel, or 'experimental,' convey a 'misleading aura of certainty.'" (*People v. Stoll* (1989) 49 Cal.3d 1136, 1155-1156, quoting *Kelly*, at pp. 30-32.) The three-prong *Kelly* test requires (1) the reliability of the method be established by showing the technique has gained general acceptance in the particular field to which it belongs; (2) any witness testifying on general acceptance be properly qualified as an expert on the subject; and (3) the proponent of the evidence demonstrate that correct scientific procedures were used in the particular case. (*People v. Venegas* (1998) 18 Cal.4th 47, 78 (*Venegas*); *Kelly, supra*, 17 Cal.3d at p. 30.)

Our Supreme Court recently explained the meaning of "general acceptance" under the first prong of the *Kelly* test: "*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.]’ [Citation.] “General acceptance” under *Kelly* means a consensus drawn from a typical cross-section of the relevant, qualified scientific community.’ [Citation.]” (*People v. Soto* (1999) 21 Cal.4th 512, 519.)

General acceptance need not be established anew in each case. “[O]nce a trial court has admitted evidence based upon a new scientific technique, and that decision is affirmed on appeal by a published appellate decision, the precedent so established may control subsequent trials, at least until new evidence is presented reflecting a change in the attitude of the scientific community.” (*Kelly, supra*, 17 Cal.3d at p. 32; accord, *Venegas, supra*, 18 Cal.4th at p. 76.)⁶ Thus, a defendant is not foreclosed from showing that a scientific test has since been invalidated or that there has been a change in the consensus of the scientific community concerning the test. (*People v. Allen* (1999) 72 Cal.App.4th 1093, 1100-1101; *People v. Smith* (1989) 215 Cal.App.3d 19, 25.)

B. Trial Court Background

Appellant filed a motion to exclude DNA evidence at trial, pursuant to *Kelly, supra*, 17 Cal.3d 24. The trial court held a hearing on the motion, and ultimately rejected appellant’s argument that a “prong one” hearing was required on issues involving interpretation of DNA data, such as allelic dropout, mixtures, and triallelism, as well as statistical calculations regarding the data. The court concluded: “The court is satisfied that STRs are acceptable science in the DNA identification process. There is no authority that I’ve read that leads me to the conclusion otherwise, and these various contentions raised in the articles [submitted by appellant] reflect concerns, but with sample analysis, repeat analysis, and availability of sample analysis by outside laboratories, a lot of the

⁶ With respect to DNA tests, our Supreme Court has held that such tests need not be identical so long as there is no “material scientific distinction between the two methodologies.” (*Venegas, supra*, 18 Cal.4th at p. 54.)

problems that are articulated by these articles can be addressed appropriately” The court ruled that it would hold a “prong three” hearing, but not a prong one hearing.⁷

C. Overview of DNA Analysis and Relevant Court Decisions

“DNA is the genetic material found in the nucleus of virtually all human cells except red blood cells. It is organized into 23 pairs of chromosomes, one chromosome in each pair being inherited from the mother and one from the father. (Nat. Research Council, *The Evaluation of Forensic DNA Evidence* (1996) pp. 60-61 ([1996 NRC Rep.]).) ‘A chromosome is a long DNA molecule in the shape of a spiral staircase. [Citation.] ‘It consists of two parallel spiral sides (i.e., a double helix) composed of repeated sequences of phosphate and sugar. The two sides are connected by a series of rungs, which constitute the steps in the staircase. Each rung consists of a pair of chemical components called bases. There are four types of bases—adenine (A), cytosine (C), guanine (G), and thymine (T). A will pair only with T, and C will pair only with G.’ [Citation.] There are over 3 billion base pairs in the 46 chromosomes of a single human cell.’ [Citation.]” (*People v. Reeves* (2001) 91 Cal.App.4th 14, 25-26 (*Reeves*).)

“Because there is no practical way to sequence all three billion base pairs in a person’s DNA, forensic scientists seek to identify individuals through variations in their base-pair sequences at polymorphic DNA locations (loci). Each variation in sequence is called an ‘allele.’ ” (*Venegas, supra*, 18 Cal.4th at p. 59.)

