Filed 7/14/03 Opinion following rehearing
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IN THE COURT OF APPEAL OF THE STATE OF CALIFORNIA

FIFTH APPELLATE DISTRICT

THE PEOPLE, Plaintiff and Respondent, v. MICHAEL ANTONIO PIZARRO, Defendant and Appellant.	F030754 (Super. Ct. No. 8517) **OPINION**

APPEAL from a judgment of the Superior Court of Madera County. Edward P. Moffat, Judge.

Lynne S. Coffin, State Public Defender, Jeffrey J. Gale and Valerie Hriciga, Deputy State Public Defenders, for Defendant and Appellant.

Bill Lockyer, Attorney General, David Druliner and Robert R. Anderson, Chief Assistant Attorneys General, Robert R. Anderson and Jo Graves, Assistant Attorneys General, Stephen G. Herndon, Paul E. O'Connor, Enid Camps, Deputy Attorneys General, for Plaintiff and Respondent.

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In 1990, defendant and appellant Michael A. Pizarro was convicted of murder, forcible lewd or lascivious act on a child under age 14, and forcible rape. The case, now on appeal for the second time, presents an unusual procedural posture. In the first appeal, Pizarro contended that the DNA (deoxyribonucleic acid) evidence against him was inadmissible because the prosecution had failed to demonstrate that the DNA restriction fragment length polymorphism (RFLP) testing conducted by the FBI was generally accepted in the scientific community. At that time, the admissibility of DNA evidence was still being debated, evaluated, and addressed by the appellate courts. We remanded the case for a thorough evidentiary (*Kelly*[1]) hearing. (*People v. Pizarro* (1992) 10 Cal.App.4th 57 (*Pizarro I*).) At that *Kelly* hearing in 1998, several new issues concerning the reliability and relevance of the DNA evidence presented to the jury were revealed for the first time. The trial court again ruled that the evidence was admissible and reentered the judgment.

After trial, the body of case law on DNA evidence developed further. (See *People v. Axell* (1991) 235 Cal.App.3d 836; *People v. Barney* (1992) 8 Cal.App.4th 798.) And, after the trial court's 1998 *Kelly* ruling in this case, the Supreme Court published *People v. Venegas* (1998) 18 Cal.4th 47 and *People v. Soto* (1999) 21 Cal.4th 512.

It is in this procedural context that defendant brings this second appeal. He contends, again, that the DNA evidence was inadmissible for various reasons.[2] In 2002, after publication of our first opinion, we granted the People's petition for rehearing to ensure that the complex issues in this case were thoroughly examined and briefed by both parties. We now reverse the judgment of conviction.

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1 *People v. Kelly* (1976) 17 Cal.3d 24.

2 For consistency and clarity, we generally refer to Pizarro as "defendant" or "Pizarro," rather than "appellant."

INTRODUCTION

Reduced to its simplest, this is a case of *insufficient evidentiary foundation.* The admission of DNA evidence to prove Pizarro's identity as the perpetrator raises foundational issues under both *Kelly* and the Evidence Code.[3] Under *Kelly* and section 405, the analysis is one of reliability and trustworthiness. Under section 403, it is one of preliminary fact and relevance.[4] The DNA evidence in this case is foundationally inadequate under both analyses. In addition, recurring thematically throughout the issues in this case are evidentiary violations founded on the improper assumption that *defendant was in fact the perpetrator* and that defendant's traits therefore could be relied upon to provide or clarify those traits of the perpetrator forming the basis of the DNA evidence.

This case demonstrates how DNA evidence brings to the fore the distinction between science and law. In the criminal legal setting, theoretical conclusions inherent to scientific discourse have different consequences. What may be an intellectual discussion in the scientific setting becomes the basis for the deprivation of a person's liberty in the legal setting. For this reason, evidentiary rules limit the admission of scientific evidence to what is reliable, trustworthy, and relevant.

I. DNA EVIDENCE

Generally, as in this case, DNA evidence consists of two distinct elements: the *match evidence* -- evidence that the defendant could be the perpetrator -- and the

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[3] All statutory references are to the Evidence Code unless otherwise noted.

[4] These analyses are ultimately interrelated in the sense that both address whether that evidence is relevant. (See *People v. Leahy* (1994) 8 Cal.4th 587, 598 ["reliability and thus the relevance of scientific evidence is determined" by the generally accepted rules of *Kelly*].)

statistical evidence -- evidence that a certain number of people in the population could be the perpetrator.[5] These differ in both purpose and effect.

The purpose of the match evidence is to establish that the defendant's genetic profile resembles or "matches" the perpetrator's genetic profile.[6] The effect of the match evidence is to directly incriminate the defendant by establishing that he genetically matches the perpetrator and therefore *could be the perpetrator*. Using a physical profile as an analogy, the match evidence might be that the defendant, like the perpetrator, has black hair, blue eyes, and 5-foot-8-inch stature. Because the defendant shares the same physical profile and therefore resembles the perpetrator, the defendant could be the perpetrator. Thus, the match evidence deems the defendant a possible perpetrator, but does not establish his identity as the perpetrator.[7]

The statistical evidence gives the match evidence its weight. It is an expression of the rarity of the perpetrator's profile, the size of the pool of possible perpetrators, and the likelihood of a random chance match with the perpetrator's profile. Specifically, the purpose of the statistical evidence is to establish *how few people* in the relevant

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[5] "Perpetrator" specifically identifies the person who committed the criminal act, while "defendant" identifies the person who is accused of committing the criminal act. Because the perpetrator in this case is likely male, we occasionally use the masculine form.

[6] In RFLP cases, the match evidence does not establish that the defendant and the perpetrator do in fact possess the *same* genetic profile because RFLP is not capable of determining definitively that two genetic profiles are truly the same. (See part III.D., *post*.) The most RFLP can determine is that two profiles are *similar enough that they could be the same*. For this reason, it is more accurate to say that the defendant's profile *closely resembles*, rather than matches, the perpetrator's profile. Henceforth, our use of the conventional term "match" in this context implies this meaning.

[7] Using a physical profile as an analogy requires the assumption that physical features, like genetic features, are essentially immutable, such that the perpetrator could not have changed the color of his hair and so on.

population genetically match the perpetrator. The relevant population is the population of possible perpetrators -- the *perpetrator's* population. Thus, the statistical evidence informs the jury of the frequency with which the perpetrator's genetic profile occurs in the perpetrator's population (i.e., the number of people in that population whose profiles are considered to be the same as the perpetrator's profile.)[8] The effect of the statistical evidence is to indirectly incriminate the defendant by allowing the jury to *infer* that because the defendant is one of the few people who genetically match the perpetrator, he is *likely to be the actual perpetrator*. Unlike the match evidence, the statistical evidence itself does not consider or rely upon the defendant; it is a statement regarding the perpetrator (his profile and his population) and it is the same regardless of who the defendant is. Continuing the physical profile analogy, the evidence might be that 1 in 10,000 Hispanics have black hair, blue eyes, and 5-foot-8-inch stature. From this statistical evidence, the jury may infer that because the defendant is one of the few Hispanics who possess these traits, he is likely to be the actual perpetrator.

As we will explain, we consider here questions such as what criteria can be used to identify the perpetrator's characteristics, whether the perpetrator can be assumed to possess a certain trait if there is insufficient evidence that he possesses that trait, and whether the rarity of that trait can then be used to establish the statistical evidence of probability.

II. PRELIMINARY FACT

In Pizarro's case, some of the issues arising from the match evidence and the statistical evidence involve preliminary foundational facts upon which the relevance of the proffered evidence rested. Under section 403, subdivision (a), the proponent of such

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8 The frequency of the perpetrator's genetic profile is also called the random match probability -- the probability that a person randomly selected from the relevant population will have a profile that is considered to match the perpetrator's profile.

evidence has the burden of producing evidence of the preliminary fact sufficient for a trier of fact to reasonably find by a preponderance of the evidence that the fact exists. (§ 403; *People v. Herrera* (2000) 83 Cal.App.4th 46, 61.)[9] Unless the preliminary fact is established, the proffered evidence depending on it is neither relevant nor admissible. (§ 403, § 210 ["'Relevant evidence' means evidence … having any tendency in reason to prove or disprove any disputed fact that is of consequence to the determination of the action"], § 350 [only relevant evidence is admissible]; *People v. Lucas, supra,* 12 Cal.4th at p. 466.).[10]

Here, the relevance of the DNA evidence relied upon the *perpetrator's genetic profile* and the *perpetrator's population* as preliminary facts. First, *the relevance of the match evidence depended on the preliminary fact of the perpetrator's profile*. The match evidence was not relevant to prove defendant's profile resembled the perpetrator's profile unless the match was based on the *perpetrator's profile*. More specifically, defendant's traits were not relevant to prove a match unless the perpetrator's traits were sufficiently

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[9] Section 403 provides in part: "(a) The proponent of the proffered evidence has the burden of producing evidence as to the existence of the preliminary fact, and the proffered evidence is inadmissible unless the court finds that there is evidence sufficient to sustain a finding of the existence of the preliminary fact, when: [¶] (1) The relevance of the proffered evidence depends on the existence of the preliminary fact …." (See, e.g., *People v. Lucas* (1995) 12 Cal.4th 415, 466-468 [evidence that defendant's car was moved and cleaned was not relevant to prove defendant's guilty knowledge unless preliminary fact that defendant was responsible for car's condition was established]; *People v. Collins* (1975) 44 Cal.App.3d 617, 628 [evidence of threatening telephone call made to witness was not relevant unless preliminary fact of caller's identity was established], superseded by statute on another ground as stated in *People v. Cole* (1982) 31 Cal.3d 568, 577-578.)

[10] The decision whether the foundational evidence is sufficiently substantial is a matter within the trial court's discretion, and the court's decision will be overruled on appeal only for an abuse of that discretion. (*People v. Lucas, supra,* 12 Cal.4th at p. 466, citing *Alvarado v. Anderson* (1959) 175 Cal.App.2d 166, 179.)

established. In the physical profile analogy, if evidence that the defendant has black hair, blue eyes, and 5-foot-8-inch stature is offered to prove he looks like the perpetrator, then the preliminary fact that the *perpetrator* has black hair, blue eyes, and 5-foot-8-inch stature must be established. This simple evidentiary requirement echoes the rule of logic stating: all possible perpetrators have black hair, blue eyes, and 5-foot-8-inch stature; the defendant has black hair, blue eyes, and 5-foot-8-inch stature; therefore, the defendant is a possible perpetrator. If the foundation of the perpetrator's profile is not laid, there is an insufficient basis to conclude the defendant possesses the same profile as the perpetrator.

Second, *the relevance of the statistical evidence (the profile frequency) depended on the preliminary facts of the perpetrator's profile and the perpetrator's population*. The profile frequency was not relevant to prove the rarity of the perpetrator's profile in the perpetrator's population unless the frequency was based on the *perpetrator's profile* and the *perpetrator's population*. In the physical profile analogy, if evidence of the number of people in the Hispanic population who have black hair, blue eyes, and 5-foot-8-inch stature is offered to prove the rarity of the perpetrator's profile in the perpetrator's population, then the preliminary facts that the *perpetrator* has black hair, blue eyes, and 5-foot-8-inch stature and that the *perpetrator* is Hispanic must be established. Logically, this evidentiary requirement is stated as follows: all possible perpetrators have black hair, blue eyes, and 5-foot-8-inch stature and are Hispanic; a certain (small) number of people in the Hispanic population have black hair, blue eyes, and 5-foot-8-inch stature; therefore, this profile is rare in the Hispanic population. If the foundation of the perpetrator's profile and the perpetrator's population is not laid, there is an insufficient basis to conclude the perpetrator's profile is rare in the perpetrator's population.

These foundational preliminary facts regarding the perpetrator's traits must be established by independent proof. In other words, the description of the perpetrator -- whether genetic or physical -- must be based on evidence of the *perpetrator's* traits. A sketch artist creates an artistic representation of the perpetrator from an eyewitness's

description of the *perpetrator's* physical features. *Then* the defendant is held up to that sketch to determine whether he possesses the perpetrator's traits. If the defendant happens to match the sketch of the perpetrator, the match provides evidence against him.

If the description of the perpetrator is instead based on evidence of the *defendant's* traits -- which are simply assumed to be the same as the perpetrator's -- the defendant no longer enjoys the presumption of innocence. It is as though the sketch artist sits with the defendant, sketches him as the perpetrator, and the prosecution introduces the sketch at trial as evidence that the defendant looks exactly like the perpetrator. The defendant's traits fill out the perpetrator's description with *facts that are not in evidence*, and the perpetrator's traits are "proved" by what is in effect a *presumption* that because the defendant possesses certain traits, the perpetrator also possesses those traits. Such a presumption operates as a substitute for proper evidence of the perpetrator's traits, thereby lightening the prosecution's burden of affirmatively proving the defendant's identity as the perpetrator and undermining the defendant's presumption of innocence.[11]

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11 "A presumption is an assumption of fact that the law requires to be made from another fact or group of facts found or otherwise established in the action. A presumption is not evidence." (§ 600, subd. (a).)

The test of the constitutional validity of a presumption is that "the device must not undermine the factfinder's responsibility at trial, based on evidence adduced by the State, to find the ultimate facts beyond a reasonable doubt. [Citations.]" (*Ulster County Court v. Allen* (1979) 442 U.S. 140, 156; *Sandstrom v. Montana* (1979) 442 U.S. 510 [instruction that law presumes person intends ordinary consequences of his voluntary acts held to be impermissible mandatory presumption that improperly relieved prosecution of burden of proving all elements beyond reasonable doubt].) A presumption "may affect not only the strength of the 'no reasonable doubt' burden but also the placement of that burden; it tells the trier that he or they *must* find the elemental fact upon proof of the basic fact, at least unless the defendant has come forward with some evidence to rebut the presumed connection between the two facts. [Citations.]" (*Id*. at p. 157.) "[The *Ulster*] court recognized that '[a] mandatory presumption is a far more troublesome evidentiary device' insofar as the reasonable doubt standard is concerned. [Citation.] Because such a presumption tells the trier of fact that it *must* assume the existence of the ultimate,

The logic is this: *the defendant is the perpetrator*; the defendant possesses certain traits; therefore, the perpetrator also possesses those traits. The defendant's guilt is the premise rather than the ultimate conclusion sought by the prosecution.

The prosecution's use of such an implicit presumption establishes for the jury, without presentation of any evidence on the topic, that the perpetrator possesses certain traits. The jurors may be either unwitting recipients or active participants in the implementation of the presumption. If the jury is unaware of the presumption (i.e., if the jury is simply informed that the perpetrator possesses certain traits), then the prosecution both creates the presumption and implements it for the jury. If, instead, the jury is informed of the presumption (i.e., if the jury is informed that the perpetrator possesses

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elemental fact from proof of specific, designated basic facts, it limits the jury's freedom independently to assess all of the prosecution's evidence in order to determine whether the facts of the particular case establish guilt beyond a reasonable doubt. For that reason, the court concluded that a mandatory presumption must be judged 'on its face,' not 'as applied' [citation], and that 'since the prosecution bears the burden of establishing guilt, it may not rest its case on [such] a presumption unless the fact proved is sufficient to support the inference of guilt beyond a reasonable doubt.' [Citation.]" (*People v. Roder* (1983) 33 Cal.3d 491, 498, fn. omitted [statutory presumption that secondhand dealer who received stolen property possessed guilty knowledge that property was stolen held to be impermissible mandatory presumption].) Under California law, the term "mandatory presumption" is redundant. (§ 600, subd. (a); *People v. Henderson* (1980) 109 Cal.App.3d 59, 64, fn. 4.)

The defendant has the right to be presumed innocent until the prosecution proves beyond a reasonable doubt every fact necessary to a finding of guilt (*In re Winship* (1970) 397 U.S. 358, 363-364; Pen. Code, § 1096 ["A defendant in a criminal action is presumed to be innocent until the contrary is proved, and in case of a reasonable doubt whether his or her guilt is satisfactorily shown, he or she is entitled to an acquittal, but the effect of this presumption is only to place upon the state the burden of proving him or her guilty beyond a reasonable doubt"]), including the defendant's identity as the perpetrator (*People v. Law* (1974) 40 Cal.App.3d 69, 85 [a defendant's identity must be established beyond a reasonable doubt]). The presumption of innocence is not a true presumption but a burden of proof on the issue of guilt. (§ 520 [party claiming person is guilty of crime or wrongdoing has burden of proof on that issue].)

certain traits *because* the defendant possesses those traits), the presumption functions as a silent instruction to the jury: "If you find that the defendant possesses certain traits, you must also find that the perpetrator possesses those traits." Implicit is the subtle message that the defendant *is* the perpetrator. This message to the jury even further lightens the prosecution's burden of proving the required facts.

The effect of these evidentiary infractions is severe. For example, since it is presumed that the perpetrator has black hair, blue eyes, and 5-foot-8-inch stature, the jurors willingly infer that because the defendant also possesses those traits, the defendant resembles the perpetrator and probably *is* the perpetrator. This ostensibly logical but entirely circular inference allows the defendant's traits to be used as incriminating evidence without any basis in proof whatsoever. The defendant necessarily possesses those traits -- to his prejudice -- because it is *his* traits that have been added to the perpetrator's description. The jury's conclusion that the defendant resembles the perpetrator is based only on the fact that the defendant possesses *his own traits*. Ironically, the *defendant* becomes the link between the perpetrator and the defendant -- the defendant's own traits establish the perpetrator's traits, and the defendant's inescapable possession of those traits incriminates him.

In this case, the FBI and the prosecution committed this fundamental violation by relying on *defendant's* traits, rather than on independent proof of the perpetrator's traits, to establish the preliminary facts necessary to render the DNA evidence relevant. Specifically, the FBI relied on proof of defendant's genetic profile to establish the preliminary fact of the perpetrator's genetic profile, and the prosecution relied on proof of defendant's ethnicity to establish the preliminary fact of the perpetrator's ethnicity.[12]

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12 As we note, *post*, the prosecution did not look to other evidence or urge other evidence as proof of the preliminary fact of the perpetrator's ethnicity. We do not

This improper reliance on defendant was founded on and legitimized by the underlying assumption that *defendant was in fact the perpetrator* and thus could be substituted for the perpetrator for the purpose of demonstrating relevance and admissibility.[13] In sum, reliance on defendant's traits added unproved traits to the perpetrator's profile and provided an illegitimate foundation for the admission of the DNA evidence.

With this brief background, we summarize the two issues in this case:

(1) A genetic profile is a compilation of several genotypes (here, three).[14] In this case, the evidence established that one of the perpetrator's genotypes (D2S44; hereafter D2) was *not discernible* from a mixed perpetrator/victim DNA sample by the standard method of autoradiograph (autorad) interpretation, and that the two alternative methods to discern the genotype were improper. The first alternative method, reference to *defendant's* genotype, was not permissible to establish the perpetrator's genotype because the perpetrator's genotype should have been determined *independently* of the defendant's genotype. The second alternative method, *band-intensity analysis*, was not permissible to discern the perpetrator's genotype because that method was subject to appropriate *Kelly* scrutiny, which it had not yet undergone. Therefore, the perpetrator's D2 genotype was discerned by an *improper scientific procedure* and the improperly discerned genotype was unreliable and inadmissible under *Kelly* and section 405. Furthermore, the FBI's subsequent use of the improperly discerned D2 genotype to declare defendant a match

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address here the issue of whether other evidence was sufficient to support the determination of the preliminary fact.

[13] We are deeply troubled by the prosecution's and the Attorney General's blurring of the lines between the perpetrator and defendant. The *Kelly* hearing record abounds with such improper references, the prosecution's papers reflect similar missteps, and the People's brief repeats them.

[14] A genotype consists of two alleles at a particular DNA region or locus. An allele is a particular segment of DNA; in the context of RFLP, alleles are identified by their lengths. See part III., *post*.

and to calculate the statistical profile frequency also amounted to *improper procedure.* In simple terms, if the FBI's determination of the perpetrator's D2 genotype was *wrong*, there was potentially no match and conceivably exoneration.

Moreover, the perpetrator's genotype was a *preliminary fact* required for the relevance of both the match evidence and the statistical evidence. Without adequate proof of that preliminary fact, there was insufficient foundation under section 403 to admit the DNA evidence.

The trial court abused its discretion by failing to find the FBI's procedure improper, by implicitly finding sufficient evidence of the preliminary fact of the perpetrator's genotype based on defendant's genotype, and by admitting the DNA evidence, which was irrelevant without that foundation.

(2) The frequency of each allele making up a genetic profile is calculated from a database containing allele frequencies collected from the perpetrator's population. In this case, the allele frequencies were calculated from a Hispanic database. Thus, the statistical evidence presented to the jury was the frequency of the genetic profile in the *Hispanic* population (1 in 250,000 Hispanics). This Hispanic profile frequency was not relevant to prove the rarity of the perpetrator's profile in the perpetrator's population unless there was sufficient evidence to establish *the preliminary fact* that the *perpetrator was Hispanic.* (§ 403.)

Although we do not decide whether there was in fact sufficient evidence to establish that the perpetrator was Hispanic, the record clearly demonstrates that the prosecution relied on *defendant's* ethnicity, rather than the perpetrator's, to establish that preliminary fact. Reference to defendant's ethnicity was not permissible to establish the perpetrator's ethnicity, which should have been determined *independently*.