California courts have recognized two methodologies that are widely used in forensic DNA typing: restriction fragment length polymorphism (RFLP) and polymerase chain reaction (PCR). RFLP analysis, which is also called VNTR (variable number of tandem repeats) analysis, is performed by examining alleles where short sequences of base pairs repeat for varying numbers of times. (*Reeves, supra*, 91 Cal.App.4th at p. 26; 1996 NRC Rep., *supra*, at p. 65.) PCR analysis is a method by which a short segment of DNA is greatly amplified and duplicated. The PCR process has several advantages over

⁷ The court subsequently found that prong three had been satisfied. Appellant does not challenge this finding on appeal.

RFLP. It is relatively simple and easily carried out in the laboratory. Results are obtained in a short time, often within 24 hours. PCR-based methods permit the analysis of extremely small amounts of DNA, which makes it easier to set aside portions of samples for repeat testing. (See 1996 NRC Rep., *supra*, at pp. 21, 23; see also *People v. Morganti* (1996) 43 Cal.App.4th 643, 662 (*Morganti*)). Only PCR methodology is at issue in this case.

“PCR forensic analysis involves three steps. First, DNA is extracted from cells in the sample. Second, select regions of the DNA are amplified. Scientists have identified these regions, also referred to as genes or genetic markers, as areas that exhibit great genetic variation among the population. One widely used marker is the DQ-alpha gene. (1996 NRC Rep., *supra*, at p. 23.) On average, only about 7 percent of the population shares the same DQ-alpha type. (*Ibid.*) Like DQ-alpha, the D1S80 locus is used in PCR testing because it contains several alleles and exhibits great variation. [Fn. omitted.] (*Id.* at p. 72.) Polymarker analysis, which amplifies several loci simultaneously, has also been validated for use in PCR testing. (*Ibid.*) After amplification, in the third and final step of PCR analysis the amplified gene is ‘typed,’ through the use of DNA probes, to identify the specific alleles it contains. (*Morganti, supra*, 43 Cal.App.4th at p. 662.) If the DNA profile[s] thus constructed differ[] in any way between the suspect and the sample, the suspect is excluded. But if the profiles match, the analyst must next determine how common the profile is in the population.” (*Reeves, supra*, 91 Cal.App.4th at pp. 28-29.)

The final step in PCR analysis requires the calculation of “the statistical probability that the DNA profile of a person, selected at random from the relevant population, would contain the same pattern of alleles represented in the evidence sample. (*Venegas, supra*, 18 Cal.App.4th at p. 65.) Databases have . . . been developed to determine population frequencies of the various alleles that may be detected using PCR. 1996 NRC Rep., *supra*, at pp. 117-119.)” (*Reeves, supra*, 91 Cal.App.4th at p. 31.)

Once population frequencies have been determined for each locus, a calculation is made regarding “the probability that a person at random would have the same

combination of matches at all loci. “The most straightforward means of making this calculation is through application of the “product rule.”’ (*Venegas, supra*, 18 Cal.4th at p. 65.) ‘The essence of the product rule is the multiplication of individual band probabilities to arrive at an overall probability statistic expressed as a simple fraction, such as 1 in 100,000.’ (*Id.* at p. 66.) Thus, the product rule is simply the multiplication of frequencies found at each locus studied. The result is a probability statistic that reflects the overall frequency of the complete DNA profile. It is often quite small. (*Ibid.*)” (*Reeves, supra*, 91 Cal.App.4th at p. 31.)

The PCR methodology generally, as well as the tests used in this case—DQ-Alpha polymarker and Profiler Plus—have been generally accepted by the relevant scientific community, as discussed in several appellate opinions. First, in *Morganti*, a panel of this Division held that DNA evidence derived from the PCR method, using the DQ-Alpha test, had achieved general acceptance in the scientific community. (*Morganti, supra*, 43 Cal.App.4th at p. 671.) The Supreme Court denied review in *Morganti*, as well as in *People v. Wright* (1998) 62 Cal.App.4th 31, 42, in which Division Five of this District held that, after *Morganti*, courts no longer need to hold prong one *Kelly* hearings on DNA evidence derived from PCR methodology. Division Three of this District likewise approved the trial court’s refusal to hold a prong one hearing in *Reeves*, where PCR DQ-Alpha, polymarker, and D1S80 tests had been used. (*Reeves, supra*, 91 Cal.App.4th at pp. 25, 31.)