Due to these foundational errors, the jury received potentially unreliable and irrelevant evidence regarding both the match between the perpetrator's and defendant's genetic profiles and the rarity of the perpetrator's profile in the population.

STATEMENT OF THE CASE

The following statement of the case is taken from our opinion in *Pizarro I*:[15]

"On August 11, 1989, an information was filed alleging [defendant] Michael A. Pizarro had committed the following crimes: count I, murder of [the victim] (Pen. Code, § 187) with the special circumstances that the murder was committed while [defendant] was engaged in the crime of rape (Pen. Code, § 190.2, subd. (a)(17)), and that the murder was committed while [defendant] was engaged in the crime of a lewd or lascivious act upon a child under age 14 (Pen. Code, § 190.2, subd. (a)(17)); count II, forcible lewd or lascivious act on a child under age 14 (Pen. Code, § 288, subd. (b)); and count III, forcible rape (Pen. Code, § 261, subd. (a)(2)).

"On August 17, 1989, [defendant] was arraigned and pleaded not guilty.

"On May 22, 1990, jury selection commenced. On May 31, 1990, during trial, a *Kelly/Frye*[16] hearing was held to determine the admissibility of the results of DNA identification evidence and the trial court ruled the results were admissible.

"On June 6, 1990, the jury returned verdicts finding [defendant] guilty of all counts and also finding the charged special circumstances to be true.

"On July 3, 1990, [defendant] was sentenced to life in prison without the possibility of parole on count I, to be served consecutively to the upper term of eight years on count II. The sentence on the rape count was stayed pursuant to Penal Code section 654.

"On July 6, 1990, [defendant] filed his notice of appeal." (*Pizarro I, supra,* 10 Cal.App.4th at pp. 60-61.)

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15 Footnotes are included and sequentially renumbered.

For consistency and clarity, we generally refer to Pizarro as "defendant" or "Pizarro," rather than "appellant."

16 "*People v. Kelly* [*supra*,] 17 Cal.3d 24 and *Frye v. United States* (D.C. Cir. 1923) 293 F. 1013" (hereafter *Kelly/Frye*).

On appeal, we remanded the case to the trial court for a full-blown evidentiary hearing to determine the general scientific acceptance of the FBI's DNA profiling procedure and the FBI's Hispanic database. (*Pizarro I, supra,* 10 Cal.App.4th at pp. 95-96.) On March 19, 1998, after a hearing conducted in 1994 and 1995, the trial court found the procedure and the database generally accepted and the evidence admissible. Defendant filed a timely notice of appeal. After publishing our opinion, we granted the People's petition for rehearing.

STATEMENT OF FACTS

The following statement of facts is also taken from *Pizarro I*:[17]

> "On June 10, 1989, [defendant], along with his wife, Sandy, and his five-month-old son, drove from Clovis to North Fork, California, to visit his family. They arrived around noon and, soon thereafter, [defendant] went to a schoolyard to play basketball with a friend. Following the basketball game, [defendant] visited the home of his friend and also spent time at Manzanita Lake. [Defendant] then returned to his mother's house and, later that evening (about 8 p.m.), he and his wife went to a party at a mobilehome park in town. [Defendant]'s 13-year-old half sister, [the victim], was also at the party.
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> "[Defendant] had consumed beer throughout the afternoon and he continued to drink at the party. Because Sandy wanted to leave before [defendant] was ready to go, she and [defendant] argued and Sandy left without him -- then returned to try to persuade [defendant] to join her. Eventually, [defendant] began walking toward his mother's house. Sandy followed in their truck and repeatedly asked [defendant] to get inside with her. [Defendant] ignored the requests and behaved erratically, crisscrossing the road, lying in front of the truck and, occasionally, hiding from Sandy. After approximately a half hour, Sandy left [defendant] in the road and drove to the home of her mother-in-law, Chris Conston.
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> "Sandy arrived at the Conston house about 1 a.m. [The victim], who had returned from the party earlier, agreed to accompany Sandy back to the

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[17] Footnotes are included and sequentially renumbered.

area where she had left [defendant]. [The victim]'s mother gave her a flashlight before she left with Sandy and the Pizarros' baby in their truck.

"Thereafter, Sandy and [the victim] saw [defendant] walking towards town but when they approached him, [defendant] ran. When Sandy turned around to follow, [defendant] ran up an embankment and Sandy shined the flashlight on him. [Defendant] then came down from the embankment and, again, began running for town. Sandy stopped the truck and [the victim], who had been holding the baby, put the child down on the seat and got out, taking the flashlight with her. Sandy watched [the victim] cross the street towards the area where [defendant] had gone. Sandy picked up her baby and closed the passenger door. When she looked up, [the victim] was gone.

"Sandy called out for [defendant] and [the victim] but there was no response. She circled her truck around and yelled for them to turn on the flashlight or say something to let her know they were all right. She then saw a flash of light coming from the area where she had last seen [the victim]. She then heard a scream and, immediately following the scream, a slight muffled sound. Frightened, she returned to the Conston house and told her mother-in-law what had happened. It was then almost 2:30 a.m.

"Chris Conston called 911 and Sandy arranged to meet sheriff's deputies at Sierra Automotive which she believed was near the area where [defendant] and [the victim] had last been seen. At 2:51 a.m., within 20 minutes after the 911 call, Madera County Sheriff's Deputy Weisert met Sandy and was directed to the place where Sandy thought [defendant] and [the victim] had gone.[**18**] Another deputy and Chris Conston also went to the area and they drove up and down the road calling for [the victim] over a public address system. There was no response and, soon after 4 a.m., the officers left the area. After waiting for Sandy's parents to come for Sandy, Chris Conston also went home.

"About 5:50 a.m., [defendant] showed up alone at his mother's house. He was dirty, sleepy and appeared to his mother to be drunk. [Defendant] told his mother that, on his way home, a man had confronted

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18 "The following day Sandy realized she had made an error and had actually last seen [the victim] and [defendant] a short distance up the road (under one-tenth of a mile away). It was in that area that [the victim]'s body was found."

him and accused him of kidnapping his sister.[19] Mrs. Conston then left to search for [the victim] at a friend's house and [defendant] went to sleep.

"Shortly after 7 a.m., officers again began searching the area which Sandy Pizarro had pointed out. When they were unable to find [the victim], Deputy Lidfors went to the Conston home at about 8 a.m. to talk to [defendant]. [Defendant] was awakened and he told the officer to look at another location approximately one-tenth of a mile farther west from the area where they had been searching. During this conversation, [defendant] did not appear intoxicated or 'hung over' to the officer.

"Deputy Lidfors, along with Deputy Nelson, went to the area described by [defendant] and there they found [the victim]'s body. [The victim]'s pants had been removed and her underpants were down around her right foot; her T-shirt and bra were pushed up above her breasts. Deputy Lidfors noticed bruises on [the victim]'s face and blood smears on her stomach and leg. Her flashlight was lying by her feet.

"An autopsy was performed and the pathologist, Dr. Gerald Dalgleish, determined that suffocation was the cause of death. He also noted the presence of bruises on the right side of the victim's face as well as swelling and discoloration around her lips and a mark on her nose. [The victim] had been alive when the injuries to her face were inflicted and the pathologist believed that the flashlight could have been the instrument which caused some of the injuries. Semen was present in [the victim]'s vagina.

"On the morning [the victim]'s body was found, [defendant] was taken to the sheriff's substation and interviewed by Sergeant Gauthier. [Defendant] told Gauthier that, after [the victim] had followed him into the brush, he told her he was mad at his wife and did not want to return to the truck. He said he then started to walk up the hill but [the victim] was mad because he had taken her flashlight. He said he was several paces away from her so he turned to toss the flashlight back to her and then left. According to [defendant], that was the last time he had seen [the victim]. At the time of the interview, Sergeant Gauthier examined [defendant]'s hands and found that the knuckles on one of [defendant]'s hands were red

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19 "[Defendant] later told Madera County Sheriff's Detective Kern that the sheriff had stopped him and made the accusation. He told Deputy Weisert that 'some cops' had met him and accused him of kidnapping."

and swollen. Gauthier collected the clothes [defendant] was wearing and arranged to have samples of [defendant]'s blood drawn.

"[Defendant] was also interviewed 10 days later by Madera County District Attorney investigator Fred Flores. [Defendant] told Flores that, after he had thrown the flashlight back to [the victim], he continued running up the hill and passed out about 100 yards later. [Defendant] claimed he did not know what occurred from that point until the time he awoke and walked to his mother's house. When Flores asked [defendant] how he would feel about being arrested, [defendant] told Flores, 'it would be a big mistake because [Flores] did not have enough proof.' [Defendant] did not specifically deny having killed his sister in that conversation. He did deny that he had undressed.[20]

"Forensic tests determined that [the victim]'s blood type was O and she was a nonsecretor. [Defendant]'s blood is type B and he is a secretor. Approximately 8 percent of the population is comprised of type B secretors. The semen which was present in the victim's vagina was from a type B secretor. Additional vaginal swabs and reference blood samples from [defendant] and victim were sent to the Federal Bureau of Investigation's (FBI) laboratory in Washington D.C. for deoxyribonucleic acid (DNA) genetic analysis.

"Dr. Dwight Adams, a special agent assigned to the FBI laboratory, performed DNA analysis on the evidence [in 1989].[21] Dr. Adams concluded the DNA from the semen on the vaginal swabs matched the known blood sample of [defendant]. Using a data base from a Hispanic population, Dr. Adams noted that the likelihood of finding another unrelated Hispanic individual with a similar profile would be approximately 1 in 250,000.[22]

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20 "Foxtails were found in the victim's hair, fist and hairband. Foxtails were also present inside and outside of [defendant]'s shorts and in his underwear."

21 "The qualifications of Dr. Adams and the methods used in conducting the analysis will be discussed, in detail, in the portion of this opinion addressing [defendant]'s contentions regarding DNA analysis admissibility."

22 "In the White population, the likelihood would decrease to 1 in 10,000,000. When a subject is half White and half Hispanic, the FBI would use the more conservative statistic applicable to the Hispanic population (here 1 in 250,000) to favor a defendant."

"Defense

"[Defendant] testified at trial. He said that he had consumed beer throughout the afternoon and evening and, by the time he arrived at the party at the mobilehome park, he was fairly intoxicated. While there, he continued to drink beer and mixed drinks. He testified that he remembered his argument with Sandy and leaving the party with the intention of walking to his mother's house. He also recalled crisscrossing the road and lying down in front of the truck.

"When Sandy returned with [the victim], he attempted to hide and ran into the brush. He testified that [the victim] followed him but he told her that he and Sandy were having problems and that she should go home. According to [defendant], he took [the victim]'s flashlight and started walking away. He said that when [the victim] asked for the light, he turned and tossed it to her.

"Throughout his testimony, [defendant] maintained he remembered nothing from the time he threw the flashlight until he woke up in the brush. [Defendant] said that, when he awoke, he did not walk back to North Fork along the dirt road but instead cut through an area of brush and trees. [Defendant] claimed to have met a man in tan pants and a white shirt who he assumed was a law enforcement officer and who accused him of kidnapping his sister. He also said that he saw a full-size pickup on the road when it was fairly light out.[23]

"[Defendant] testified that the injury to his hand had occurred at work. [Defendant] denied telling investigating officers that he had not removed his underwear or clothes, and claimed that he had actually told them he did not 'believe' he had undressed. He also said investigator Flores had mischaracterized his response to the question of how he would feel about being arrested. Rather than stating to Flores that it would be a mistake because there 'wasn't enough proof,' [defendant] testified that he told Flores that Flores would be making a mistake 'because [he] didn't kill [the victim].'

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23 "[Defendant] said that Detective Gauthier was mistaken in reporting that [defendant] had previously stated that he saw the truck after he had run into the brush away from [the victim]."

"[Defendant] also testified that he had, in the past, suffered blackouts and loss of consciousness after drinking excessively and that such episodes began to occur more frequently after he suffered a head injury in 1985. He also admitted that he told an investigator that alcohol made him violent.

"[Defendant]'s mother also testified for the defense. She said [defendant] and [the victim] had been close. Although [defendant] had scratches on him when he appeared at her home in the morning, the scratches did not appear to her to have been made by a person; she assumed he had been scratched by bushes. Mrs. Conston recalled that, when [defendant] learned his sister was dead, he put his head in her lap and cried.

"Guy Clements was the final defense witness at trial. Mr. Clements was working as a newspaper delivery person on June 11, 1989. He testified that he was driving near the area where [the victim]'s body was found, about 1:30 a.m., when he saw a red Datsun pickup stopped in the middle of the road. It appeared to him that there was a man inside the truck.[24]" (*Pizarro I, supra,* 10 Cal.App.4th at pp. 61-66.)

DISCUSSION

Defendant contends proper scientific methods were not followed in this particular case. He raises his contentions under the third prong of *Kelly*, in which the Supreme Court articulated this three-step test for the admission of evidence generated by a new scientific procedure:[25] (1) the reliability of the procedure must be sufficiently established to have gained general acceptance in the relevant scientific community; (2) the witness providing the evidence must be properly qualified as an expert; and (3) the evidence must

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[24] "On the morning that the crime was discovered, a year before trial, Mr. Clements reported that he had seen a yellow gold, newer model Nissan truck with a young White male inside."

[25] We consider the terms "procedure," "technique," and "methodology" interchangeable in this context.

establish that, in the particular case, the correct and accepted scientific procedure was actually followed. (*People v. Kelly, supra,* 17 Cal.3d at p. 30.)[26]

Specifically, defendant argues that proper scientific procedures were not followed in this case because (1) all possible genotypes in a mixed sample were improperly unaccounted for; (2) evidence of the Hispanic profile frequency was improperly admitted without sufficient evidence that the perpetrator was Hispanic; (3) the statistical window was too small; (4) the statistical window was improperly centered on the average of the perpetrator's and defendant's allele measurements; (5) the H2 Hispanic database was defective; (6) evidence of the possibility of laboratory error should have been presented in addition to the profile frequency; and (7) evidence of a confidence interval should have been presented in addition to the profile frequency.[27] Defendant also argues that, in the event we find the evidence admissible, he should receive a new trial so his evidentiary challenges can be heard by the jury that determines his guilt, and, lastly, that his counsel was ineffective for failing to properly contest the DNA evidence.

I. *KELLY*

In *Kelly*, the Supreme Court spoke to the dangers of scientific evidence and its power to mystify and impress a jury. The court formulated a test composed of three prongs, the first and third of which specifically address the scientific procedures used to generate the scientific evidence against the defendant. The first prong requires that the

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[26] Although the federal *Frye* analysis has been superceded by the Federal Rules of Evidence (28 U.S.C.), as held in *Daubert v. Merrell Dow Pharmaceuticals, Inc.* (1993) 509 U.S. 579, the California Supreme Court reaffirmed the *Kelly-Frye* test in this state (*People v. Leahy, supra,* 8 Cal.4th at p. 611). The foundational requirement is now referred to as the *Kelly* test. (*Id.* at p. 612; *People v. Soto, supra,* 21 Cal.4th at p. 515, fn. 3.)

[27] In light of our conclusions on the first two issues, we need not address appellant's remaining arguments.

scientific procedures be *reliable*, as shown by their general acceptance by scientists in the relevant field. The third prong requires that the reliable, generally accepted procedures were *actually followed* or *complied with* in the particular case before the court. (*People v. Kelly, supra*, 17 Cal.3d at p. 30.) The party offering the evidence has the burden of proving its admissibility by a preponderance of the evidence. (*People v. Ashmus* (1991) 54 Cal.3d 932, 970.)

The *Kelly* test is an evidence-screening device that targets highly sophisticated scientific evidence that to the average juror would be not only incomprehensible in process but also irresistibly convincing in result. The test requires that such evidence pass the court's scrutiny before it is submitted to the jury -- it "is intended to forestall the jury's uncritical acceptance of scientific evidence or technology that is so foreign to everyday experience as to be unusually difficult for laypersons to evaluate. [Citation.] In most other instances, the jurors are permitted to rely on their own common sense and good judgment in evaluating the weight of the evidence presented to them. [Citations.] [¶] DNA evidence is different." (*People v. Venegas, supra,* 18 Cal.4th at p. 80.) "Lay jurors tend to give considerable weight to 'scientific' evidence when presented by 'experts' with impressive credentials." (*People v. Kelly, supra,* 17 Cal.3d at p. 31.) "'[S]cientific proof may in some instances assume a posture of mystic infallibility in the eyes of a jury ....' [Citation.]" (*Id.* at p. 32.) "Unlike fingerprint, shoe track, bite mark, or ballistic comparisons, which jurors essentially can see for themselves," questions concerning sophisticated scientific concepts, procedures, and laboratory compliance require educated expert testimony. (*People v. Venegas, supra,* 18 Cal.4th at p. 81.)

"'It is our duty … , where the life or liberty of a defendant is at stake, to be particularly careful that there is not only substantial evidence to support the implied finding of [defendant's] identity but that the finding is based upon admissible and nonprejudicial evidence.'" (*People v. Kelly, supra,* 17 Cal.3d. at p. 36.) Because of the

immense power of scientific evidence, the *Kelly* test goes to the admissibility, not the weight, of the evidence. (*Id.* at pp. 30-32.)

A. KELLY'S FIRST PRONG

In the *Kelly* review process, the trial judge serves as gatekeeper, allowing only evidence that is sufficiently reliable and trustworthy to reach the jurors. In performing this function in the context of scientific evidence, the judge must rely on the educated testimony of scientific experts. Thus, the first prong of the *Kelly* test -- the general acceptance of the procedure by the relevant scientific community -- is intended to confirm the reliability of a procedure too sophisticated or technical for the average lay person to readily understand. (See *People v. Kelly, supra,* 17 Cal.3d at pp. 30-32; *Frye v. United States*, *supra*, 293 F. 1013.)[28] The first prong "assures that *those most qualified to assess the general validity of a scientific method will have the determinative voice*."

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28 A determination under *Kelly*'s first prong is a determination under section 405, requiring the court to make a final determination regarding the existence of the preliminary fact that the scientific procedure has been generally accepted by the scientific community and thus the scientific evidence is reliable and trustworthy. It is not a question under section 403 of whether there is evidence sufficient to permit a jury to decide the question. (See *People v. Herrera, supra,* 83 Cal.App.4th at p. 63; see also § 405 Com. of Assem. Com. on Judiciary (West 1995 ed.) ["Section 405 deals with evidentiary rules designed to withhold evidence from the jury because it is too unreliable to be evaluated properly …."]; see generally Mendez, Expert Testimony and the Opinion Rule: Conforming the Evidence Code to the Federal Rules (2003) 37 U.S.F.L.Rev. 411, 426 (hereafter Mendez) ["Since *Kelly* is designed to withhold expert testimony that is too unreliable to be evaluated properly, the question whether the underlying scientific principle or technique has been generally accepted by the relevant scientific community should be governed by section 405 of the California Evidence Code. Under section 405, the judge should exclude the expert testimony unless the proponent convinces the judge by a preponderance of the evidence that the principle or technique in question meets the *Kelly* standards of acceptance. If after the hearing it is unclear to the judge whether the required scientific consensus has developed, the judge should exclude the expert evidence." (Fns. omitted.)].) As we explain, the Supreme Court has held that appellate courts review the trial court's first-prong *Kelly* determinations independently. (*People v. Venegas, supra,* 18 Cal.4th at p. 85.)

(*People v. Kelly, supra,* 17 Cal.3d at p. 31.) It is "intended to interpose a substantial obstacle to the unrestrained admission of evidence based upon new scientific principles…. [A] '... misleading aura of certainty … often envelops a new scientific process, obscuring its currently experimental nature.' [Citations.] … [¶] Exercise of restraint is especially warranted when the identification technique is offered to identify the perpetrator of a crime. "'When identification is chiefly founded upon an opinion which is derived from utilization of an unproven process or technique, the court must be particularly careful to scrutinize the general acceptance of the technique."' [Citation.]" (*Id.* at pp. 31-32.)

The question of general scientific acceptance may be answered by prior case law: "once 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." (*People v. Kelly, supra,* 17 Cal.3d. at p. 32; *People v. Venegas, supra,* 18 Cal.4th at p. 54 [trial court could properly rely on a published appellate decision as establishing general scientific acceptance].) However, the published decision does not serve as precedent when there is proof of a "material scientific distinction" between the methodology approved by the published case and that used in the case before the court; materially distinct procedures must pass first-prong scrutiny independently. (*People v. Venegas, supra,* 18 Cal.4th at p. 54.)

B. KELLY'S THIRD PRONG

The third *Kelly* prong is a case-specific inquiry that asks: were the proper scientific procedures (those that have been deemed generally accepted under the first prong) *followed in this case*? (*People v. Venegas, supra,* 18 Cal.4th at p. 78.) Or, here, did the FBI scientists follow correct scientific procedures when they performed the DNA testing in Pizarro's case?

The *Venegas* court comprehensively explained *Kelly*'s third prong:

"The *Kelly* test's third prong … assumes the methodology and technique in question has already met [the general acceptance] requirement. Instead, it inquires into the matter of whether *the procedures actually utilized in the case* were in compliance with that methodology and technique, as generally accepted by the scientific community. [Citation.] The third-prong inquiry is thus case specific; 'it cannot be satisfied by relying on a published appellate decision.' [Citation.]