This same conclusion was reached in *People v. Hill* (2001) 89 Cal.App.4th 48 (*Hill*), in which the Second District upheld the trial court’s refusal to hold a prong one hearing on the Profiler Plus test kit. The *Hill* court rejected “the argument that each new PCR/STR test kit must, as a matter of law, be subjected to a *Kelly* prong one analysis to determine scientific reliability.” (*Id.* at p. 58.) The *Hill* court also observed that the FBI, the California Department of Justice, and the majority of forensic laboratories conducting DNA tests use the Profiler Plus kit. (*Id.* at pp. 58-59.)

D. *The Trial Court's Refusal to Hold a Prong One Hearing*

Appellant contends his offer of proof, which consisted of various scientific publications, undermined prior court rulings with regard to the admissibility of the results of PCR/STR typing of the sort used here showed that such testing was no longer considered reliable by the relevant scientific community.⁸

1. *Allelic Dropout and Null Alleles*

Appellant first argues that his offer of proof showed that the PCR/STR testing in question was no longer considered reliable due to the problem of allelic dropout and null alleles.

Prosecution witness Lisa Calandro explained the concept of allelic dropout or null alleles during her testimony at trial: “Allelic dropout refers to an instance where you might have a heterozygote, let’s say someone who’s an 11, 12, and only one of the two alleles is actually amplified. That has been detected with Profiler Plus. [¶] . . . [¶] It’s also a possibility, when you have very low quantities of DNA, that you only detect one type and the other one falls below your detection limit or doesn’t get amplified because there’s so little DNA. [¶] . . . [¶] . . . Another possible cause of allelic dropout might be inhibition where you have a substance that is actually inhibiting the ability of the amplification to take place. There are certain things, like soil and botanical material, that could potentially cause the amplification not to perform optimally. [¶] Again, you can usually determine that that’s going on by looking at the overall data.”

Appellant’s offer of proof contained articles published between 1998 and 2001 that discuss the rare phenomenon of allelic dropout or null alleles. For example, a 2001 article noted that “STRs have become almost the exclusive tool of genetic scientists in

⁸ We observe that appellant’s offer of proof contained only published articles and letters; he proffered no expert testimony to support his contention that the views of the relevant scientific community have changed such that DNA evidence derived from the PCR/STR typing of the type used in this case is no longer generally accepted by that community. We also note that, at trial, neither of appellant’s experts testified that such testing was no longer generally accepted.

forensic typing work. Consequently, large numbers of samples are genotyped and the detection of rare abnormalities is to be expected.” (*Variations in primer sequences are the origin of allele drop-out at loci D13S317 and CD4*, Int. J. Legal Med. (2001), 114:295-297.) Authors of two other 2001 articles recommended caution in the interpretation of results obtained using, inter alia, the Profiler Plus kit. (*VWA STR genotyping: further inconsistencies between Perkin-Elmer and Promega kits*, Int. J. Legal Med. (2001) 115(2):97-9; *Non-amplification of an allele of the D8S1179 locus due to a point mutation*, Int. J. Legal Med. (2001) 115:45-47.) Finally, a 2000 article stated, “It is well known that some polymorphic loci that are used for forensic profiling purposes, on occasions, can be affected by mutations that cause allelic dropout (e.g., 13-16). The AmpFLSTR Profiler Plus system is a classic example of one of the current systems that has taken action to reduce the effects of known mutations that cause primer mismatch through the use of degenerate primers In any case, with STR profiling, the worst implications of these mutations would be a full allelic dropout that results in a false homozygous genotype. Such mutations usually remain undetected and have little effect on the significance of a match, so long as the mutation is inherited throughout the somatic and sex cells of the individual and the same primer set is used on both unknown and reference samples.” (*A Rare Mutation in the Amelogenin Gene and Its Potential Investigative Ramifications*, J. Forensic Sci. (2000) 45(5):1016, 1018-1019.) The article then noted that, when measuring phenotypic traits, such as gender, the discrepancies can have dramatic effects and, therefore, advised verification of gender of specimens from an independent locus, if necessary. (*Id.* at p. 1019.)