"... 'Due to the complexity of the DNA multisystem identification tests and the powerful impact that this evidence may have on a jury, satisfying *Frye* [i.e., satisfying *Kelly's* first prong] alone is insufficient to place this type of evidence before a jury without a preliminary critical examination of the actual testing procedures performed....' [Citation.] [¶] … [¶]

"[Q]uestions concerning whether a laboratory has adopted correct, scientifically accepted procedures for [DNA testing] or determining a [profile] match depend almost entirely on the technical interpretations of experts. [Citations.] Consideration and affirmative resolution of those questions constitutes a prerequisite to admissibilit*y* under the third prong of *Kelly*.

"The *Kelly* test's third prong does not, of course, cover all derelictions in following the prescribed scientific procedures. Shortcomings such as mislabeling, mixing the wrong ingredients, or failing to follow routine precautions against contamination may well be amenable to evaluation by jurors without the assistance of expert testimony. Such readily apparent missteps involve 'the degree of professionalism' with which otherwise scientifically accepted methodologies are applied in a given case, and so amount only to '[c]areless testing affect[ing] the weight of the evidence and not its admissibility' [citation].

"The *Kelly* third-prong inquiry involves further scrutiny of a methodology or technique that has already passed muster under the central first prong of the *Kelly* test, in that general acceptance of its validity by the relevant scientific community has been established. The issue of the inquiry is whether the procedures utilized in the case at hand complied with that technique. Proof of that compliance does not necessitate expert testimony anew from a member of the relevant scientific community directed at evaluating the technique's validity or acceptance in that community. It does, however, require that the testifying expert understand the technique and its underlying theory, and be thoroughly familiar with the

procedures that were in fact used in the case at bar to implement the technique. [Citations.]" (*People v. Venegas, supra,* 18 Cal.4th at pp. 78-81.)[29]

"The third-prong hearing 'will not approach the "complexity of a full-blown" *Kelly* hearing. [Citation.] "All that is necessary in the limited third-prong hearing is a foundational showing that correct scientific procedures were used." [Citation.]' [Citation.] Where the prosecution shows that the correct procedures were followed, criticisms of the techniques go to the weight of the evidence, not its admissibility. [Citations.]" (*People v. Brown* (2001) 91 Cal.App.4th 623, 647.) Similarly, where there is substantial evidence showing both that the procedures were followed and that they were not followed, the question is one for the jury to resolve. (*People v. Venegas, supra,* 18 Cal.4th at p. 91.) But where defense evidence establishes a failure in procedure, and that failure is not contradicted by substantial evidence, then the scientific evidence produced as a result of that incorrect procedure is inadmissible. (See *id.* at pp. 91-92.)

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29 A determination under *Kelly*'s third prong is also a determination under section 405, requiring the court to make a final determination regarding the existence of the preliminary fact that proper scientific procedures have been followed and thus the scientific evidence is reliable and trustworthy. Again, it is not a question under section 403 of whether there is evidence sufficient to permit a jury to decide the question. (See *People v. Herrera, supra,* 83 Cal.App.4th at p. 63; see generally Mendez, *supra*, 37 U.S.F.L.Rev. at p. 426 ["Moreover, the question whether specific protocols or methodologies have been followed also should be governed by section 405. The failure to follow correct procedures in applying the novel principle or technique involved could give rise to opinions that are as unreliable as opinions based on principles and techniques rejected by the relevant scientific community. Accordingly, the failure to follow the appropriate procedures should result in the exclusion of the expert opinion even if the proponent has demonstrated general acceptance by the pertinent scientific community of the scientific principles or techniques underlying the opinion." (Fns. omitted.)].) The Supreme Court has held that appellate courts review the trial court's third-prong determinations for abuse of discretion. (*People v. Venegas, supra,* 18 Cal.4th at p. 91.)

C. STANDARDS OF REVIEW

1. First Prong: De Novo

When the trial court relies on a published appellate decision finding general scientific acceptance of a scientific procedure, the appellate court upholds the trial court's ruling unless there is proof of a material scientific distinction between the accepted procedure and that used in the particular case. (*People v. Venegas, supra,* 18 Cal.4th at pp. 53-54.) But when the trial court independently concludes that a new scientific technique has been generally accepted, the appellate court independently reviews that conclusion. (*Id.* at p. 85.) "The preliminary showing of general acceptance of the new technique in the relevant scientific community is a mixed question of law and fact. [Citations.]" (*People v. Axell, supra,* 235 Cal.App.3d at p. 854.) "[I]n reviewing the scientific acceptance of [a methodology] de novo under *Kelly*, we are not required to decide whether such methodology is 'reliable as a matter of "scientific fact," but simply whether it is generally accepted as reliable by the relevant scientific community.' [Citation.] '"General acceptance" under *Kelly* means a consensus drawn from a typical cross-section of the relevant, qualified scientific community.' [Citation.] The *Kelly* test does not demand 'absolute unanimity of views in the scientific community .... Rather, the test is met if use of the technique is supported by a clear majority of the members of that community.' [Citation.]" (*People v. Venegas, supra,* 18 Cal.4th at p. 85.) Conversely, the test fails if "'"scientists significant either in number or expertise publicly oppose [a technique] as unreliable."' [Citations.]" (*People v. Axell, supra,* 235 Cal.App.3d at p. 854.) "In determining the question of general acceptance, courts '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 ....' [Citation.]" (*People v. Venegas, supra,* 18 Cal.4th at p. 85.)

"Because the technical complexity of many new scientific procedures may prevent lay judges from determining the existence, degree, or nature of a scientific consensus without the testimony and interpretation of qualified experts in the field, *Kelly/Frye* properly emphasizes the record made at trial. [Citation.]" (*People v. Axell, supra,* 235 Cal.App.3d at p. 854.) In addition to reviewing the trial court record, the appellate court may also independently survey the scientific literature and case law to determine whether acceptance of the procedure does indeed exist. (*Ibid.*)

2. Third Prong: Abuse of Discretion

In contrast to first-prong issues, the trial court's third-prong conclusions that proper procedures were followed in the particular case are reviewed for abuse of discretion. (*People v. Venegas, supra,* 18 Cal.4th at p. 91.) The appellate court is "required to accept the trial court's resolutions of credibility, choices of reasonable inferences, and factual determinations from conflicting substantial evidence. [Citation.]" (*Ibid.*) We thus consider whether there is substantial evidence in the record to support the conclusion that the procedures were in fact performed in a manner fully consistent with the underlying science such that they produced reliable results. (*Id.* at pp. 91-92.)

"'This standard is *deferential*. [Citations.] But it is not empty. Although variously phrased in various decisions [citation], it asks in substance whether the ruling in question "*falls outside the bounds of reason*" under the applicable law and the relevant facts [citations].'" (*People v. Garcia* (1999) 20 Cal.4th 490, 503.) "Abuse may be found if the trial court exercised its discretion in an arbitrary, capricious, or patently absurd manner, but reversal of the ensuing judgment is appropriate only if the error has resulted in a manifest miscarriage of justice. [Citations.]" (*People v. Coddington* (2000) 23 Cal.4th 529, 587-588, overruled on other grounds in *Price v. Superior Court* (2001) 25 Cal.4th 1046, 1069, fn. 13.) "The governing canons are well established: 'This discretion ... is an impartial discretion, guided and controlled by fixed legal principles, to be exercised in conformity with the spirit of the law, and in a manner to subserve and not

to impede or defeat the ends of substantial justice. [Citations.]' [Citation.] 'Obviously the term is a broad and elastic one [citation] which we have equated with "the sound judgment of the court, to be exercised according to the rules of law." [Citation.]' [Citation.] Thus, '[t]he courts have never ascribed to judicial discretion a potential without restraint.' (*Ibid*.) … '[A]ll exercises of legal discretion must be grounded in reasoned judgment and guided by legal principles and policies appropriate to the particular matter at issue.' [Citation.]" (*People v. Superior Court* (*Alvarez*) (1997) 14 Cal.4th 968, 977.)

"A trial court abuses its discretion when the factual findings critical to its decision find no support in the evidence.… '[I]t would seem obvious that, if there were no evidence to support the decision, there would be an abuse of discretion.'" (*People v. Cluff* (2001) 87 Cal.App.4th 991, 998.) Thus, when the defense establishes that proper scientific procedures were not followed, and the prosecution fails to present "substantial evidence upon which to base a contrary conclusion," the prosecution has failed to carry its burden and the trial court's admission of the evidence constitutes an abuse of discretion. (*People v. Venegas, supra,* 18 Cal.4th at p. 93.)

II. RELEVANT HISTORY

In *People v. Axell, supra,* 235 Cal.App.3d 836 , filed in October 1991, the court ruled that the general RFLP methodology used by Cellmark had gained general scientific acceptance. (*Id.* at pp. 853-863.) In August 1992, the court in *People v. Barney, supra,* 8 Cal.App.4th 798, relying primarily on *Axell*, rejected challenges to the general acceptance of the preparatory RFLP procedures (up to the statistical analysis) conducted by both Cellmark and the FBI. (*People v. Barney, supra,* 8 Cal.App.4th at pp. 811-814; see also *People v. Venegas, supra,* 18 Cal.4th at p. 77.)

In October 1992, we filed our first opinion in the present case (*Pizarro I, supra,* 10 Cal.App.4th 57), in which defendant claimed the FBI's RFLP methodology had not been deemed generally accepted. Concerned by the differences between the protocols

used by Cellmark in *Axell* and by the FBI in this case, and by the lack of evidence that the protocols were the same, we held the evidence insufficient to establish general scientific acceptance of the FBI's technique (*Pizarro I, supra,* at pp. 79-80), and remanded the case for a complete *Kelly* hearing. That hearing took place in 1994 and 1995. In its 1998 ruling, the trial court stated that we remanded the matter for a *Kelly* hearing to determine (1) whether the DNA testing method used by the FBI in this case was generally accepted by the scientific community, and (2) whether the database used by the FBI in this case was generally accepted by the scientific community. The trial court found the evidence admissible, ruling as follows: "There is general acceptance in the scientific community of the DNA testing method used by the F.B.I." and "The data base used by the FBI to calculate statistical probability estimates was, and is, accepted in the scientific community." The court did not directly mention third-prong issues regarding whether the FBI followed correct scientific procedures. The court denied the motion to exclude the DNA evidence and confirmed the conviction.

Two months after the trial court's ruling, the Supreme Court published *Venegas*, which concluded that "the *Axell* and *Barney* opinions clearly established the general scientific acceptance, under *Kelly*'s first prong, of the basic RFLP methodology utilized by the FBI …." (*People v. Venegas, supra,* 18 Cal.4th at p. 79.) Unless there was proof the FBI's procedure was materially distinct from the basic RFLP procedure deemed approved by *Axell* and *Barney*, these opinions served as precedent for a first-prong challenge. (*Id.* at pp. 53, 78-79.)[30] In effect, *Venegas* determined that, once the basic procedure was deemed accepted, the burden fell on the opponent of the evidence to show that the procedure in the case before the court differed materially from the accepted basic

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30 We note that this conclusion by *Venegas* calls into question the principle that one appellate court's decision is not binding on another appellate court. (See, e.g., 9 Witkin, Cal. Procedure (4th ed. 2001) §§ 934-935, pp. 971-974 and cases cited therein.)

procedure. If the opponent could not do so, then the first prong remained satisfied by precedent.

We review this case in light of these developments.

III. SCIENCE[31]

A. INTRODUCTION

As we have stated, forensic DNA profiling is intended to demonstrate two facts -- first, that *the defendant could be the perpetrator because his genetic profile matches the perpetrator's*, and, second, that *a certain number of people in the population could be the perpetrator because their genetic profiles match the perpetrator's*. The first fact allows the prosecution of the defendant to continue (a profile nonmatch would exonerate him); the second allows the jury to weigh the value of the first. (See National Research Council, DNA Technology in Forensic Science (1992) p. 51 (hereafter NRCI).)

A genetic profile is much like a physical profile or composite sketch -- it is a compilation of traits to describe the perpetrator. The profiler or sketch artist attempts to include as many of the perpetrator's traits as possible because the more traits described, the more specific the sketch of the perpetrator and the more limited the pool of possible perpetrators. A physical profile that describes a perpetrator as having black hair, blue eyes, and 5-foot-8-inch stature limits the pool of possible perpetrators to people with

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31 We generally refer to the parties and their DNA samples as defendant (rather than suspect), perpetrator (rather than evidence or evidentiary), and victim. We recognize that what we refer to as the perpetrator's sample is more accurately referred to as the evidentiary sample because it may contain DNA from someone other than the perpetrator. But, for clarity and simplicity, and to stress the distinction between the perpetrator and the defendant, we generally adhere to this scheme.

Our reference to scientific literature is to provide the background necessary for the understanding of the issues in this case, not to resolve those issues. Although we cite various scientific sources, our discussion of the science and procedure of RFLP is derived in great part from a report entitled The Evaluation of Forensic DNA Evidence (hereafter NRCII), prepared in 1996 by the National Research Council.

these three traits. If a fourth trait -- prominent ears, for example -- is added to the profile, the description becomes more specific and the pool of possible perpetrators decreases further. In the same way, a genetic profile that describes a perpetrator as having certain genetic characteristics at three DNA loci limits the pool of possible perpetrators to people with those three traits. Again, if more loci are added to the profile, the description's specificity increases and the pool of possible perpetrators decreases.

There are three basic theoretical steps or inquiries in RFLP genetic profiling. (1) What is the perpetrator's profile? (2) Does the defendant match that profile? (3) How rare is that profile in the population? (NRCI, *supra*, at p. 51.)

B. THEORETICAL SUMMARY

Returning to the physical description scenario, we summarize these three theoretical steps, mindful that the genetic loci used for the genetic profiling have nothing to do with physical features; the comparison is strictly illustrative.

(1) Profiles -- What is the perpetrator's profile?

Metaphorically: The perpetrator has black hair, blue eyes, and 5-foot-8-inch stature.

Genetically: The perpetrator possesses certain alleles at three particular DNA loci.

(2) Matching -- Does the defendant match that profile?

Metaphorically: Does the defendant also have black hair, blue eyes, and 5-foot-8-inch stature?

Genetically: Does the defendant's genetic profile match the perpetrator's at each allele of the three loci?

If so, the defendant resembles the perpetrator and cannot be excluded as a possible perpetrator; the case against the defendant may proceed.

If not, the defendant does not resemble the perpetrator and is excluded as a possible perpetrator; the defendant is exonerated.

(3) Statistical Probability -- How many people in the relevant population match the perpetrator's profile?

Metaphorically: How many people have black hair, blue eyes, and 5-foot-8-inch stature? (Or, how often would we expect to find a person with black hair, blue eyes, and 5-foot-8-inch stature?)

Genetically: How many people have alleles that match the perpetrator's alleles? (Or, how often would we expect to find a person whose alleles match the perpetrator's alleles?)

If the perpetrator's traits occur together *commonly*, the profile is common and the pool of possible perpetrators is fairly large. A common profile such as this *benefits* the defendant (who shares this profile). He will say, "A lot of people look like the perpetrator. The fact that I look like him too is nearly meaningless."

If the perpetrator's traits occur together *rarely*, the profile is rare and the pool of possible perpetrators is very small. A rare profile such as this *incriminates* the defendant. The prosecutor will say, "Almost no one looks like the perpetrator. The fact that you look like him means you probably *are* him."

C. PROCEDURAL SUMMARY

In RFLP, these three theoretical steps are implemented with three procedural steps: a molecular biology protocol to process the DNA and produce the genetic profiles; a matching protocol to determine whether, accounting for measurement imprecision, the perpetrator's and defendant's profiles match; and a statistical protocol to determine the rarity of the profile and the probability of a match. (NRCI, *supra*, at p. 51.)

(1) Profiles[32]

1. Extraction and isolation of the DNA samples (perpetrator, victim, and defendant)

2. Cutting (digestion) of the DNA with a site-specific enzyme to create an enormous number of fragments

3. Separation of the DNA fragments according to size by gel electrophoresis

4. Transfer (blotting) of the separated DNA fragments from the gel onto a nylon membrane for convenience

5. Sequential probing (hybridization) of the separated DNA fragments attached to the membrane with various radioactive probes that attach to only two VNTR regions on the fragments (one region from each parent)

6. Autoradiography of each hybridization to memorialize the results on X-ray film

When this procedure is completed, the autorads are analyzed to determine whether the defendant's profile matches the perpetrator's.

(2) Matching[33]

1. Preliminary visual examination of the autorads to determine whether each of the defendant's alleles appears to be the same

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32 These well-established molecular biology steps are described on pages 3-19 of the FBI's protocol received into evidence as Exhibit 7. (See also NRCII, *supra*, at pp. 15-18, 42, 65-67; Congress of the United States Office of Technology Assessment, Genetic Witness: Forensic Uses of DNA Tests (1990) pp. 44-46 (hereafter OTA); DNA in Forensic Science: Theory, Techniques and Applications (Robertson, et al. eds., 1990) pp. 68-70 (hereafter Robertson); Easteal, et al., DNA Profiling: Principles, Pitfalls and Potential (1991) pp. 149-161 (hereafter Easteal); Coleman & Swenson, DNA in the Courtroom (1994) pp. 36-41 (hereafter Coleman).)

33 Matching steps are described on pages 20 and 21 of the FBI's protocol (Exhibit 7). (See also NRCII, *supra*, at pp. 18-19, 43-44, 68-69; Easteal, *supra*, at pp. 161-163.)

size as each of the perpetrator's alleles (to eliminate obvious mismatches)

2. Computerized examination to measure the size of each allele

3. Calculation of "uncertainty windows" around each allele measurement (to account for measurement imprecision)

4. Determination of whether, for each allele, the defendant's uncertainty window overlaps the perpetrator's uncertainty window (so that the alleles could actually be the same size)

5. Declaration of a matching profile if overlap of uncertainty windows is found to occur at each allele

Last, the frequency or statistical probability of the perpetrator's profile in the population is calculated.

(3) Statistical Probability[34]

1. Calculation of a "statistical window" for each of the perpetrator's alleles

2. Reference to database frequencies (using the statistical window) to assign a frequency to each of the perpetrator's alleles

3. Calculation of the overall frequency of the perpetrator's complete DNA profile in the database population (also called the random match probability)[35]

We now address in more detail these three steps -- profiles, matching, and statistical probability -- discussing both theory and procedure.

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34 The FBI's protocol (Exhibit 7) does not address statistical probability. (But see NRCII, *supra*, at pp. 20-21, 44-45, 68-69; Coleman, *supra*, at p. 45; part III.E., *post*.)

35 We recognize there is commentary stating that in complicated cases there may be a distinction between the frequency of the perpetrator's profile and the probability of a random match. (See, e.g., Weir, DNA Match and Profile Probabilities: Comment on Budowle et al. (2000) and Fung and Hu (2000) (2001) Forensic Science Communications.) However, this case apparently does not present such complications.

D. PROFILES AND MATCHING

1. Theory

a. Profiles

Determination of a person's genetic profile using RFLP relies on the differences in *length* of certain DNA regions, or alleles. (NRCII, *supra*, at p. 65.) In *People v. Brown, supra,* 91 Cal.App.4th 623, this court summarized the basis of variation between alleles and its utility to forensic DNA profiling. There, we analogized DNA to text:[36]

> "The genetics of a human cell can be compared to a library, the *genome*, composed of 46 'books,' each a single *chromosome*. The 'text' contained in the books is written in *DNA*, the chemical language of genetics. The 'library' is compiled by the owner's parents, each of whom contributes 23 books, which are then matched up and arranged together in 23 paired sets inside the sacrosanct edifice of the *nucleus*. During embryonic development, the original library is copied millions of times so that each cell in the human body contains a copy of the entire library.[37]
>
> "Twenty-two of the twenty-three paired sets of books are entitled 'Chromosome 1' through 'Chromosome 22'; externally, the two paired books of each set appear to be identical in size and shape. However, the 23d set, which contains information on gender, consists of one book entitled 'Chromosome X' (given by the mother) and one book entitled either 'Chromosome X' or 'Chromosome Y' (given by the father and determining the sex of the library's owner). The 22 sets comprising 'Chromosome 1' through 'Chromosome 22' address an enormous variety of topics describing the composition, appearance, and function of the owner's body. In addition, they include a considerable amount of what

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36 Footnotes are included and sequentially renumbered.

37 "There are a few exceptions, the two most significant being red blood cells and sex cells. Red blood cells contain no nucleus and therefore no chromosomes. Egg and sperm cells contain half the number of chromosomes of the rest of the body's cells, so that upon fertilization the complete number of chromosomes will be restored rather than doubled. Blood can be used to test a person's DNA because white blood cells contain DNA; sperm cells can be used because enough cells are tested that collectively the entire complement of DNA is represented. ([NRCII, *supra*, at] p. 12 ….)"

appears to be nonsense. The two paired books of each set, one book from each parent, address identical topics, but may contain slightly different information on those topics. Thus, two paired books opened to the same page contain corresponding 'paragraphs,' but the text within those corresponding paragraphs may vary between the two books. For example, within the paragraph addressing eye color, one book may describe blue eyes while the other book of the set may describe brown eyes.[38]

"The two corresponding, but potentially variant, paragraphs in the two paired books are called *alleles*. If, for a particular topic (i.e., at a particular region or *locus* on the DNA), the allele from the mother is A and the corresponding allele from the father is B, the *genotype* at that locus is designated AB. The text of two corresponding alleles at any locus may be identical (a *homozygous* genotype, e.g., AA) or different (a *heterozygous* genotype, e.g., AB). Regardless, one person's genetic text is, in general, extremely similar to another person's; indeed, viewed in its vast entirety, the genetic text of one human library is 99.9 percent identical to all others. As a result, the text of most corresponding paragraphs varies only slightly among members of the population.

"Certain alleles, however, have been found to contain highly variable text. For example, alleles are composed of highly variable text when they describe structures requiring enormous variability. Also, some alleles appear to contain gibberish that varies greatly, or repeated strings of text that vary not in text but in repeat number. These variants (*polymorphisms*) found at certain *loci* render each person's library unique[39] and provide forensic scientists a method of differentiating between libraries (people) through the use of forensic techniques that rely on the large number of variant alleles possible at each variable locus…. Since each person receives two alleles for each locus, the number of possible combinations is further increased.

"When a sample of DNA -- usually in the form of hair, blood, saliva, or semen -- is left at the crime scene by a perpetrator, a forensic genetic

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38 "The physical characteristic exhibited by the library's owner generally depends on the dominance or recessiveness of those two descriptions. Paragraphs describing a physical characteristic such as eye color, or describing a particular cellular product or function, are called *genes*. By definition, they contain a discrete amount of text sufficient to describe a particular thing or function."

39 "Identical twins, however, share essentially identical DNA."

> analysis is conducted. First, DNA analysts create a genetic 'profile' or 'type' of the perpetrator's DNA by determining which variants or alleles exist at several variable loci. Second, the defendant's DNA is analyzed in exactly the same manner to create a profile for comparison with the perpetrator's profile. If the defendant's DNA produces a different profile than the perpetrator's, even by only one allele, the defendant could not have been the source of the crime scene DNA, and he or she is absolutely exonerated.[40] If, on the other hand, the defendant's DNA produces exactly the same genetic profile, the defendant could have been the source of the perpetrator's DNA -- but so could any other person with the same genetic profile. Third, when the perpetrator's and the defendant's profiles are found to match, the statistical significance of the match must be explained in terms of the rarity or commonness of that profile within a particular population -- that is, the number of people within a population expected to possess that particular genetic profile, or, put another way, the probability that a randomly chosen person in that population possesses that particular genetic profile.[41] Only then can the jury weigh the value of the profile match. [Citation.]."[42] (*People v. Brown, supra,* 91 Cal.App.4th at pp. 627-629; see NRCII, *supra*, at pp. 12-14, 60-65; NRCI, *supra*, at pp. 1-3, 32-33; OTA, *supra*, at pp. 3-6, 41-43; Kirby, DNA Fingerprinting (1992) pp. 7-34 (hereafter Kirby); Robertson, *supra*, at pp. 1-8, 31-33.)

The RFLP procedure used in Pizarro's case exploits genetic polymorphisms called variable number of tandem repeats (VNTRs), repeated sequences that abut one another without interruption. These DNA regions, which have no known product or function, vary greatly in repeat unit number and hence in length. The repeat unit is generally 15 to 35 base pairs (bp) long, and the total length of the allele usually ranges from 500 bp to

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40 "This, of course, assumes there was no error in handling of evidence or in laboratory procedure and analysis."

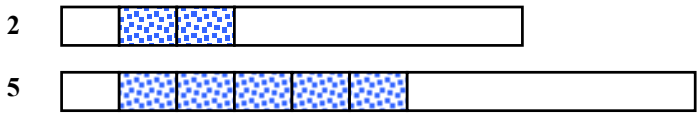
41 "This probability is often called the random match probability."

42 "'A determination that the DNA profile of an evidentiary sample matches the profile of a suspect establishes that the two profiles are consistent, but the determination would be of little significance if the evidentiary profile also matched that of many or most other human beings. The evidentiary weight of the match with the suspect is therefore inversely dependent upon the statistical probability of a similar match with the profile of a person drawn at random from the relevant population.' [Citation.]"

10,000 bp.[43] The variation in allele length provides a method of comparison between the two alleles of a single person and between the alleles of different people. (NRCII, *supra*, at pp. 14-15, 65; NRCI, *supra*, at pp. 34-36, 38; OTA, *supra*, at pp. 43-44; Robertson, *supra*, at pp. 27-28.)

This concept can be explained schematically. Assume, for example, that the two alleles, one from each parent, possessed by the perpetrator at a particular locus are hypothetically referred to as 2 and 5 (rather than A and B, to denote their lengths). The perpetrator's genotype at this locus is 2,5. Schematically, the alleles, which have been enzymatically cut out of the long DNA molecule,[44] might appear as follows:

Perpetrator:



Since one locus or trait does not specifically describe the perpetrator and thus does not narrow down the possible perpetrators significantly, just as describing the perpetrator as having black hair does not significantly reduce the field of possible perpetrators, additional genetic traits must be examined to flesh out the genetic sketch.

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[43] Base pairs are the "letters" in the text of DNA. The term "allele" technically refers to a variant of a *gene*, but for convenience it is also used to refer to a variant of a polymorphic locus.

[44] The DNA has been cut with an enzyme that recognizes a specific sequence known not to exist within the VNTR sequence. Thus, the cuts occur outside of and without disturbing those regions. (NRCII, *supra*, at p. 66.)

The alleles at a second locus might appear as follows:

Perpetrator:

6

6

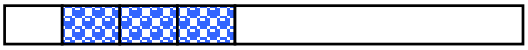
The perpetrator's genotype at this locus is 6,6.

The alleles at a third locus might appear as follows:

Perpetrator:

7

3



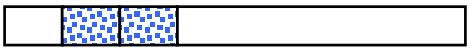
The perpetrator's genotype at this locus is 7,3. The genetic sketch of the perpetrator now consists of three loci and six alleles. (See NRCI, *supra*, at pp. 35-36; 45-46.)

b. Matching

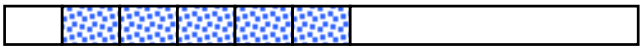
The matching step determines whether each of the defendant's alleles match the perpetrator's alleles -- that is, whether the defendant *could be* the perpetrator. Assume that the following sets of alleles are revealed at the first locus for the perpetrator and the defendant:

Perpetrator:

2



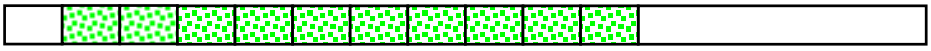
5



Defendant:

5

10

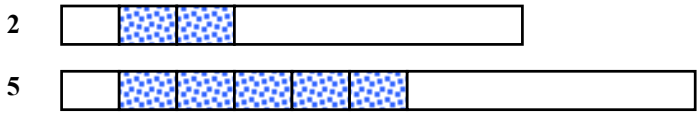


Although the perpetrator and the defendant share one allele (5), they do not share both, and therefore the defendant is excluded as a possible perpetrator. Identity between all of the alleles is required. When this lack of identity exists for even one allele at one locus, the defendant is exonerated. Stated metaphorically, the defendant's "hair color"

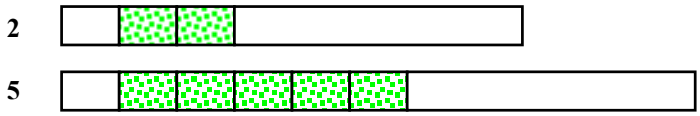
(5,10) is not the same as the perpetrator's (2,5) and thus the defendant cannot be the perpetrator.

Assume instead that the following alleles are revealed for the perpetrator and the defendant at the first locus:

Perpetrator:



Defendant:



Now, both alleles at this locus match and the defendant is not excluded as a possible perpetrator. The defendant's "hair color" matches the perpetrator's. If all of the defendant's alleles at the remaining two loci match the perpetrator's, the overall profiles match, and the defendant is a possible perpetrator. If, on the other hand, even one of the defendant's alleles fails to match, the defendant is no longer a candidate. (NRCII, *supra*, at p. 18; NRCI, *supra*, at p. 4.)

While these diagrams suggest otherwise, the unfortunate reality of RFLP analysis is that it cannot display the actual alleles or measure their exact lengths.[45] Thus, determination of a match between two alleles is complicated by the system's measurement imprecision. (NRCII, *supra*, at p. 139; NRCI, *supra*, at pp. 38, 61.) We

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[45] If, however, each allele were directly sequenced to determine its exact length, an allele from the perpetrator and the corresponding allele from the defendant could be compared unambiguously. If the base pair lengths were identical, the allele lengths would be the same. If the base pair lengths were off by even a single base pair, the allele lengths would be different and the defendant would be excluded.

turn next to the procedure by which RFLP determines whether an allele from the defendant is the "same" length as the corresponding allele from the perpetrator.

2. Procedure

***a. Profiles*[46]**

1. Extraction of DNA

In practice, comparison of allele lengths by RFLP begins with the extraction of DNA from the crime scene evidence -- from hair, a blood stain, a saliva stain, or, as in this case, a vaginal swab. This evidentiary sample will likely contain the perpetrator's DNA. For comparison, blood samples are taken from the victim and the defendant, and DNA is extracted from those samples also.

2. Enzymatic Digestion of DNA

Once purified, the DNA in the three separate samples is cut into millions of fragments of varying lengths by a restriction enzyme that cuts at a specific short sequence wherever it exists in the DNA. The spacing of these cutting sites on the DNA varies slightly from person to person, and thus the array of fragments produced by the cutting will vary slightly from person to person. If the array of fragments in two samples is the same -- that is, if the *lengths* of the fragments are the same -- then the DNA in the two

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46 For an overview of the following molecular biology procedure, see NRCII, *supra*, at pages 15-18, 42-45, 65-69; NRCI, *supra*, at pages 36-40; and Robertson, *supra*, at pages 74-79. Unless otherwise noted, in this section (part III.D.2.a.) we rely on NRCII, *supra*, at pages 15-18, 42-43, 66-68; NRCI, *supra*, at pages 36-40; OTA, *supra*, at pages 46-47; Kirby, *supra*, at pages 51-73, 94-104, 110-116; Robertson, *supra*, at pages 62-65, 69-70; Coleman, *supra*, at pages 36-37, 40-41; and Easteal, *supra*, at pages 85-87.

samples could be from the same person. Consequently, to determine whether the perpetrator and the defendant could be the same person, the fragments in their DNA samples must be compared.

3. Gel Electrophoresis of DNA Fragments

To accomplish this, the DNA fragments are first separated according to size using gel electrophoresis. This electrophoretic step serves two purposes: (1) it spreads out the invisible contents of each DNA sample, preparing the DNA fragments for further study, and (2) it allows estimation of the sizes of the DNA fragments. A portion of each DNA sample is added to separate wells near the end of a horizontal slab of dense gel (the wells do not penetrate through to the bottom of the gel). The gel is then placed in an electrical field. The DNA fragments, which are negatively charged, travel through the gel toward the positive pole, their speeds depending on their size and ability to maneuver through the gel structure. The gel is something of a molecular obstacle course -- the shorter, more agile DNA fragments move through it more quickly and advance farther down the gel in a given amount of time than the longer, more cumbersome fragments. When the electrical current is turned off, the DNA fragments in a sample are spread down a lane

extending from the well to the other end of the gel. The fragments of DNA form what are called bands. For reference, size standards (often called molecular weight markers), which are DNA fragments of known sizes, are also run on the gel. (Fig. 1.)

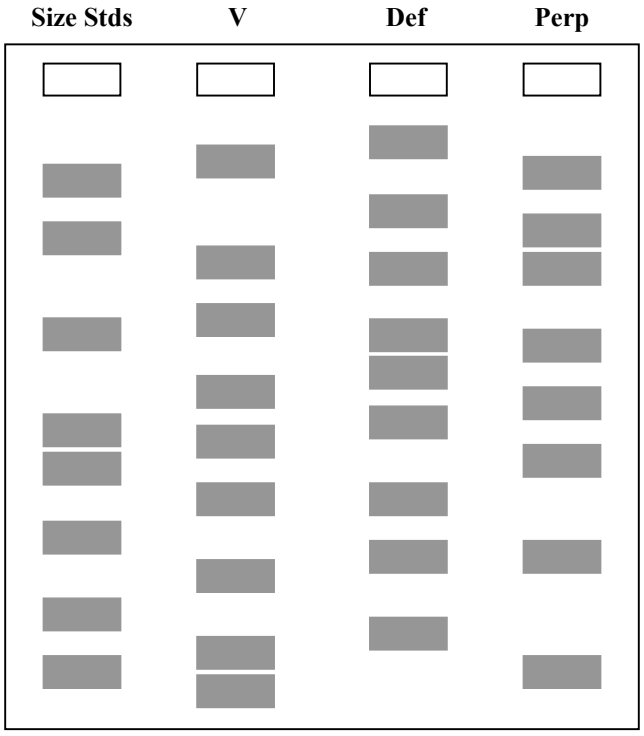

Fig. 1. ***Bands of DNA on Gel.***[47]
NOTE: View looking down on the horizontal gel. The wells are at the top of the gel. The smallest fragments travel farthest and are at the bottom of the gel; the largest fragments remain near the top of the gel. In all diagrams, Size stds = size standards; V = victim; Def = defendant; Perp = perpetrator.

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47 Our diagrams are schematic and imprecise. They are intended only to aid the reader. (The autorad scans (figs. 4-6, *post*), however, are representations of the evidence in this case.)

4. Blotting of DNA Fragments onto Membrane

Since the gel is fragile and short-lived, the DNA fragments are transferred (blotted) from the gel onto a durable nylon membrane, the DNA retaining the same band formation. But before the gel is blotted, it is soaked in a chemical that separates or "unzips" the two strands of every DNA fragment within the gel (i.e., the double-stranded DNA fragments are denatured into single-stranded fragments). Now the single-stranded DNA fragments adhered to the membrane can be analyzed.

5. Hybridization with Radioactive Probes

RFLP seeks to identify the polymorphic VNTR regions that vary in length. After the DNA is cut into fragments, the two specific VNTR regions possessed by a person are contained in two of the many fragments now spread down the lane of the gel. It is impossible, however, to tell which fragments contain the VNTR regions by simply looking at the DNA fragments on the gel or membrane. These regions must be sought out and flagged by a molecular probe. The highly specific bonds formed between the two strands of DNA make this possible. The single-stranded DNA fragments immobilized on the membrane are available for bonding with other single-stranded DNA fragments, but only if the sequences of the two fragments are complementary. Thus, if a known sequence is being sought in the DNA (e.g., a specific VNTR region), a short single-stranded DNA fragment (probe) with a complementary sequence can be created to seek out that sequence among the fragments attached to the membrane. Each probe molecule is radioactively tagged to allow visualization of the (invisible) DNA fragments later.

Many copies of the radioactive probe are added to liquid in a container, then the membrane is added and sloshed about for several hours. When a probe molecule happens to wash across a complementary DNA fragment attached to the membrane, it will bind tightly (hybridize) to it. Then, when the excess probe is washed off the membrane, the remaining probe molecules are bound only to the VNTR regions in the two alleles per DNA sample. The hybrids formed between the radioactive probe molecules and the complementary VNTR regions on the membrane are radioactive and will be visualized in the next step. (Other radioactive probe molecules specific to the size standards are also added to the hybridization liquid so the standards will also be identifiable.) (Fig. 2.)

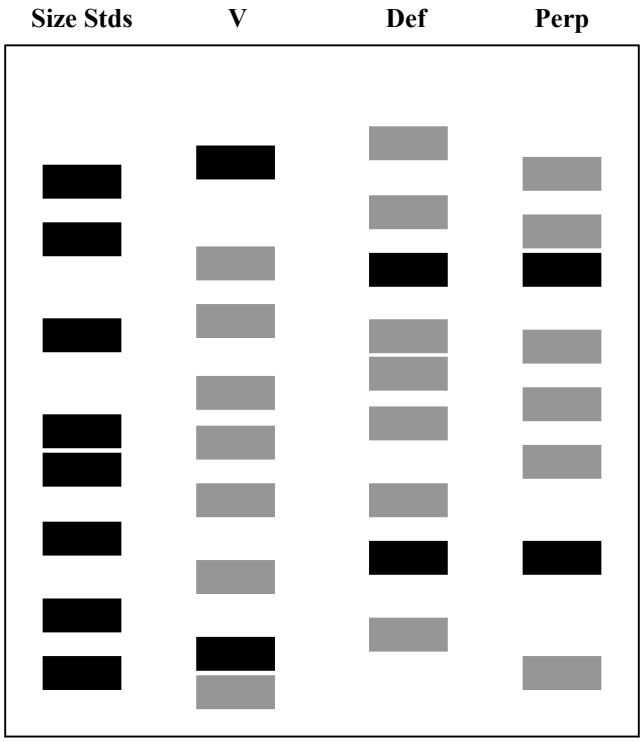

Fig. 2. ***Bands of Probe-Bound DNA on Membrane.***
NOTE: The probe binds to two alleles per DNA sample, represented by the two black bands in the V, Def, and Perp lanes. Different probe binds to the size standards so they too will be visible later.

6. Autoradiography

When an X-ray film is placed over the membrane, the radioactive tags reveal the positions of the invisible probe-bound alleles and size standards. The other nonradioactive DNA bands remain invisible. (Fig. 3.) Once an autorad has been made from the hybridized membrane, the probe is chemically stripped off the membrane, and the procedure is repeated with a different probe specific to another VNTR locus. The membrane can be reused for several different probes (but there is a limit because the DNA attached to the membrane is gradually stripped off).

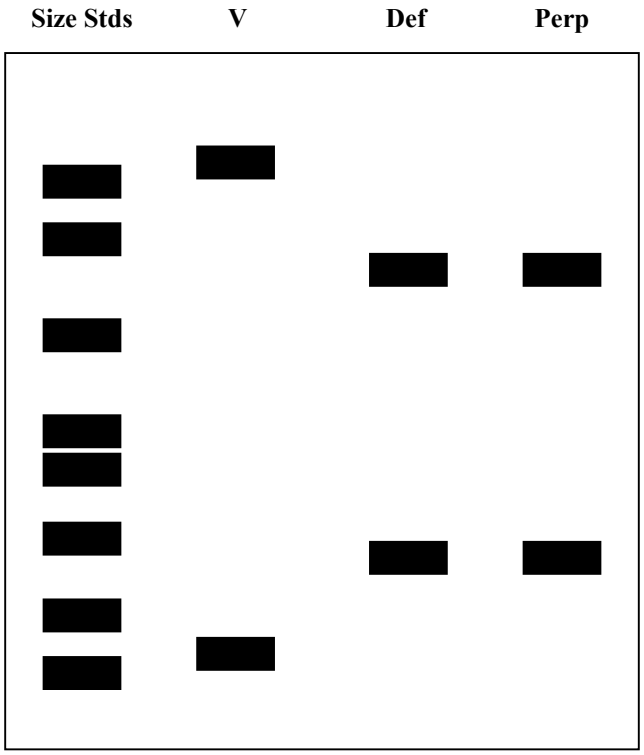

Fig. 3. ***Bands of Probe-Bound DNA on Autorad.***
NOTE: The bands of probe-bound DNA are finally visible on the X-ray film.

This molecular biology procedure reveals the two VNTR alleles possessed by the perpetrator, the defendant, and the victim at each locus tested. If three loci are tested, three autorads are produced, each showing one or two bands in each person's DNA sample. Usually, the two alleles possessed by a person are different lengths and therefore appear as two bands (a heterozygous genotype). If the two alleles are the same or a very

similar length, they will appear as a single band (a homozygous genotype). (NRCII, *supra*, at p. 69; Aitken, Statistics and the Evaluation of Evidence for Forensic Scientists (1995) p. 207.) A person's alleles, discerned from all the autorads, together make up that person's genetic profile.

b. Matching[48]

To determine whether the defendant's alleles match the perpetrator's alleles, the scientists first visually compare one of the defendant's bands with the corresponding perpetrator's band on an autorad to see if they appear to be the same size (i.e., are in the same position because they traveled the same distance on the gel). If the two bands are an obvious mismatch, the analysis ends. If the bands appear to match (as in figure 3, *ante*), they are measured by the computer, using the size standards on the same autorad for comparison. If the bands are within a certain size range of each other, they are considered a match.

E. STATISTICAL PROBABILITY[49]

A match between all the defendant's alleles and all the perpetrator's alleles (i.e., between their profiles) does not signify an *absolute* match between the entirety of the perpetrator's DNA and the entirety of the defendant's DNA, which would absolutely prove the perpetrator and the defendant are the same person. The match is actually between only a few or several regions of an enormous amount of DNA, and therefore it does not absolutely prove identity. What it does prove is that the defendant *could be* the perpetrator. However, this information standing alone is not particularly helpful to the

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48 In this section (part III.D.2.b.) we rely on NRCII, *supra*, at pages 7, 18-20, 43-45, and 139-142.

49 Unless otherwise noted, in this section (part III.E.) we rely on NRCII, *supra*, at pages 7, 18-22, 30, 44-45, 95, 114, 122, 127, 139-145, 161-162, and 177, and NRCI, *supra*, at pages 77-79 and 85-86.

jury; it is in fact unwieldy, overwhelming, even irresistible. If the jury is told simply that the defendant's genetic profile matches the perpetrator's profile and thus the defendant could be the perpetrator, the jury, awed by the sophistication and incomprehensibility of the DNA evidence, will naturally respond by assuming the match absolutely proves identity. For this reason, courts have insisted that the prosecution provide comprehensible evidence regarding the meaning or significance of the match. (See NRCII, *supra*, at pp. 192-199; NRCI, *supra*, at pp. 9-11, 44; Easteal, *supra*, at pp. 90-91.)