None of these articles even suggests a changed attitude in the scientific community toward the PCR/STR methodology. Instead, the articles emphasize the need for caution in interpretation of data pursuant to such testing as well as the persistence of rare problems. They also show that the existence of allelic dropout or null alleles has been recognized for several years, and was well known when two appellate courts reaffirmed the admissibility of STR evidence in *People v. Smith* (2003)107 Cal.App.4th 646, 666-672 (*Smith*) and *People v. Henderson* (2003) 107 Cal.App.4th 769 (*Henderson*).

We further observe that, in *U.S. v. Trala* (D.Del. 2001) 162 F.Supp.2d 336, 349, the district court found that, “[i]n 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.” (Affd., *U.S. v. Trala* (3d Cir. 2004) 386 F.3d 536, 542 [“[T]he district court’s painstaking opinion provides a thorough and compelling analysis of the court’s rejection of Trala’s challenges to the DNA evidence”];⁹ cf. *Henderson, supra*, 107 Cal.App.4th at p. 773 [added complication of analyzing a multiple source DNA sample goes to weight, not admissibility, of evidence]; *Smith, supra*, 107 Cal.App.4th at pp. 671-672 [same].)

Because appellant has not provided any new evidence showing that PCR/STR testing is no longer considered reliable due to the problem of allelic dropout or null alleles, the trial court did not err when it refused to hold a prong one hearing on this issue.

2. *Mixture Studies and Analysis*

Appellant also argues that his offer of proof undermined prior court rulings with respect to mixture analysis. According to appellant, the articles he submitted to the trial court show that mixtures (evidentiary samples that contain DNA from more than one person) cannot be reliably interpreted using the Profiler Plus kit.

However, appellant’s most recent article on this subject is from 2001, and, in 2003, two appellate court opinions found STR analysis of mixtures to be generally accepted. (See *Henderson, supra*, 107 Cal.App.4th at pp. 785-787; *Smith, supra*, 107 Cal.App.4th at pp. 666-672; accord, *U.S. v. Trala, supra*, 162 F.Supp.2d at p. 349 [rejecting defendant’s claim that STR typing of mixed samples was unreliable].)

In *Smith*, the appellate court concluded that the trial court’s “finding that the mixed sample analysis of [DNA] 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

⁹ It is appropriate to consider cases from other jurisdictions in determining general acceptance of a scientific technique. (*Morganti, supra*, 43 Cal.App.4th at p. 663.)

testimony, and exhaustive review of the literature and case law. Moreover, any challenges regarding errors in multiple sample [DNA] analysis should be directed to the weight of the evidence and not its admissibility.” (*Smith, supra*, 107 Cal.App.4th at pp. 671-672; accord, *Henderson, supra*, 107 Cal.App.4th at p. 773 [“We also conclude that the added complication of analyzing a multiple source DNA sample did not affect the admissibility of the evidence, but, instead was a consideration for the jury in weighing the evidence and determining the credibility and accuracy of the DNA test results”].)

Given that appellant’s offer of proof failed to provide new evidence undermining the reliability of mixed-source analysis and that, in 2003, two California appellate opinions found STR analysis, including analysis of mixtures, to be generally accepted, the trial court did not err in refusing to hold a prong one hearing on this issue.

3. *Triallelism*

Appellant further argues that the trial court erred when it refused to hold a prong one hearing regarding the issue of triallelism, which Dr. Shields described as a rare occurrence in which an individual has three alleles at one locus instead of two alleles, which could erroneously indicate there is a mixture.

Appellant submitted one article, from a study conducted in 1999, that briefly addressed triallelism, describing, inter alia, three-branded patterns as a procedural problem that needed to be addressed by some of the laboratories participating in the study on which the article was based. The article further noted that typing of single-donor samples was a non-issue for participating laboratories. (*Results from the 1999 NIST Mixed Stain Study #2: DNA Quantitation, Differential Extraction, and Identification of Unknown Contributors* (2000) Promega Meeting, p. 3.)