The determination of what is often called the "significance of the match" is a statistical assessment of *how incriminating* it is that the defendant's profile matches the perpetrator's. It quantifies the rarity of the perpetrator's profile in the population, thereby allowing the jury to weigh the evidence that the defendant possesses the same profile. It is a numerical assessment that asks, in essence, are there multitudes of people who possess the perpetrator's profile, or exceedingly few people who possess the perpetrator's profile? The rarer the profile, the more incriminating the defendant's possession of it. (See NRCII, *supra*, at p. 127; NRCI, *supra*, at p. 44.)

First, a numerical frequency is determined for each of the perpetrator's alleles, one at a time; then the genotype frequency (for an allele pair) at each locus (for each autorad) is calculated; and finally the overall frequency of the perpetrator's complete DNA profile is calculated to determine how many people in the relevant population would be expected to possess or match the perpetrator's profile (or, stated differently, the probability that a random person in the relevant population would possess that profile). (See NRCII, *supra*, at pp. 90-93, 122, 127; NRCI, *supra*, at pp. 44, 77-79.) The product is expressed as, for example, 1 in 10,000 or 1 in 500 million.[50]

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50 "[The overall] numerical probability is generally calculated using the 'product rule,' which posits that the probability of several things occurring together is the product of their separate probabilities. [Citation.] For example, the probability of 'heads' coming

Frequencies such as these are easily estimated using population databases. We explained the underlying idea in *Brown*:

> "For example, if the victim reports that the perpetrator had blue eyes and abnormally short fingers (brachydactyly), forensic scientists will need to know how rare the combination of blue eyes and brachydactyly is in the population. That determination requires knowledge of the *separate* frequencies of these two traits in the population -- how many people have blue eyes and how many people have brachydactyly. But it is impractical to actually examine the entire population to count every person with blue eyes and every person with brachydactyly; instead, scientists create a database of randomly selected people, and use the frequencies of the traits of that group of people to represent the entire population. If among the people used to compile the database the occurrence of blue eyes is fairly common and the occurrence of brachydactyly is very uncommon, then the probability of the two traits occurring *together* will be extremely rare. That determination, derived from the database, is presumed to apply to the entire population the database was created to represent. Therefore, the reasoning goes, if very few people are expected to have both traits -- that is, if the profile is rare -- the probability is greater that a defendant who possesses both traits is in fact the perpetrator.
>
> "In reality, forensically important alleles do not manifest themselves in obvious physical traits, but the idea is the same. Because allele frequencies cannot be determined from external appearances, preparation of a database requires collection of DNA samples (usually blood) from

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up on three successive coin tosses is the probability of heads on the first toss (1 in 2), multiplied by the probability of heads on the second toss (1 in 2), multiplied by the probability of heads on the third toss (1 in 2), resulting in an overall probability of 1 in 8. Similarly, if a set of paired alleles (a genotype) is known to occur in 1 in 3.47 people and another set of paired alleles is known to occur in 1 in 18.52 people, then the probability of *both* sets occurring in the *same* person is 1/3.47 multiplied by 1/18.52, or 1 in 64.26 people. When more alleles are examined, the probability of a multilocus profile can be exceedingly rare, even one in hundreds of billions, and therefore the profile is highly distinctive." (*People v. Brown, supra,* 91 Cal.App.4th at p. 630, fn. omitted.) "Obviously, there are situations in which the result of the product rule calculation exceeds the size of the particular population on earth. In that case, the result must be viewed in its alternative sense -- the numerical probability that a person randomly chosen from that population will possess the same genetic profile." (*Id.* at p. 630, fn. 14.)

> unrelated individuals in the relevant population, genetic analysis of each DNA sample to determine the alleles present at each locus tested, tally of the various alleles at each locus, and statistical analysis of the tallied results to determine the frequency of each allele … at each locus. These database frequencies become standard values from which a perpetrator's profile can be given a numerical probability of existing in a population." (*People v. Brown, supra*, 91 Cal.App.4th at pp. 629-630, fns. omitted.)

The "relevant" database population for calculating the profile frequency is the *perpetrator's* population, the population that contains all possible perpetrators. (NRCII, *supra*, at p. 30 [calculation should be made from relevant population database]; *id.* at p. 114 [calculation should be made from database that reflects ethnicity of person who left crime-scene DNA sample, if it is known]; *id*. at p. 122 [same]; *id.* at p. 127 [relevant population is "population of possible suspects"].) Scientists often use an *ethnic* population, rather than a more general population. For example, if there is proof that the perpetrator is Asian, the scientists may utilize the Asian database to estimate how many Asians possess the perpetrator's profile and therefore could be the perpetrator.[51]

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51 Courts often refer to this as the "relevant" (e.g. *People v. Venegas, supra,* 18 Cal.4th at pp. 63-64) or "target" (*People v. Barney, supra,* 8 Cal.App.4th at p. 809) population. Apparently, it was, and still may be, the practice of many laboratories to report only the frequency from the ethnic database to which the *defendant* belongs. (See, e.g., *Venegas, supra,* 18 Cal.4th at pp. 69-70 [FBI's 1991 report reported only a Hispanic frequency "as it was at that time the FBI's practice to report only the frequency for the racial group to which the suspect belonged…. Later, the FBI started routinely reporting Hispanic, Black, and Caucasian frequencies in every case."].)

IV. AUTORADIOGRAPHS

In Pizarro's case, three autorads were used to create the genetic profiles and to determine a match between the perpetrator's and defendant's profiles. Because our discussion refers extensively to this evidence, we include scans of the D1S7 (hereafter D1), D2, and D4S139 (hereafter D4) autorads.[52]

Each autorad is made from the same gel and hybridization membrane and thus the same underlying DNA fragments. The autorads look different because each memorializes a hybridization with a different probe that attached to and "lit up" different DNA fragments on the membrane.

Each autorad displays 12 vertical lanes. Four lanes contain size standards to which the unknown fragments can be compared and sized. The standards are run in several lanes on the gel to account for slight variations in electrical current in different regions of the gel. (Note that corresponding bands across the width of the autorads are not in perfect alignment.) One lane contains a control sample to ensure there has been no obvious failure in the system. The remaining lanes contain the DNA samples specific to this case. In summary, the autorads display the following samples:

lanes 1, 5, 9 & 12	Size Stds:	size standards
lane 2	C:	control sample
lane 3	V:	victim's reference blood sample
lane 4	Def:	defendant's reference blood sample
lanes 6 & 7	$V_{(ev)}$:	victim's vaginal epithelium fraction of evidentiary sample[53]
lanes 10 & 11	Perp:	perpetrator's sperm fraction of evidentiary sample

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[52] The D17S79 (hereafter D17) autorad was inconclusive.

[53] The evidentiary samples from two vaginal swabs were divided into sperm and vaginal cell DNA fractions, resulting in two sets of evidentiary DNA samples (4 lanes).

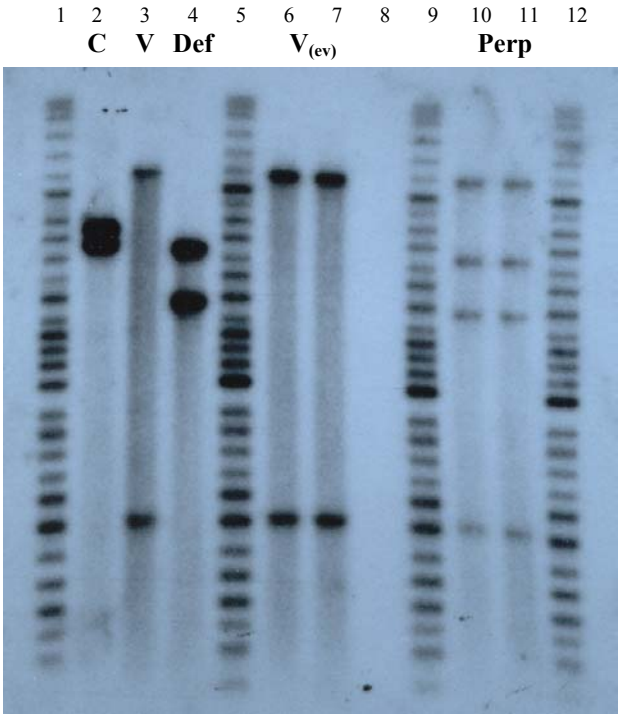

Fig. 4. ***D1 Autorad.***
NOTE: C = control; V = victim; Def = defendant; $V_{(ev)}$ = victim's (vaginal epithelium) fraction of evidentiary sample; Perp = perpetrator's (sperm) fraction of evidentiary sample. (Exhibit Y)

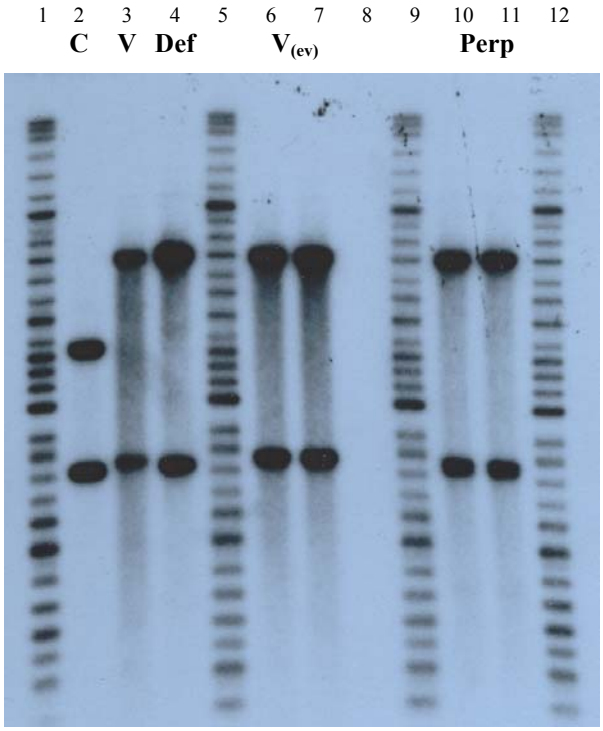

Fig. 5. ***D2 Autorad.***
NOTE: C = control; V = victim; Def = defendant; $V_{(ev)}$ = victim's (vaginal epithelium) fraction of evidentiary sample; Perp = perpetrator's (sperm) fraction of evidentiary sample. (Exhibit 2)

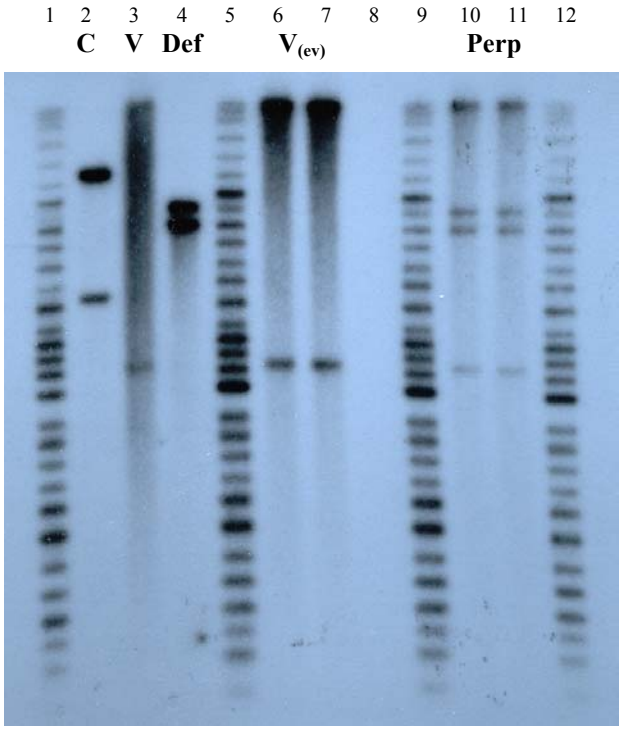

Fig. 6. ***D4 Autorad.***
NOTE: C = control; V = victim; Def = defendant; $V_{(ev)}$ = victim's (vaginal epithelium) fraction of evidentiary sample; Perp = perpetrator's (sperm) fraction of evidentiary sample. (Exhibit Am)

V. MIXED DNA SAMPLE

Defendant contends that the FBI's procedure with regard to the D2 genetic locus did not comport with correct scientific procedures under *Kelly*'s third prong, and that the resulting profile frequency therefore failed to meet the preliminary fact foundational requirements of section 403.

Specifically, defendant argues that the perpetrator's genotype at the D2 locus was not discernible from the D2 autorad because the perpetrator's DNA was contaminated by the victim's DNA, creating a complicated pattern. He asserts that the pattern represents *three different possible genotypes* for the perpetrator, all of which should have been accounted for in the FBI's frequency calculation. Instead, he claims, the FBI assumed the perpetrator's true genotype was the same as defendant's. He argues that reliance on defendant's genotype to determine the perpetrator's genotype was based on the assumption that defendant was the perpetrator, depriving defendant of the presumption of innocence, due process, and a fair trial. The FBI's method, defendant contends, amounted to improper scientific procedure under *Kelly*'s third prong. The People reply that defendant's claim is without merit because there was no realistic chance that the perpetrator possessed either of the other two possible genotypes (the two not matching defendant's) since defendant and the victim were half-siblings, and because the relative intensities of the bands on the D2 autorad allowed the scientists to discern the perpetrator's genotype from the mixture.

We conclude that the two methods utilized for discerning the perpetrator's genotype at the D2 locus were improper, one because it relied on defendant's genotype, the other because it required *Kelly*'s first-prong scrutiny. Thus, the FBI discerned the perpetrator's D2 genotype using improper procedure under *Kelly*'s third prong. Furthermore, the FBI's subsequent use of the improperly discerned genotype to declare defendant a match and to calculate the frequency of the perpetrator's profile was also improper procedure. Finally, because the D2 genotype was not properly discerned, the

DNA evidence admitted at trial, which relied upon proof of that genotype as preliminary fact, was introduced without sufficient foundation. (§ 403.)

A. INTRODUCTION AND SCIENCE

As we have explained, the initial step in genetic profiling is the determination of the lengths of the perpetrator's two alleles (his genotype) at each locus. Normally, this is a straightforward procedure -- the scientist observes one or (the usual) two bands in the perpetrator's lane on the autorads and sizes the bands by comparing their locations to the locations of the size standards. Figure 7 is an example of a typical autorad.[54]

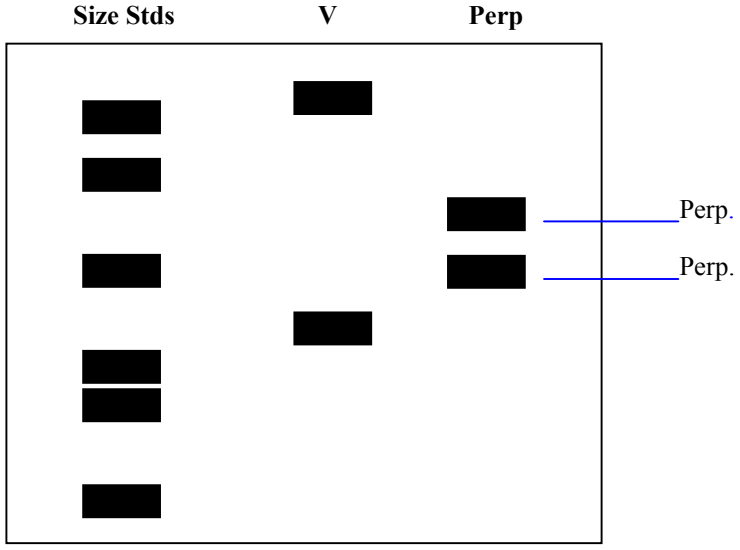

Fig. 7. ***Normal Two-Band Perpetrator's Sample.***

In Pizarro's case, however, we are presented with a critical issue specific to cases in which discernment of the perpetrator's alleles is more complicated because *the perpetrator's DNA is mixed with (contaminated by) another person's DNA*. In these situations, it may be difficult if not impossible to locate the perpetrator's bands on the autorad. (NRCII, *supra*, at p. 129; NRCI, *supra*, at pp. 59, 66.)

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54 In all our examples, the victim is heterozygous, like the victim in this case.

Mixed DNA is a potential problem with postrape vaginal swab samples because they typically contain both perpetrator sperm cells and victim vaginal epithelial cells. (NRCII, *supra*, at p. 129; NRCI, *supra*, at pp. 65-66.) To separate the DNA from inside the two types of cells, scientists use a procedure called differential extraction, which relies on the different resistances of sperm nuclei and epithelial cell nuclei to breaking open.[55] (NRCI, *supra*, at pp. 65-66; Easteal, *supra*, at pp. 152-153; Butler, *supra*, at p. 32; Kirby, *supra*, at pp. 63-64; Robertson, *supra*, at pp. 54-55, 82-83.) Sometimes the procedure is not completely successful and some victim epithelial cell DNA may remain in the sperm fraction. When the autorads are produced, the scientist can usually see that the perpetrator's DNA contains more than the normal two bands and that one or two of the bands match the victim's bands. These findings reveal that the two types of DNA were not completely separated and that the DNA is mixed. (See NRCII, *supra*, at p. 129.)

The perpetrator/victim DNA mixture necessarily contains two alleles from the perpetrator and two alleles from the victim. Accordingly, autorads of mixtures generally reveal four separate and distinguishable bands, one for each of the four alleles in the mixture. The two victim's bands in the mixture can be discerned by comparing the mixed sample to the victim samples on the same autorad. The two bands that match the victim's bands can logically be subtracted out of the mixture to leave the two remaining bands as the perpetrator's. (NRCII, *supra*, at p. 129 ["In many cases, one of the

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55 "The differential extraction procedure involves preferentially breaking open the female epithelial cells with an incubation in a SDS/proteinase K mixture. Sperm nuclei are subsequently lysed by treatment with a SDS/proteinase K/dithiothreitol (DTT) mixture. The DTT breaks down the protein disulfide bridges that make up sperm nuclear membranes [citation]. Differential extraction works because sperm nuclei are impervious to digestion without DTT." (Butler, Forensic DNA Typing (2001) at p. 32 (hereafter Butler).)

contributors -- for example, the victim -- is known, and the genetic profile of the unknown is readily inferred."].) Thus, in a four-band perpetrator/victim mixture, the mere locations of the four bands can provide adequate information for discerning the perpetrator's alleles. Figure 8 shows two examples of two-band perpetrator's samples, four-band mixtures, and the subtraction out of the victim's bands from the mixtures.

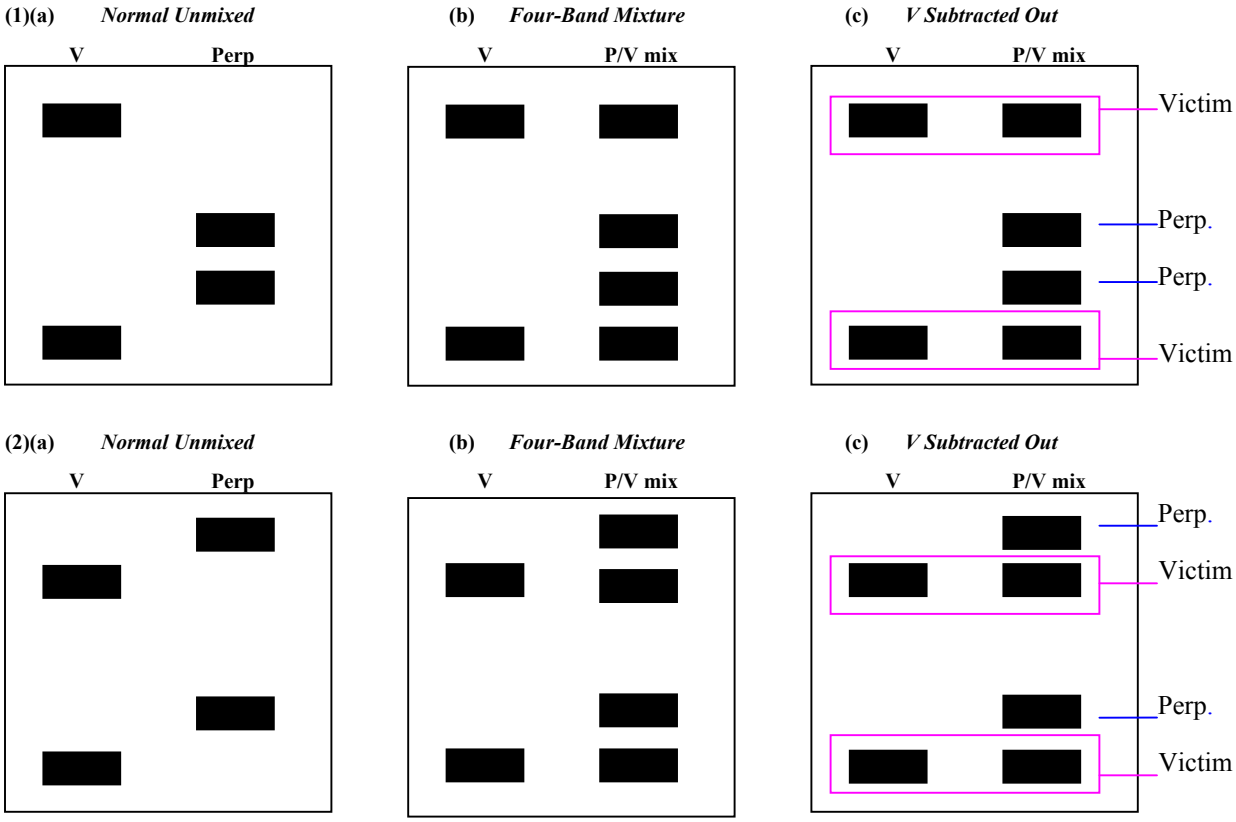

Fig. 8. ***Two Examples of Four-Band Perpetrator/Victim Mixtures and Subtraction Out.***
NOTE: In (1)(c) and (2)(c), the victim's bands in a four-band mixture can be identified and subtracted out of the mixture to leave the perpetrator's bands. In (1)(c), the first and fourth bands in the mixture belong to the victim and can be subtracted out. In (2)(c), the second and fourth bands in the mixture belong to the victim and can be subtracted out. In both examples, the remaining two bands belong to the perpetrator. P/V mix = perpetrator/victim mixture fraction of evidentiary sample.

When the two victim's bands are subtracted out, the two remaining bands then represent the perpetrator's profile (genotype) at that locus. The two bands will later be compared to the defendant's bands, and, if a match is found, used in the statistical calculations to determine the perpetrator's overall profile frequency.

A more complicated situation arises, however, when a mixture contains only two or three bands, rather than four. Because every person possesses two alleles at each

locus, the presence of fewer than four bands in the mixture means one or more of the bands is probably *masked* by (superimposed on or coalesced with) another band. In these situations, the victim's alleles cannot simply be subtracted out to reveal both of the perpetrator's alleles; the superimposed bands may conceal the perpetrator's genotype.[56] (NRCI, *supra*, at p. 66 [two-band mixture: "if the sperm fraction shows a genotype that matches that of the victim, one cannot conclude that this represents the genotype of the perpetrator, inasmuch as it could be due to residual vaginal epithelial cells"].) (Fig. 9.)

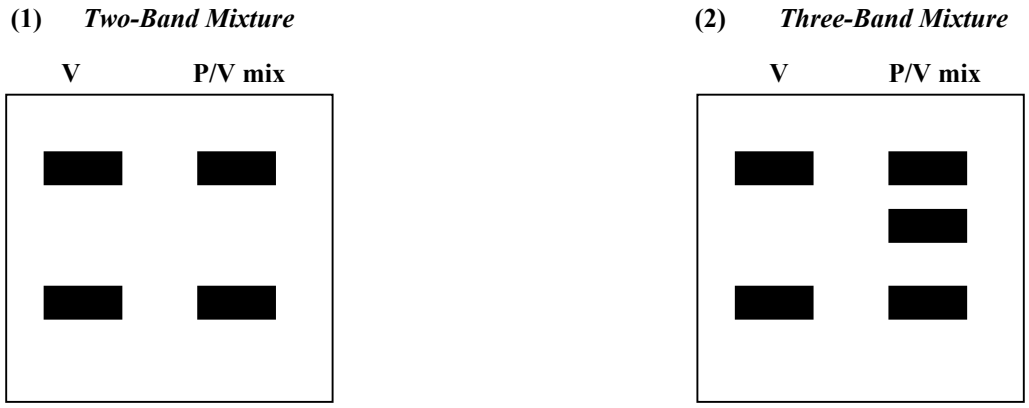

Fig. 9. ***Indistinguishable Two- and Three-Band Mixtures.***
NOTE: Four alleles are now contained in only two or three bands in the P/V mix.
The perpetrator's bands are no longer discernible by subtracting out the victim's bands.

In a two-band mixture, as in this case and as in figure 9(1), the perpetrator's masked profile may be one of three profiles or genotypes, as established by uncontroverted testimony, *post*. These three perpetrator profiles are shown schematically in figure 10: (1) heterozygous, sharing both bands with the victim (there are two alleles within each band), (2) homozygous for one allele, sharing one band (there are three alleles within one band and one allele within the other), or (3) homozygous for the other allele, sharing one band (there is one allele within one band and three within the other). (See NRCII, *supra*, at p. 162 [a two- or three-band mixture may mean that one of the contributors produced a single band.])

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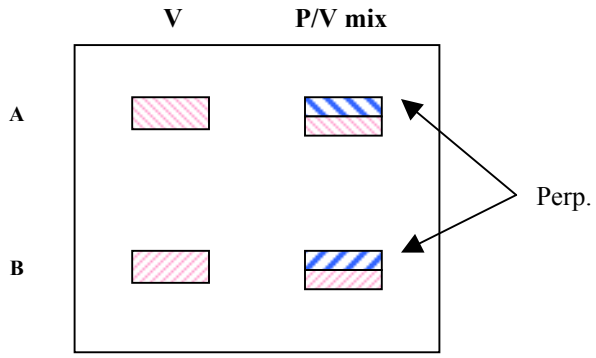
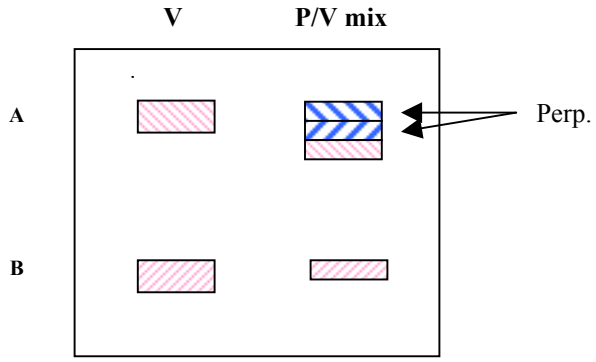
56 For the sake of simplicity, we ignore band intensity for the moment.

(1) Perpetrator is *heterozygous* (AB):



(2) Perpetrator is *homozygous* for top band (AA):



(3) Perpetrator is *homozygous* for bottom band (BB):

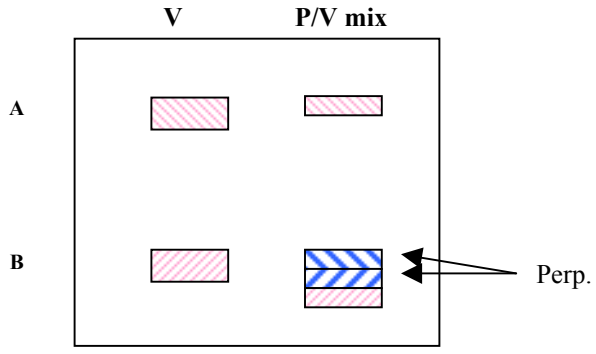


Fig. 10. ***Three Possible Perpetrator Profiles within Two-Band Mixture.***
NOTE: = V's 1st allele; = V's 2d allele; = Perp's 1st allele; = Perp's 2d allele. Each allele or group of alleles constitutes a single band. All bands should be presumed to be approximately the same size/intensity despite their schematic appearance.

In the present case, two of the three autorads (D1 and D4) contained four bands in the perpetrator's sample (as in fig. 8(1)(b) and (c), *ante*), two of which matched the victim's bands, demonstrating that the perpetrator's and victim's DNA were mixed. (Figs. 11 & 12, lanes 10 & 11.) The DNA was therefore mixed on *all* autorads. (Although a mixture may be *revealed* by only one or some autorads, it *exists* identically on all of them. (NRCII, *supra*, at p. 162 ["It is also possible that there are only two bands, but other loci indicate that the stain is mixed"].)) Autorads D1 and D4 were four-band mixtures from which the victim's bands could be subtracted out to reveal the perpetrator's bands. (Figs. 11 & 12.)

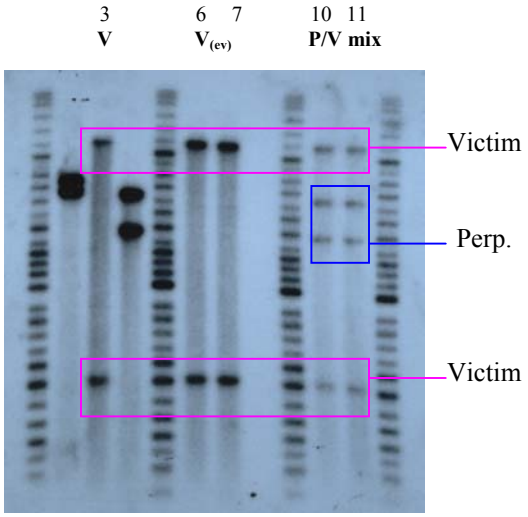


Fig. 11. ***D1 Autorad.***

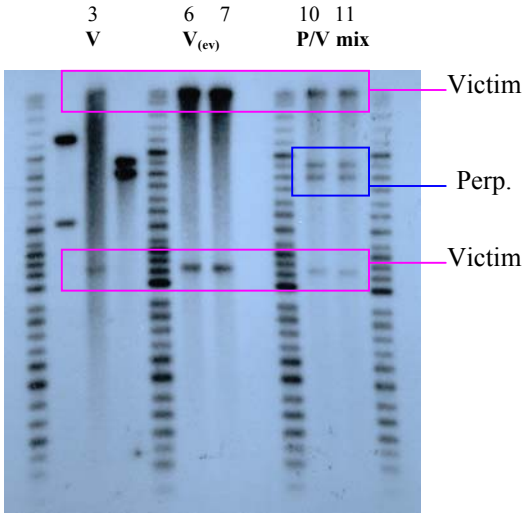


Fig. 12. ***D4 Autorad.***

NOTE: Four-band mixture was present in lanes 10 and 11 of both autorads. The victim's bands in the mixture were discernible by comparison to the victim's known bands in lanes 3, 6, and 7. Once the victim's bands were subtracted out, the perpetrator's bands were also discernible.

The D2 autorad, however, presented the more complicated two-band mixture in which both bands were shared by the heterozygous victim, as in figure 9(1), *ante*. (Fig. 13.) The mixture still contained four alleles, but they now existed in some combination within only two bands.

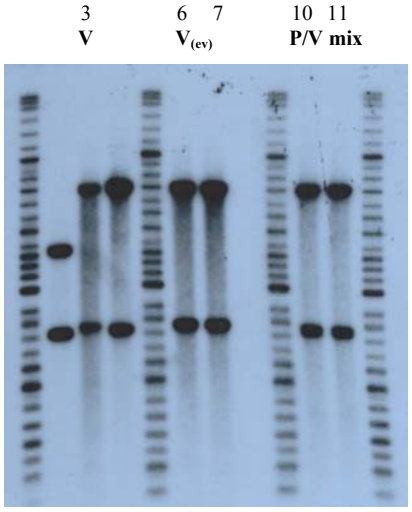


Fig. 13. ***D2 Autorad.***
NOTE: Two-band mixture in lanes 10 and 11.
The victim's bands could not be subtracted out.

The FBI scientists determined that the perpetrator was *heterozygous* at the D2 locus, as in figure 10(1), *ante*. In other words, the FBI concluded that the two-band perpetrator/victim mixture on the D2 autorad should be interpreted as representing two heterozygous individuals (AB and AB), in two sets of superimposed bands. The FBI then multiplied the frequency of this heterozygous genotype by the other two genotype frequencies (from the D1 and D4 autorads) to obtain the perpetrator's overall profile frequency.

At the *Kelly* hearing, the prosecution presented evidence of two procedures for discerning the perpetrator's heterozygous D2 genotype from the mixture. These two procedures refer to (1) defendant's profile and (2) relative band intensities. We summarize the rationale of these procedures as follows:

(1) **Defendant's Profile --**

Reference to *defendant's* profile explained any ambiguity in the perpetrator's profile because:

> *defendant* was heterozygous (AB), and his bands matched the two bands in the perpetrator/victim mixture.

(2) **Relative Band Intensities --**

Reference to relative band intensities established that the two bands in the perpetrator/victim mixture each contained the *same amount of DNA* -- one contained two A alleles and the other contained two B alleles --because:

(a) the intensities of the two bands in the D2 mixture were *equal*; therefore the four alleles in the mixture must be divided equally in sets of two superimposed alleles (AA and BB) (as in fig. 10(1), *ante*);

(b) the intensities of the bands in the two-band D2 mixture were *twice as strong* as the intensities of the bands in the four-band D1 and D4 mixtures; therefore the D2 bands must contain twice as much DNA as the D1 and D4 bands, which were known to contain one allele each.

We address these two procedures in turn, examining the evidence supporting and refuting the propriety of each.

B. REFERENCE TO DEFENDANT'S PROFILE

The People assert that reference to defendant's genetic profile provided guidance in the interpretation of the D2 autorad's perpetrator/victim mixture. In other words, because defendant was heterozygous at that locus, *the perpetrator could be assumed to be heterozygous also*.

1. Prosecution Testimony

a. Sensabaugh

George Sensabaugh, Jr., professor in the School of Public Health at the University of California, Berkeley, explained on cross examination that "the most straightforward inference [from the two-band D2 mixture] is that in this case both individuals share

indistinguishable typing at this particular locus [i.e., both individuals are heterozygous]." Defense counsel then asked Sensabaugh whether he was aware of the method in which all possible genotype frequencies in a mixture are added together.[57] Sensabaugh responded:

> "[SENSABAUGH:] That would be -- that is appropriate in some situations. If one has a four-band pattern and in making comparisons of the four-band pattern one cannot exclude the possibility of various combinations, then all the non-excluded frequencies of all the non-excluded combinations are put together."

He then explained that the National Research Council's recommendation (in NRCI) to add the frequencies for mixtures is "a bit naïve to anyone who has actual forensic practice," notwithstanding the NRCI report, on which Sensabaugh was a signatory. He agreed, however, that the two-band mixture on the D2 autorad could represent a mixture of the heterozygous victim and a homozygous perpetrator who shared one band with the victim (see fig. 10(2) & (3), *ante*), and that the frequency would be affected if this possibility were taken into account as NRCI recommends. Nevertheless, Sensabaugh stated:

> "[W]hen the presentation is as straightforward as this is[,] those numbers are not, in my experience, usually calculated. It is usually in more complex mixture cases that -- where there may be known and unknown individuals mixed together that one engages in that exercise."

On redirect, the prosecutor asked Sensabaugh if he knew of any fact in this case that would make it more likely that the victim and defendant would share the same alleles. Sensabaugh responded that it was his understanding that they were half siblings, and, in light of this fact, the bands were where Sensabaugh would expect to see them if

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57 Because two-band mixtures present three possibilities, some authorities, including NRCI, recommend that the statistical calculations account for all three genotypes by adding their frequencies. (NRCI, *supra*, at pp. 58-59.)

the mixture contained the victim's and defendant's DNA. He thought the results were "interpretable."

b. Chakraborty

Ranajit Chakraborty, professor of population genetics, biometry, and international health at the University of Texas Health Science Center, testified that the D2 autorad revealed that the profiles of the victim and defendant were very similar, and, "as a consequence," the profiles of the victim and the perpetrator/victim mixture were also very similar.[58] Chakraborty stated that the half-sibling relationship of defendant and victim might explain that occurrence. Chakraborty's calculations indicated that the chance of two shared alleles is five times greater in half siblings than in unrelated persons. Chakraborty explained that this calculation did not require any assumption about the source of the evidentiary sample because the D2 autorad showed defendant's profile matched the perpetrator's profile, and the victim's profile matched the victim's fraction of the evidentiary sample. It is very unusual to observe a defendant's profile so similar to the victim's profile, but given the fact that they were half siblings in this case, the similarity was expected.

On cross-examination, Chakraborty stated there is no way of telling whether the two bands in the D2 mixture came from the perpetrator or the victim. But the autorad did not exclude defendant as a possible perpetrator. Chakraborty did not disagree with the NRCI recommendation to add all possible combinations for mixed samples.

Chakraborty did not know of any laboratories that excluded autorads when the victim and defendant's profiles matched; he had heard of the concept, but did not

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58 Chakraborty said: "And as a consequence the evidentiary samples, female fraction and male fraction DNA profiles were also very similar."

understand its logic. He agreed that excluding the D2 autorad would change the frequency of the profile "substantially."

c. Adams

Dwight Adams, who oversaw the FBI's DNA analysis in this case, testified that he did not see sufficient reason to exclude the D2 autorad from the calculations,[59] although he agreed that excluding an autorad can make a significant difference in the resulting frequency. He stated that it is impossible to determine the source of a band on an autorad. He was not aware of NRCI's recommendation to add all possible profile frequencies in the case of a mixture such as the one on the D2 autorad, and he did not believe NRCI did in fact suggest such an approach. But he explained that when the mixture contains only two bands, it is impossible to discern whether the mixture consists of two homozygous people; it is impossible to tell which bands are contributed by the victim and which by the perpetrator.

d. Conneally

On direct examination, Patrick Michael Conneally, professor of medical genetics at Indiana University Medical Center, explained that the D2 autorad should not be excluded from the calculation because half siblings would be expected to share a band more often. He stated:

> "[CONNEALLY:] … The defendant and the victim shared a band in common there. And that's always a possibility to share a band. And, in fact, if the defendant were the perpetrator would he not be -- I understand that they were related, so this would not be unusual at all. Half siblings would be expected to share one band out of six. So, I do believe that there was no reason to -- there is no reason to exclude the results of D2S44."

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[59] His reasons for this conclusion fall under the second procedure, Reference to Relative Band Intensities, *post.*

On cross-examination, Conneally stated it is impossible to tell from a band on an autorad whether the band was contributed by the victim, the perpetrator, or both, and in what quantities.

2. Defense Testimony

a. Shields

William Shields, professor of biology at the State University of New York, testified that in a two-band mixture there is no way to determine whether the bands were contributed by the victim or by someone else. When the victim's fraction and the perpetrator's fraction of the evidentiary sample both contain the same bands (have the same profile), Shields believed the autorad should be excluded from the calculation. It is possible that the perpetrator is either homozygous or heterozygous. (See fig. 10, *ante*.) If, for example, the perpetrator is homozygous and the defendant is heterozygous, the defendant is actually excluded as a potential perpetrator (i.e., he is exonerated). There is no way to know what the mixture means. For these reasons, when there is even one shared band between the victim and the defendant, the autorad should be excluded entirely.

b. Zabell

Sandy Lew Zabell, professor of mathematics and statistics at Northwestern University, explained that a mixture containing only two bands is a very different situation than a mixture containing four bands. When there are four bands, the victim's bands can be subtracted out, leaving the two bands that presumably belong to the perpetrator. But when the mixture contains only two bands, there are several possible perpetrator profiles represented by those two bands. First, the perpetrator could be homozygous for one band, or appear to be homozygous for that band because his two bands are so close together as to coalesce into one band on the autorad. (See fig. 10(2), *ante*.) Second, the perpetrator could be homozygous, or apparently homozygous, for the other band. (See fig. 10(3), *ante*.) Third, the perpetrator could be heterozygous for the

same two bands as the victim. (See fig. 10(1), *ante*.) Fourth, the perpetrator could be heterozygous for one of the same bands as the victim, but his second band "ran off" the end of the gel and is not visible on the autorad. Fifth, the perpetrator could be heterozygous for the other band, but his second band ran off the end of the gel and is not visible on the autorad. Sixth, both of the perpetrator's bands, whether homozygous or heterozygous, could have run off the gel and are not visible on the autorad. Ignoring the unlikely cases of run-off, there are three possible profiles for the perpetrator represented by a two-band mixture.

Zabell noted that the FBI's calculation, however, took into account only the single possibility that the perpetrator was heterozygous, sharing both bands with the heterozygous victim. (See fig. 10(1), *ante*.) Zabell explained that when calculating the match probability -- the chance that a randomly chosen person will match the profile -- it is incorrect to account for only one possibility as the FBI did in this case. If only the defendant's profile is used to calculate the perpetrator's profile, an assumption is being made that the defendant is the perpetrator.

Zabell testified that the proper procedure is to add up the frequencies for all the possible explanations for the banding pattern to determine how frequently a match of any possible kind could arise. This procedure significantly increases the likelihood of a random match in this case. When the frequency in this case was recalculated (using the updated H4 database) to take into account the three possible profiles (adding their frequencies together, but otherwise using the FBI's method), the frequency of the perpetrator's overall profile became 1 out of 20,000, instead of 1 out of 894,000.[60]

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60 For Pizarro's trial, the 1-in-250,000 frequency was calculated from the H2 Hispanic database. At the time of the *Kelly* hearing on remand, an expanded H4 Hispanic database had been developed. The two frequencies to which Zabell referred were calculated using the H4 database.

Zabell stated that the existence of mixtures in forensic samples is not an uncommon or new phenomenon. Scientists expect that taking into account the extra possibilities presented by a mixture can cause the profile to become substantially more common. NRCI plainly stated that all possible genotype frequencies should be added together in the case of mixtures. In the two-band mixture situation, some labs exclude the autorad from the frequency calculation; others add up the possible frequencies. Zabell knew of "no one who would say that when more than one profile could match a pattern you should not add up the frequencies for the different profiles." He believed that, when more than one profile could be declared to match the evidence sample's profile, there was "essentially unanimity" among the scientific community that "those other frequencies must be taken into account in the calculations." The "clear con[s]ensus" was that the calculations should be performed in this manner for the D2 autorad in this case.

Zabell explained that to disagree with this principle one would have to argue that, if defendant were homozygous, he would be excluded as a possible perpetrator. To avoid such a conclusion, the other two possible perpetrator profiles must be included in the calculation to account for all possible matches with the profile.