This article does not suggest that the rare occurrence of triallelism has led to a change of attitude toward PCR/STR testing in the relevant scientific community. Moreover, the article was published in 2000, and, as previously discussed, two appellate court opinions from 2003 have found STR analysis of mixtures to be generally accepted. (See *Henderson, supra*, 107 Cal.App.4th at pp. 785-787; *Smith, supra*, 107 Cal.App.4th at pp. 666-672; accord, *U.S. v. Trala, supra*, 162 F.Supp.2d at p. 349.) Both cases further

found that concerns involving interpretation of mixtures—which would include triallelism—go to the weight, not the admissibility, of the evidence. (*Henderson, supra*, 107 Cal.App.4th at p. 773; *Smith, supra*, 107 Cal.App.4th at p. 672.)

The trial court did not err in failing to hold a prong one hearing on this issue.

4. *Validation*

Finally, appellant argues that each STR method must be individually validated and that, in this case, the lack of substantial validation by the manufacturer for the type of STR testing conducted in this case required that the San Francisco Police Department Crime Laboratory perform internal validation. Appellant asserts that the Technical Working Group on DNA Analysis Methods (TWGDAM) and the DNA Advisory Board (DAB) have created mandatory guidelines that must be followed by all test developers and laboratories using a particular test. According to appellant, in this case, the San Francisco Police Department Crime Laboratory has not performed sufficient validation to cure the lack of validation studies by the manufacturer.

As the appellate court in *Hill, supra*, 89 Cal.App.4th 48 explained, the guidelines in question are advisory, not mandatory. (*Id.* at p. 59.) “The DAB recommendations, which supersede TWGDAM guidelines, do not require that scientists developing new DNA technologies publish developmental validation studies in peer reviewed scientific journals.” (*Ibid.*)

The *Hill* court also recounted testimony regarding validation studies and Profiler Plus by Lisa Calandro, the lab supervisor at Forensic Analytical, who also testified in this case. Calandro “testified that TWGDAM guidelines are recommended guidelines and that developmental validation ‘may be done by the manufacturer or it may be done in other laboratories outside of the manufacturer. In this case, it was done both by manufacturer and in other laboratories.’ Calandro stated that the Profiler Plus test kit has been extant since 1997 and that the California Department of Justice and the Santa Clara County Crime Laboratory have conducted developmental validation tests on the Profiler Plus test kit. Calandro testified that the majority of DNA laboratories, including the FBI and the California Department of Justice use the Profiler Plus test kit and that the

California DNA database and the national DNA database are ‘being switched over to Profiler Plus’ because ‘PCR-based systems are very discriminating.’ ” (*Hill, supra*, 89 Cal.App.4th at pp. 59-60, fn. omitted.)

As to appellant’s argument that no development validation studies have yet been published with respect to capillary electrophoresis in combination with the GeneScan and Genotyper programs, in *Henderson*, Cellmark Diagnostics had used the Profiler Plus and Cofiler system kits to amplify DNA evidence and then had analyzed the DNA fragments by the process of capillary electrophoresis with the ABI Prism 310 Genetic Analyzer. (*Henderson, supra*, 107 Cal.App.4th at p. 776.) The appellate court concluded: “Our independent review of the trial testimony, including the description of the validation studies performed at Cellmark and the discussion of the sampling of literature available on the subject, leads to the conclusion that capillary electrophoresis has gained general acceptance in the scientific community.” (*Id.* at p. 785.)

The trial court did not err in refusing to hold a prong one hearing regarding lack of validation.

In conclusion, we find that the trial court did not err in refusing to hold a prong one hearing in this case because appellant’s offer of proof did not constitute new evidence that PCR-based DNA typing involving STRs was no longer generally accepted by the relevant scientific community. (See *Kelly, supra*, 17 Cal.3d at p. 32; *Venegas, supra*, 18 Cal.4th at p. 76.)

II. *The Trial Court’s Refusal to Give Special Instructions*

Regarding the Jury’s Consideration of DNA Evidence

A. Trial Court Background

Appellant contends the trial court erred in refusing to give special defense instructions regarding the jury’s consideration of DNA-typing evidence and the relationship between such evidence and reasonable doubt.

Appellant requested two special instructions related to the DNA evidence presented at trial. The first special instruction stated: “To evaluate evidence of a DNA inclusion, you must consider the possibility of a coincidental inclusion between two

different persons who happen to have the same genetic characteristics. To help you evaluate this possibility, you have been given statistical estimates of the frequency of the inclusion characteristics in various populations as well as the error rate for DNA testing.