On cross-examination, Zabell stated that, although the likelihood of a three-locus match is "in general … a quite rare event[, w]e're in a special case here. And that's the single biggest concern I would have for the calculations. We do have a mixture and that obviously affects the frequency."

Later, the following colloquy took place:

> "[PROSECUTOR:] I understand that you have to assume the defendant is the perpetrator in order for them to calculate the significance as they did [in this case].
>
> "[ZABELL:] Well, strictly speaking what the significant calculation does is it doesn't refer to -- it doesn't refer to the defendant or suspect at all. They say[, ']suppose we choose someone at random, what's the chance that

it would match the evidence profile[?'] So the calculations [*sic*] in certain instances does not refer at all to the suspect.

"[PROSECUTOR:] There's nothing inconsistent between the defendant's profile and the questioned sample, is there?

"[ZABELL:] That's right. When you use the statistical match rule, the defendant's profile [is] declared to match the [evidentiary] bands, yes.

"[PROSECUTOR:] So you are not calling into question the FBI's call of a match in this case?

"[ZABELL:] No."

In regard to the mixture on the D2 autorad, the following exchange occurred:

"[ZABELL:] … I think the FBI is wrong. [¶] … [¶] If we have a [two-band] mixture then we have to do the calculation for all three potential profiles. The perpetrator is heterozygous for the top band A and the bottom band B, homozygous for band A or homozygous for band B. All those three possibilities would be taken into account because that is precisely because of [the mixture revealed by the] D1 and D4 [autorads].

"[PROSECUTOR:] What about the relationship between Mr. Pizarro and the victim in this case? What effect does that have on your interpretation of this autorad?

"[ZABELL:] None because you remember the way the calculation is phrased. I mean I did see Dr. Chakraborty made some reference to that, which puzzled me the way the calculations go. You were saying[, ']here's the evidence sample, the evidence profile, and we have declared a match with the suspect.[']

"Now, the question is[, ']given the evidence profile, suppose we went out and picked an unrelated person.['] That's often investigated in the summary of the calculation. [']Suppose we chose someone who's unrelated, what would be the chance that we would get a matching profile?['] … The fact that the suspect is or isn't related is really irrelevant to that calculation.

"[PROSECUTOR:] But the fact is this suspect is related to the victim in this case, at least in hindsight [that fact] must affect the way you -- affect the autorad.

"[ZABELL:] Guess I don't see that, Counselor. I mean, it's true that because Mr. Pizarro is related to the victim that he would have a higher chance of matching up at any of the loci at one of the bands.

"[PROSECUTOR:] Which is what happened here.

"[ZABELL:] But, again, I mean, the calculation doesn't -- I mean, the calculation really does not refer to that. The calculation says, 'Here's the evidence sample.' The calculation in effect says, 'We don't have a suspect. Here's the evidence sample, suppose I chose someone at random, what's the chance they would match up?' Right. There is nothing in that sentence that refers to the suspect."

c. Bakken

Aimee Hayes Bakken, associate professor of zoology at the University of Washington, stated that in the case of the two-band D2 mixture there was no way to tell whether the perpetrator was heterozygous, homozygous for the top band, or homozygous for the bottom band. (See fig. 10, *ante*.)

d. Muller

Lawrence Muller, associate professor of population genetics at the University of California at Irvine, explained: "The genetic constitution of the perpetrator [in the D2 mixture] is somewhat ambiguous …. It's going to have DNA from the victim … and [DNA] from the perpetrator. But the perpetrator can have a variety of genetic constitutions …." The perpetrator's profile could be represented by just the top band, just the bottom band, or both bands. (See fig. 10, *ante*.)

"All those alternative genetic states for the perpetrator produce an evidence sample that's consistent with a match. We can't distinguish whether the perpetrator is [the first, second, or third possibility]."

People who possess any of these three possible profiles could not be excluded from the pool of possible perpetrators.

"Now, it happens that Mr. Pizarro only has the [heterozygous] combination. Statistically, we have to take into account that if he [were homozygous for one band], we couldn't have excluded him. Had he [been homozygous for the other band], we couldn't have excluded him. So, all those combinations need to be taken into account because of the particular

> results in this case, which are that the DNA from the victim and suspect [*sic*] have not been completely separated."[61]

Muller stated that, if only one of the possible profiles were considered, the result would grossly underestimate the number of people in the population who might possess the perpetrator's profile. Incorporating all possible profiles into the calculation would make the profile "significantly more common." Further justification for including all possible profiles is the fact that, if the perpetrator were indeed homozygous for either one of the bands, Pizarro would be completely excluded as a possible perpetrator. Muller stated, "We have the possibility that the evidence may, in fact, be inconsistent with the conclusion that [the perpetrator's and defendant's profiles] match. So, the information from this particular locus [the D2 autorad] is not interpretable as a definitive match."

Muller noted that Chakraborty testified that he agreed with NRCI's recommendation to add all possible profiles in a mixture. Muller interpreted Chakraborty's testimony as follows:

> "[MULLER:] Generally, what he said is, given that the suspect and victim have a genetic relationship, they can share alleles in common. The finding of the evidence of completely overlapping bands for the victim and the suspect is five times more likely in this case. Therefore, he's not surprised at all by seeing this pattern. To my mind, it means he thinks he understands the nature of that pattern.
>
> "[DEFENSE COUNSEL:] Another way of saying that is, he's assuming, because Mr. Pizarro, the defendant, has a two-banded pattern that it must be him in [the evidence sample]. He's only going to count the possibility that it's Mr. Pizarro or somebody else with two bands, right? I mean, he's using information about the suspect to make inferences about

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61 Defense witness Muller's mistaken use of "suspect" rather than "perpetrator" demonstrates the ease with which such an error can be made. Further proof of the potential for inadvertent misuse is found in this court's footnote 12 in the recent case of *People v. Brown, supra,* 91 Cal.App.4th at page 630. There, as Pizzaro's appellate counsel noted at oral argument in this case, we also mistakenly used the term "suspect" for "perpetrator."

the pattern in the evidence, which is akin to assuming that the suspect's DNA must be in the evidence sample?

"[MULLER:] But, of course, that's exactly why we do a DNA analysis at trials, to determine [to] what extent that's a reasonable conclusion.

"[DEFENSE COUNSEL:] And it's fair to say that when you're calculating the significance of a match, that's the exact opposite of what your [*sic*] supposed to do? You're trying to find out how many people other than your defendant could fit the pattern?

"[MULLER:] Right. The presumption is if they think there's a match, if we were to choose people at random, what's the likelihood that people chosen at random would match in the fashion seen here? And the fashion of the match we've seen here, as I explained earlier for D2S44, is somewhat ambiguous, because there's [*sic*] several different genetic patterns the suspect could have and be declared a match here.

"That level of ambiguity has to be taken into [account.] … Mr. Pizarro's particular genetic relationship to the victim [is] completely irrelevant for assessing that level of ambiguity, because, as we said earlier, it presumes his DNA is in the evidence [sample], which, of course, is the whole focus of this study."

Muller also commented on Sensabaugh's testimony, noting that Sensabaugh testified he was a signatory on the NRCI report that recommended adding frequencies in such a case and testified that frequencies should be added together when mixed samples contain a known and unknown source. Muller commented that this is "precisely the kind of situation we have here" -- a two-person mixture in which one person, the victim, is known, and the other, the perpetrator, is unknown.

3. Analysis

As this testimony demonstrates, the perpetrator's genotype in the D2 perpetrator/victim mixture was uncertain -- it could have been one of three possible genotypes. Some witnesses explained that the perpetrator's genotype could be discerned by reference to *defendant's* genotype. Other witnesses testified that the perpetrator's genotype could not be discerned and therefore all three possible genotypes should be accounted for to decrease the rarity of the profile. One witness maintained that evidence

of the undiscernible D2 genotype should be excluded altogether because of its potential to exonerate defendant. As we will explain, we reject all theories but the last.[62]

The defense witnesses explained extensively and unequivocally that the two-band mixture on the D2 autorad represented three possible profiles and that the perpetrator's true profile could not be discerned from the autorad bands. The perpetrator could be heterozygous or homozygous. Shields recommended that autorads with mixtures such as this be entirely excluded from the statistical calculations, in part because two of the three possible perpetrator profiles would actually exclude defendant as a suspect. Zabell and Muller explained that the proper procedure in such a case is to take into account all three possible profiles by adding their frequencies, thereby increasing the commonness of the profile and the likelihood of a random match in the population.

The prosecution witnesses did not contradict the defense theory that the perpetrator could have been homozygous at the D2 locus. Sensabaugh agreed that the two-band mixture on the D2 autorad could represent a homozygous perpetrator and that

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62 We are aware NRCII has modified NRCI's position to add together the frequencies of all possible genotypes, now suggesting that this method is "hard to justify, because it does not make use of some of the information available, namely, the genotype of the suspect." (NRCII, *supra*, at pp. 129-130.) NRCII recommends using a likelihood ratio that takes into account the defendant's profile because likelihood ratios are especially useful "provided that prior odds are available on the hypothesis that the two DNA profiles have the same source. (Prior odds are the odds that the two DNA samples came from the same person on the basis of [*evidence*] *other than the DNA*.)" (*Id.* at pp. 130-131, italics added.) Bayes's theorem, invoked when the prior odds are multiplied by the likelihood ratio (*ibid.*), is used regularly in paternity cases, but rarely in criminal cases (*id*. at pp. 131-132, 200). As NRCII explains, "The main difficulty is probably an unwillingness of the courts to ask juries to assign odds on the basis of non-DNA evidence." (*Id.* at p. 132.)

We too see great difficulties with this approach; nevertheless, it was not taken in this case. Here, the FBI calculated the *profile frequency* (or *random match probability*), not the likelihood ratio and prior odds; thus there was no occasion for consideration of defendant's profile in the calculation.

consideration of such a possibility would affect the frequency calculation. Chakraborty stated it was impossible to discern whether the two bands came from the victim or the perpetrator and he did not disagree with the recommendation to add all possible profiles for mixed samples. Adams testified that it is impossible to determine the source of a band, and in a two-band mixture it is impossible to determine whether the mixture contains a homozygous individual and whether the bands come from the victim or the perpetrator. Conneally also agreed it is impossible to discern who contributed a band in a mixture, and in what quantities.

Prosecution evidence that could be portrayed as contradictory on this specific issue was consistently and expressly based on the assumption that the DNA mixture contained *defendant's* DNA rather than the *perpetrator's* DNA. Sensabaugh stated that "the most straightforward inference" is that both people in the mixture were heterozygous. He explained that NRCI's recommendation to add all possibilities is naïve and that such an approach is usually limited to cases in which there is a mixture of "known and unknown individuals." As defense witness Muller noted, Sensabaugh's description precisely fit the situation in this case: the victim was known and the perpetrator was unknown. Sensabaugh deemed the results of the D2 autorad "interpretable" because the autorad displayed the results he would expect to see if the mixture contained the victim's and *defendant's* DNA. Chakraborty explained that the perpetrator and victim profiles were similar because the *defendant* and victim profiles were similar. Conneally said the results would not be unusual at all if *defendant* was the perpetrator.

But the assumption that defendant was the perpetrator was improper and the FBI therefore should not have relied on defendant's genotype to "prove" the perpetrator's genotype, which was a preliminary fact required to render the match evidence and the statistical evidence relevant under section 403. Specifically, defendant's heterozygous D2 genotype was not relevant to prove defendant matched the perpetrator unless it was

established that the *perpetrator* possessed a heterozygous D2 genotype. And, the profile frequency (calculated as including a heterozygous D2 genotype) was not relevant to prove the rarity of the perpetrator's profile, unless it was established that the *perpetrator's profile* included the heterozygous D2 genotype. These preliminary fact requirements can be restated in the context of the physical profile analogy as follows: the defendant's black hair is not relevant to prove the defendant looks like the perpetrator unless it is established that the *perpetrator* has black hair. And, the profile frequency (calculated as including black hair) is not relevant to prove the rarity of the perpetrator's profile unless it is established that the *perpetrator's profile* includes black hair.[63]

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63 Again, the People's assumption that defendant was the perpetrator persists on appeal. The People's brief goes so far as to remind us the perpetrator and defendant were the *same person*: "it is clear that there are two sets of two bands [in the D2 mixture]: one set for the victim, the other set for appellant (the perpetrator)." The brief concludes that because the defendant was heterozygous, there was no realistic probability of a homozygous perpetrator because "[n]either appellant nor the evidence suggests this possibility."

We note that various commentators agree that the perpetrator's genetic profile must be ascertained independently of the defendant's profile. DNA bands "must be identified separately and independently in [the perpetrator's and defendant's] samples. It is not permissible to decide which features of [a perpetrator's] sample to count and which to discount on the basis of a comparison with a [defendant's] sample, because this can bias one's interpretation." (NRCI, *supra*, at p. 53.) "In all cases, each lane must be evaluated independently -- the presence of a band in one lane must not influence whether a questionable signal in another lane should be identified as a band." (OTA, *supra*, at p. 65.) Indeed, "[c]ommentators have noted a disturbing tendency for forensic analysts to resolve ambiguities in DNA patterns in a manner consistent with the expected result. The analyst may, for example, infer that a discrepancy between two DNA profiles on one autorad *must* be an artifact (rather than a true genetic difference) because there is a match on the other autorads or, worse yet, because other evidence in the case suggests the two profiles have a common source. Professor Eric Lander has condemned this kind of bootstrap interpretation in forensics because 'one runs the risk of discounting precisely those differences that would exonerate an innocent defendant.' An analyst who too readily dismisses discrepancies in a DNA test that do not fit with other evidence can mistakenly conclude that weak, equivocal evidence is quite powerful, and thereby mislead the trier of fact." (Thompson, *Evaluating the Admissibility of New Genetic*

We conclude that, if the perpetrator's D2 genotype was discerned solely by reliance on defendant's D2 genotype, the perpetrator's genotype was discerned by an improper procedure. Furthermore, that genotype served as inadequate foundation for the relevance of the DNA evidence. (§ 403.)[64]

We digress to discuss the suggestion by defendant and several witnesses that because the perpetrator's genotype cannot be discerned, all possible genotypes should have been accounted for. We recognize that this approach, once promoted by NRC, is an attempt to make the uncertain evidence less damaging to the defendant, but it is defeated by one simple yet critical fact: *the perpetrator's genotype has not been established*. When evidence is lacking on a certain fact such that the fact cannot be established, the situation does not justify consideration of *all possible alternatives* to that fact. Only the one fact is relevant. If, in our analogy, the eyewitness is uncertain about the perpetrator's hair color, but can narrow the color down to black, brown, or blond, should all three possibilities be taken into account? The logic supporting an affirmative answer states: all possible perpetrators have black, brown, or blond hair; the defendant has black hair; therefore, the defendant is a possible perpetrator. Although initially appealing, this logic ignores the fact that the perpetrator has only one hair color and thus only that one hair color is relevant to his profile; more importantly, it ignores the fact that if the perpetrator actually has brown or blond hair, the defendant simply *is not* the perpetrator. The correct logic requires a *choice* of these three possible syllogisms: (1) all possible perpetrators

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Identification Tests: Lessons From the "DNA War" (1993) 84 J. Crim. Law & Criminol. 22, 53-54, fns. omitted (hereafter Thompson).)

64 We disagree with the People that the Evidence Code issues are waived for failure to raise them in the post-hearing brief. We consider the lack of foundation and relevance that resulted from the D2 genotype error (which defense counsel carefully argued and briefed) inherent to that issue. Again, this issue is critical to the reliability of the DNA evidence.

have *black* hair; the defendant has black hair; therefore, the defendant is a possible perpetrator; (2) all possible perpetrators have *brown* hair; the defendant has black hair; therefore, the defendant is not the perpetrator; (3) all possible perpetrators have *blond* hair; the defendant has black hair; therefore, the defendant is not the perpetrator. It would defy the principles of evidence to allow the eyewitness to testify that the perpetrator has black, brown, or blond hair when there is no way of establishing which one hair color the perpetrator actually possesses. This testimony is neither relevant nor probative, but it *is* potentially damning because it draws the defendant into the pool of possible perpetrators when in reality it more likely excludes him -- two of the three possibilities *exonerate* him.

Similarly, only the perpetrator's one D2 genotype was relevant to his genetic profile. If the prosecution could not establish which genotype the perpetrator possessed at that locus, there was no relevant evidence to admit from that locus. But, as in the analogy, the most compelling reason for demanding proof of the perpetrator's genotype and for refusing to admit evidence of all three possible genotypes was that the other two possible genotypes were more than irrelevant -- they potentially proved defendant's *innocence*. Thus, the evidence that was admitted to incriminate defendant actually had a greater chance of exonerating him. If the perpetrator was not heterozygous (i.e., if he was either homozygous for the top band or homozygous for the bottom band), defendant did not match the perpetrator and he was *excluded* as a possible perpetrator. Only if the perpetrator was heterozygous did defendant match and become a possible perpetrator.

We turn now to the remaining procedure -- reference to relative band intensities -- presented by the prosecution as a method for discerning the perpetrator's D2 genotype from the perpetrator/victim mixture.

C. REFERENCE TO RELATIVE BAND INTENSITIES

The admissibility of the D2 autorad evidence hinged on the People's remaining argument that band-intensity analysis -- *the comparison of visually observable band intensities on the autorads* -- established that the perpetrator's D2 genotype was heterozygous.

1. Prosecution Testimony

a. Sensabaugh

Sensabaugh stated that heavier and broader bands are an indication of DNA quantity. When bands in a four-band mixture have different intensities, it may be possible to infer which two bands come from one person (i.e., the intensity of two of the four bands may match, and the intensity of the other two may match). But in the case of the D2 two-band mixture, the bands gave no clue which bands went together or whether they came from a male or female.

b. Chakraborty

Chakraborty stated generally that band intensity is affected by DNA quantity.

c. Adams

Adams did not believe there was sufficient reason to exclude the D2 autorad from the frequency calculation "based on the totality of the results." He explained, in reference to comparisons between the autorads, that relative band intensities can reveal information about DNA quantity. He explained that the other autorads clearly demonstrated there was a mixture of two people's DNA in the perpetrator's lanes because there were four bands of equal concentrations. Because the D2 mixture showed only two bands, "about double in strength" (compared to the bands in the four-band mixtures on the D1 and D4 autorads), he concluded that two people's alleles were present, "but at the same locations." The D2 mixture bands appeared twice as intense as the single-allele bands in the four-band mixtures on the D1 and D4 autorads and therefore they contained twice the DNA (two alleles each). (See fig. 14.)

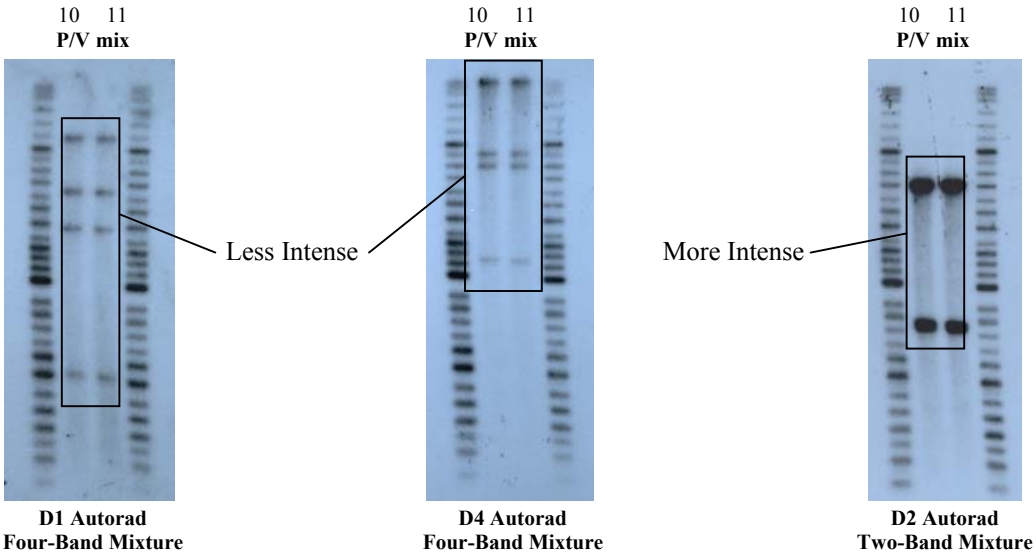

Fig. 14. ***Band Intensity Comparison Between Perpetrator/Victim Mixture Bands On Different Autorads.***

NOTE: Adams testified that the D2 P/V mix bands were twice as intense as the D1 and D4 P/V mix bands.

2. Defense Testimony

a. Zabell

Zabell stated that it is "very risky business" to make inferences regarding DNA quantity from band intensities, although a sharp difference in intensity may give a hint as to quantity.

b. Bakken

Bakken testified that it is an invalid argument to say that both the victim and perpetrator were heterozygous (see fig. 10(1), *ante*) based on relative band intensities. Experience teaches that this prediction cannot be made. Bakken explained there are many studies that instruct against making an assessment of DNA quantity based on band intensity. The argument that the perpetrator could not be homozygous (see fig. 10(2) & (3), *ante*) because the two D2 bands were of equal intensity was invalid and based on faulty reasoning. Bakken pointed to an example of the failure of this theory found on the D2 autorad itself. He noted that the two bands in the control lane were of differing intensities although it was known that each band contained the same amount of DNA

(because the two alleles were inherited in equal proportions from the mother and father). (Fig. 15, lane 2.)