“You may rely on these statistical estimates to help you evaluate how rare or common the inclusion may be. The statistical estimates do not however, indicate the likelihood that two similar samples are or are not from the same person.

“You must consider all of the evidence in this case, not just DNA evidence.

“The burden is on the government to prove beyond a reasonable doubt that the defendant is the person who committed the crimes with which he is charged.

“If after considering the circumstances of the DNA evidence and any other evidence in the case, you have a reasonable doubt [whether] the defendant was the person who committed the crime, you must give the defendant the benefit of that doubt and find him not guilty.”

The second special instruction stated: “DNA evidence and testimony regarding DNA evidence has been received in this trial for the purpose of identifying the defendant as the perpetrator of the crime charged. In determining the weight to be [given] DNA evidence, you should consider the reliability of the evidence as well as other factors which bear upon the accuracy of the DNA evidence, including but not limited to any of the following:

“The validity and reliability of the test methods used;

“The accuracy and reproducibility of the test results;

“The risk of contamination;

“The extent to which the defendant either fits or does not fit the genetic profile of the evidence;

“The risk of a false positive or false negative result based on the laboratory error;

“Any other evidence relating to the DNA evidence and its ability to link or not link the defendant to the charged crime.”

After a discussion with counsel about these two requested instructions, the trial court refused to give them, explaining: “The specials of defendant now. Special number

one, DNA. I'm inclined not to give the special on DNA, because the jury is told how to evaluate evidence generally, and the rules on how to deal with experts, how to evaluate expert opinion, resolving conflicts amongst experts. They're told about the burden of proof. I mean, this is just an argument. [¶] . . . [¶] I think basically, the jury is told generally how to evaluate expert testimony, and circumstantial evidence and the burden of proof, and that should cover it all."

After further discussion, the court reiterated: "I am not going to give them. The jury is going to be fully instructed on traditional rules. We've had evidence from physical sciences, fingerprint evidence in the past, blood evidence in the past, no specific highlighting of legal principles of how to evaluate that evidence that's been generated in the cases. And I think they become argument, not necessarily otherwise. And I'm not going to give them. [¶] . . . [I]t's a circumstance the jury can consider, and it unnecessarily focuses on one item of reasonable doubt, whereas the standard of reasonable doubt is the government's case, not a particular item of evidence. And the jury has to evaluate all the evidence, and a reasonable doubt is based upon the comparison of all the evidence, not just a particular item."¹⁰

B. *Legal Analysis*

"Upon request, a trial court must give jury instructions 'that "pinpoint[] the theory of the defense," ' but it can refuse instructions that highlight ' "specific evidence as such." ' [Citations.] Because the latter type of instruction 'invite[s] the jury to draw inferences favorable to one of the parties from specified items of evidence,' it is considered 'argumentative' and therefore should not be given. [Citations.]" (*People v. Earp* (1999) 20 Cal.4th 826, 886.) "[T]he effect of certain facts on identified theories 'is

¹⁰ Later, during the hearing on appellant's motion for a new trial, the trial court rejected appellant's analogy of his proposed instructions to pinpoint instructions regarding the factors the jury should consider with respect to eyewitness evidence: "Well, the eyewitness identification instruction that you suggest should have been given, vis-à-vis DNA evidence, there is no other pinpoint instruction that's, I think, in case law, which deals with scientific identifying evidence as opposed to human identifying evidence; is there?" The trial court ultimately denied the new trial motion.

best left to argument by counsel, cross-examination of the witnesses, and expert testimony where appropriate.’ [Citation.]” (*People v. Wharton* (1991) 53 Cal.3d 522, 570.) Moreover, “an instruction incorporating a particular expert’s opinion would deprive the jury of its independence in judging the weight to be given to such expert opinion.” (*People v. Wright* (1988) 45 Cal.3d 1126, 1143.) Finally, the trial court need not give a requested instruction that is duplicative of a standard instruction that is given to the jury, even where the requested instruction expressly states a point only implied in the instructions. (*Id.* at p. 1134.)

In the present case, we conclude the trial court properly refused to give appellant’s two special instructions because those instructions were argumentative in that they, in effect, told the jury to focus on the testimony of appellant’s two expert witnesses regarding the weaknesses of DNA testing and those experts’ opinions regarding possible flaws in the evidence. Such language belonged in the arguments of counsel, not in the jury instructions. (See *People v. Wright, supra*, 45 Cal.3d at p. 1135; see also *People v. Earp, supra*, 20 Cal.4th. at p. 886)

Furthermore, the language of the proposed instructions relating the DNA evidence to the requirement that every element of the offense be proven beyond a reasonable doubt was covered by CALJIC No. 2.90 [regarding prosecution’s burden to prove defendant’s guilt beyond a reasonable doubt], and language regarding the weight to be given the expert testimony presented in this case was covered by CALJIC No. 2.80, which informed the jury, inter alia, that “an opinion by an expert is only as good as the facts and the reasons on which it is based. If you find that any fact has not been proved, or, in fact, has been disproved, you must consider that determination in determining the value of the expert opinion. Likewise, you must consider the strengths and the weaknesses of the reasons upon which the expert opinion is based.” Thus, those portions of the special instructions that may not have been argumentative were duplicative of other instructions. (See *People v. Berryman* (1993) 6 Cal.4th 1048, 1080; see *People v. Wright, supra*, 45 Cal.3d at p. 1134.)

Moreover, even were we to find the court should have given the requested instructions, any such error would be harmless in that it is not reasonably probable that had the jury been given defendant's proposed pinpoint instruction, it would have come to any different conclusion in this case. (*People v. Watson* (1956) 46 Cal.2d 818, 836.)¹¹ That is because the issues raised in these special instructions regarding the reliability of the DNA testing and the result produced were "put before the jury at trial by means of several vehicles," including expert testimony, counsel's arguments, and the instructions the court did give. (*People v. Wright, supra*, 45 Cal.3d at p. 1146; accord, *People v. Earp, supra*, 20 Cal.4th at p. 887.)

As already indicated, the trial court instructed the jury regarding the prosecution's burden of proving guilt beyond a reasonable doubt (CALJIC No. 2.90), and also gave various instructions regarding circumstantial evidence (CALJIC Nos. 2.00, 2.01, 2.02) and expert testimony (CALJIC Nos. 2.80, 2.81, 2.82, 2.83). These instructions fully conveyed the relevant legal and evidentiary standards, and nothing in the instructions precluded the jury from considering the evidentiary concerns raised in the proposed special instructions. (See *People v. Wharton, supra*, 53 Cal.3d at p. 572.)

In addition, appellant's expert witnesses testified at length regarding perceived weaknesses in DNA testing as a means of identifying a suspect, as well as regarding the dangers of contamination and laboratory error. Defense counsel also presented a lengthy argument to support the defense claim that the DNA evidence was contaminated, there was laboratory error, and the laboratories misinterpreted the results.

¹¹ Appellant claims the federal standard for determining prejudice is applicable. (See *Chapman v. California* (1967) 386 U.S. 18, 24.) We disagree. First, appellant does not challenge respondent's statement that appellant did not raise a constitutional claim in the trial court. (See *People v. Rodrigues* (1994) 8 Cal.4th 1060, 1116, fn. 20, 1119-1120, fns. 22, 23, 1126, fn. 30 [constitutional claims waived by failure to raise them in trial court].) Second, appellant does not demonstrate any unique factors in this case that would require us to utilize a different standard than that used by our Supreme Court in assessing error in this context. (See, e.g., *People v. Earp, supra*, 20 Cal.4th at p. 887; *People v. Wharton, supra*, 53 Cal.3d at p. 571; *People v. Wright, supra*, 45 Cal.3d at p. 1144.)

Finally, the evidence as a whole was quite strong. Two laboratories concluded, based on separate testing of two different samples, that appellant was the source of the sperm found in Velma S.'s vagina. Even appellant's experts acknowledged that the likelihood of a mistaken identification based on laboratory error when two laboratories reach the same result is low. This evidence, along with other non-DNA circumstantial evidence, was sufficiently strong to make a different result highly unlikely.

Thus, in light of the court's instructions, the expert testimony presented, the arguments of counsel, and the overall strength of the evidence, any error in refusing to give the two requested instructions was harmless. (See *People v. Wright, supra*, 45 Cal.3d at pp. 1144-1145.)

DISPOSITION

The judgment is affirmed.

Kline, P.J.

We concur:

Haerle, J.

Lambden, J.