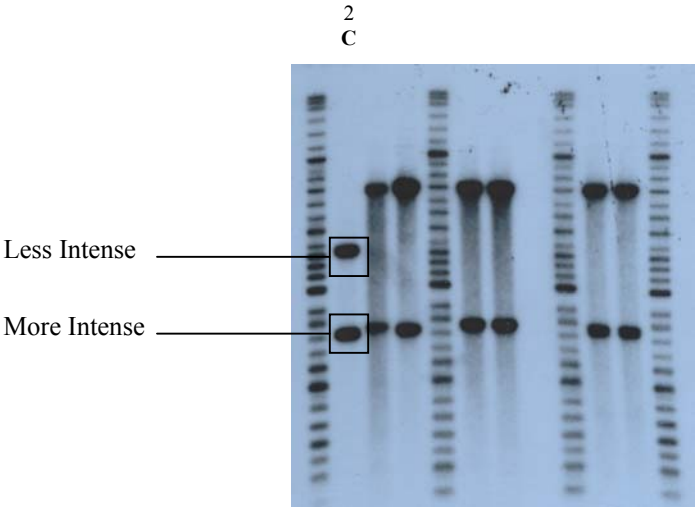

Fig. 15. ***D2 Autorad.***
NOTE: Bakken testified to an intensity disparity between bands within lane 2.

Another example, Bakken testified, could be seen in one of the four-band mixtures where there was a difference in the intensity between the two victim's bands, again known to contain the same amount of DNA. Bakken did not specify whether he was referring to the D1 or D4 autorad, but based on the distinctive pattern Bakken described it appears he was referring to the four-band mixture on the D4 autorad in which the top victim's band was significantly more intense than the bottom band. (Fig. 16, lanes 10 & 11.)

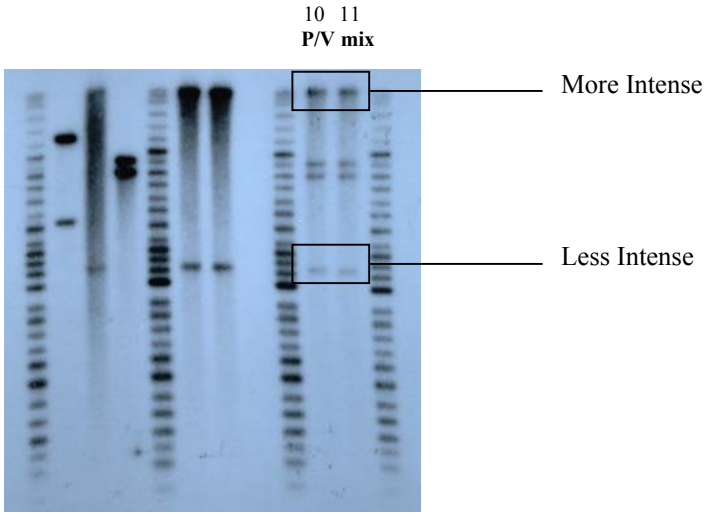

Fig. 16. ***D4 Autorad.***
NOTE: Bakken testified to an intensity disparity between the top and bottom band.

3. Analysis

a. Applicability of Kelly

Complicated scientific procedures must pass *Kelly* scrutiny before their results are submitted to the jury. Under *Kelly*'s first prong, the reliability of these procedures must be determined by the court, which asks: can this procedure *reliably be used* for this purpose? -- or more loosely, *should* this procedure be used for this purpose? Expert opinions responding to this question go to admissibility, not credibility. Such expert opinions include criticisms of the procedure as subjective, inconsistent, irreproducible, and so on. While *Kelly*'s first prong considers expert opinions regarding the procedure itself, including its theory, the third prong considers expert opinions regarding proper *use* of the procedure. Both prongs are part of *Kelly*'s admissibility screening. (*People v. Kelly, supra,* 17 Cal.3d at pp. 30-32; *People v. Venegas, supra*, 18 Cal.4th at pp. 78-81.)

The *Kelly* test is required because sophisticated scientific procedures and their results are not only incomprehensible but also irresistibly impressive to jurors. *Venegas* stressed that a procedure's complexity and incomprehensibility are key to the *Kelly* requirement, and that procedures "readily understandable by laypersons … need not be screened under *Kelly/Frye* before being admitted into evidence." (*People v. Venegas,*

supra, 18 Cal.4th at p. 83.) In *Venegas*, the Attorney General argued that "the procedures for determining the statistical significance of a match are immune from the requirements of *Kelly/Frye*" because the procedure "requires no more than well-established mathematical formulae such as those used to calculate the frequency of blood-group markers [citation]." (*Id.* at p. 82.) Disagreeing, the court explained that the statistical RFLP calculation is "much more complicated" than the blood marker calculation, and therefore requires *Kelly* scrutiny. (*Ibid.*)

> "*It is the very complexity of the issues* surrounding the propriety of the various recognized methods of computing RFLP probability frequencies *that draws them under the Kelly/Frye umbrella*. 'To ... leave it to jurors to assess the current scientific debate on statistical calculation as a matter of weight rather than admissibility, would stand *Kelly-Frye* on its head. We would be asking jurors to do what judges carefully avoid -- decide the substantive merits of competing scientific opinion as to the reliability of a novel method of scientific proof.... The result would be predictable. The jury would simply skip to the bottom line -- the only aspect of the process that is readily understood -- and look at the ultimate expression of match probability, without competently assessing the reliability of the process by which the laboratory got to the bottom line. This is an instance in which the method of scientific proof is so impenetrable that it would "' ... assume a posture of mystic infallibility in the eyes of a jury ....' [Citation.]" [Citation.]' [Citation.] The statistical calculation phase of RFLP analysis therefore requires *Kelly/Frye* screening of evidence on statistical probabilities of random matches at VNTR loci to assure that (1) the methodology used is generally accepted in the scientific community, and (2) the calculations in the particular case followed correct scientific procedures." (*People v. Venegas, supra*, 18 Cal.4th at pp. 83-84, italics added.)

Similarly, the propriety of band-intensity analysis is a complicated issue beyond the understanding of laypersons. It requires an understanding of genetic principles, knowledge and experience in molecular biology methods, particularly electrophoresis and autoradiography, and a trained eye for reading subtle variations on X-ray films. Lacking these, jurors are not equipped to competently consider opposing scientific opinions regarding whether the procedure is scientifically grounded, reliable, and generally

accepted in the scientific community. Yet, without the court's first-prong *Kelly* scrutiny, jurors are left to resolve questions such as these: Does superimposed DNA cause more intense bands? Does band intensity reliably and predictably correlate with DNA quantity? Can a simple visual examination of autorads provide a reliable evaluation of superimposed bands? Can the perpetrator's masked alleles reliably be discerned from the superimposed bands of a two-band mixture using band-intensity analysis? These are scientific questions to be considered and answered by the *scientific community*, not by jurors. And it is the *court's* responsibility to determine whether the scientific community accepts band-intensity analysis as a reliable procedure for discerning masked bands from a two-band mixture. In this way, the court discharges its first-prong duty to screen the scientific evidence and ensure that jurors hear only reliable and trustworthy scientific evidence.

Thus, we conclude band-intensity analysis requires independent *Kelly* scrutiny.

b. Kelly's First Prong

Our analysis under *Kelly*'s first prong proceeds as follows:

1) Has band-intensity analysis, *specifically*, already been deemed generally accepted by a published appellate opinion?

2) If so, under *Venegas*, the trial court could properly rely upon that opinion as precedent to satisfy the first prong.

3) If not, has another similar procedure -- which is *not materially distinct* from band-intensity analysis -- already been deemed generally accepted by a published appellate opinion?

4) If so, under *Venegas*, the trial court could properly rely upon that opinion as precedent to satisfy the first prong.

5) If not, band-intensity analysis has not been deemed generally accepted and the trial court was required to conduct a thorough hearing on that matter before admitting the D2 autorad evidence.

Accordingly, our first step is to determine whether band-intensity analysis, *specifically*, has already been deemed generally accepted. We look to the case law to see

whether an opinion has set a precedent, assuming precedent can be so established, for the general acceptance of band-intensity analysis. Because we find no opinion addressing band-intensity analysis specifically, we move to the next step to determine whether any opinions have already deemed similar procedures generally accepted, and whether those procedures are materially distinct from band-intensity analysis. (*People v. Venegas, supra,* 18 Cal.4th at p. 53.)

c. Already Accepted Procedure[65]

As *Venegas* concluded, *Axell* and *Barney* have established the general acceptance of the *basic* RFLP procedure (up to the statistical analysis). Thus, we must determine exactly what the relevant procedure described in those cases entails, and whether band-intensity analysis is effectively the same procedure or, instead, a materially distinct procedure.

Venegas explained that *Axell* established general acceptance of the basic RFLP steps of "generat[ing] autorad displays of bands indicating sizes of DNA fragments" and "compar[ing] those bands with one another and declar[ing] a match." (*People v. Venegas, supra*, 18 Cal.4th at pp. 76-77.) Similarly, *Venegas* noted that *Barney* established the general acceptance of "the basic procedures applied to compare and match bands depicted on the autorads." (*Venegas, supra*, at p. 79.) Thus, *Venegas* concluded that

> "for purposes of the trial of this case, the *Axell* and *Barney* opinions clearly established the general scientific acceptance, under *Kelly*'s first prong, of the basic RFLP methodology utilized by the FBI in (1) producing autorads with bands reflecting the base-pair sizes of forensic samples at particular DNA locations, and (2) comparing the bands in order to determine whether the samples matched at those locations." (*Ibid*.)

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65 We use the shorthand phrase "already accepted procedure" for convenience, but it is intended to imply that the procedure has already been *deemed generally accepted* by a published appellate opinion.

Axell itself explained that RFLP involves the step of

> "… autoradiography in which a film is developed on top of the nylon membrane, revealing the location of the DNA by bands on the X-ray film, called an autoradiogram or autorad.... [¶] The autorads must be interpreted and the bands produced by the migration of DNA in the gel in different lanes examined to ascertain if they match. Essentially the bands on the autorad from the victim's, suspect's, and crime scene evidence samples are 'eyeballed' to see if they match within a certain measurement…." (*People v. Axell, supra*, 235 Cal.App.3d at p. 846.)

In *Barney,* the court described the relevant steps as "*processing* of DNA from the suspect and the crime scene to produce X-ray films which indicate the lengths of the polymorphic fragments" and "examination of the films to determine whether any sets of fragments *match* …." (*People v. Barney, supra*, 8 Cal.App.4th at p. 806.) *Barney* explained these steps in more detail:

> "The last two substeps enable visualization of the lengths of the sample DNA fragments by producing X-ray films which show the distance the fragments traveled as a result of electrophoresis…. [¶] … [¶]
>
> "The location of a band on the X-ray film indicates the distance a fragment traveled as a result of electrophoresis, and hence the length of the fragment. The size-marker fragments also appear on the films, enabling measurement of the base-pair lengths of the sample fragments.
>
> "… The bands are arrayed in varying positions, which indicate the distance the selected DNA fragments traveled during electrophoresis and hence the various lengths of the fragments." (*Id*. at pp. 807-808.)

From *Venegas*, *Axell*, and *Barney*, we gather the following statements of accepted procedure for the relevant step of discerning bands and identifying alleles from autorads:

- production of "autorad *displays of bands*" that "*indicat[e] sizes of DNA fragments*" (*People v. Venegas, supra*, 18 Cal.4th at pp. 76-77, italics added);
- production of autorads to which "*basic procedures* … to compare and match *bands depicted on the autorads*" can be applied (*id.* at p. 79, italics added);

- production of "autorads with *bands reflecting the base-pair sizes*" of the DNA fragments (*ibid.*, italics added);

- production of autorads "*revealing the location of the DNA by bands*" (*People v. Axell, supra*, 235 Cal.App.3d at p. 846, italics added);

- production of autorads that "*indicate the lengths of the [DNA] fragments*" (*People v. Barney, supra*, 8 Cal.App.4th at p. 806, italics added);

- production of autorads that "*show the distance the fragments traveled*" and thus "*enable visualization of the lengths* of the sample DNA fragments" (*id.* at p. 807, italics added);

- production of autorads "with *bands arrayed* in varying positions, which *indicate[] the distance* the selected DNA fragments traveled … and hence *the various lengths of the fragments*" (*id.* at p. 808, italics added).

It is apparent that *Venegas*, *Axell*, and *Barney* address the typical cases in which the "basic" procedure is adequate -- the cases in which the autorads do indeed display and depict the perpetrator's bands, and do indicate, reflect, and reveal the locations/sizes of the perpetrator's alleles. In these typical cases, the locations of the perpetrator's bands are readily apparent and the sizes of the alleles can be determined from the size standards using "basic procedures" (*People v. Venegas, supra*, 18 Cal.4th at p. 79). Each band accounts for one allele and band locations reveal allele sizes. When the sample is not mixed, the perpetrator's one or two bands can readily be discerned because they are the only bands in the perpetrator's lane. And, even when the sample is mixed, there are usually four bands from which the perpetrator's two bands can readily be discerned, as on the D1 and D4 autorads. We believe these are the situations for which *Venegas*, *Axell*, and *Barney* serve as precedent for the general acceptance of discerning bands from autorads.

d. Material Scientific Distinction

In our opinion, band-intensity analysis constitutes a *materially distinct procedure* for discerning the perpetrator's alleles from an autorad, not merely an immaterial variation on the accepted basic autorad analysis approved by *Venegas*, *Axell*, and *Barney*. As the Supreme Court's decisions have established, materially distinct approaches to the same general purpose must independently pass *Kelly*'s first-prong scrutiny. In *Venegas*, the court deemed accepted the modified ceiling method for determining the statistical significance of a match. (*People v. Venegas, supra*, 18 Cal.4th at pp. 84-90.) Then, in *Soto*, the court separately examined and deemed accepted the unmodified product rule method for determining the statistical significance of a match. (*People v. Soto, supra,* 21 Cal.4th at pp. 518-519.) Both procedures interpret the RFLP data, and both are approaches to the same general purpose of calculating the profile frequency, but they address different theoretical concerns and can produce significantly different results. The court gave each procedure independent first-prong scrutiny.

The accepted autorad analysis addressed by *Venegas*, *Axell*, and *Barney* compares the locations of the perpetrator's *displayed* bands to the locations of the size standard bands to determine the sizes of the perpetrator's alleles. This procedure in fact involves very little subjectivity or interpretation. As *Axell* and *Barney* determined, "'interpretation of bands on an autorad is fairly straightforward and involves a minimal amount of subjective analysis.' [Citation.]" (*People v. Barney, supra*, 8 Cal.App.4th at pp. 813-814.) On the other hand, *visual* resolution of a superimposed mixture using band-intensity analysis is not a straightforward, objective comparison of band locations to determine allele sizes. Unlike the accepted autorad interpretation procedure of *Venegas*, *Axell*, and *Barney*, band-intensity analysis addresses the anomalous situation in which the alleles in a mixture are *superimposed* into only two or three bands; all the bands are *not* displayed or depicted, and those that are do not by their presence indicate, reflect, or reveal the size of the perpetrator's alleles. The locations of the bands are entirely

inadequate to permit determination of the perpetrator's alleles because there are too few bands to account for all four alleles, some of which are masked by others.[66] Band-intensity analysis is a subjective visual evaluation of subtle variations between bands to discern the alleles from a mixture that contains too few bands to yield readily discernible results. Furthermore, use of band-intensity analysis can significantly affect the resulting statistical calculation. We think *Venegas*, *Axell*, and *Barney* plainly do not speak to this methodology, and therefore do not encompass band-intensity analysis in the procedure they deem generally accepted. Band-intensity analysis of superimposed mixtures is a separate and distinct procedure for interpreting autorad bands and it must therefore independently "pass[] muster under the central first prong of the *Kelly* test." (*People v. Venegas, supra*, 18 Cal.4th at p. 81.) Because it has not, the evidence produced by that procedure -- the FBI's conclusion that the D2 autorad revealed a heterozygous perpetrator whose genotype matched defendant's -- was unreliable and inadmissible.[67]

e. Lack of Evidentiary Foundation

We express no opinion as to whether band-intensity analysis is in fact generally accepted by the scientific community,[68] but we note that the evidence in this case appears to present instances in which band intensity did not correlate with DNA quantity. At the *Kelly* hearing, although the prosecution presented testimony that relative band intensities can correlate with DNA quantity and that the intensities of the bands in the two-band D2 mixture appeared to be approximately twice as strong as those in the four-band mixtures, the defense presented strong evidence that band intensity does not reliably and

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66 This situation is very different than when the perpetrator's sample contains only *one* band but the sample is not mixed (i.e., the perpetrator has a homozygous genotype).

67 This is not to say that the FBI's conclusion would be unreliable and inadmissible if band-intensity analysis passes first-prong scrutiny.

68 We simply find an inadequate evidentiary showing here.

consistently correlate with DNA quantity. Bakken pointed to instances in this case in which two bands on the same autorad, expected to contain the same quantity of DNA, displayed significantly different intensities -- the control bands on the D2 autorad, and the victim's bands in the four-band mixture on the D4 autorad.[69] (See figs. 15 & 16, *ante*.) Figures 17 through 21 illustrate other possible inconsistencies.

(1) defendant's bands on the D2 autorad:

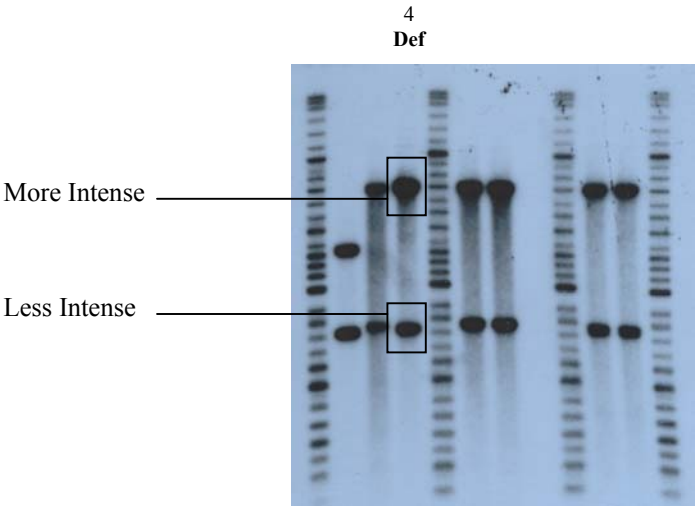

Fig. 17. ***D2 Autorad.***
NOTE: Intensity disparity between bands within lane 4.

[69] Again, we assume Bakken was referring to the D4 autorad.

(2) the control bands on the D4 autorad:

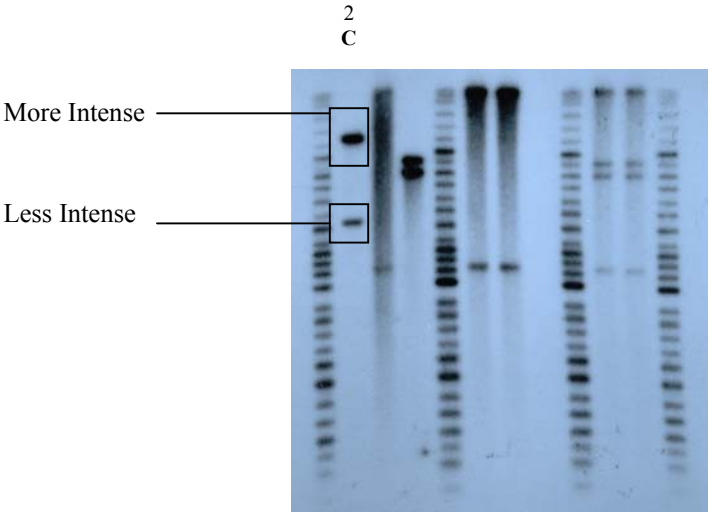

Fig. 18. ***D4 Autorad.***
NOTE: Intensity disparity between bands within lane 2.

(3) the victim's (evidentiary) bands on the D4 autorad:

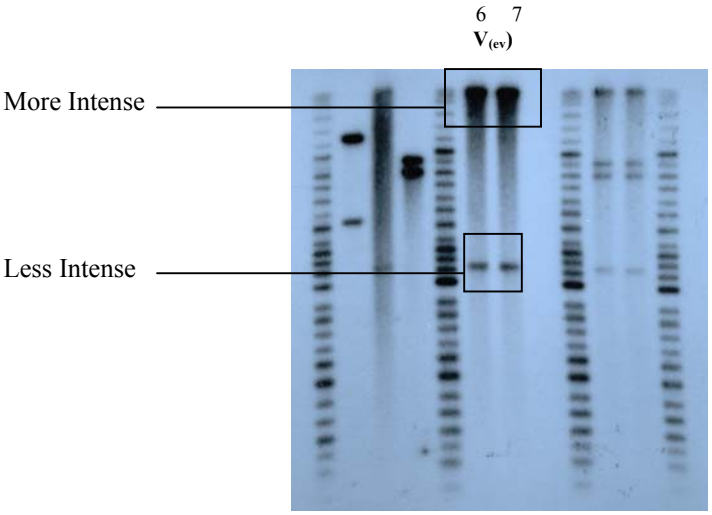

Fig. 19. ***D4 Autorad.***
NOTE: Intensity disparity between bands within lanes 6 and 7.

(4) the victim's bands on the D1 autorad:

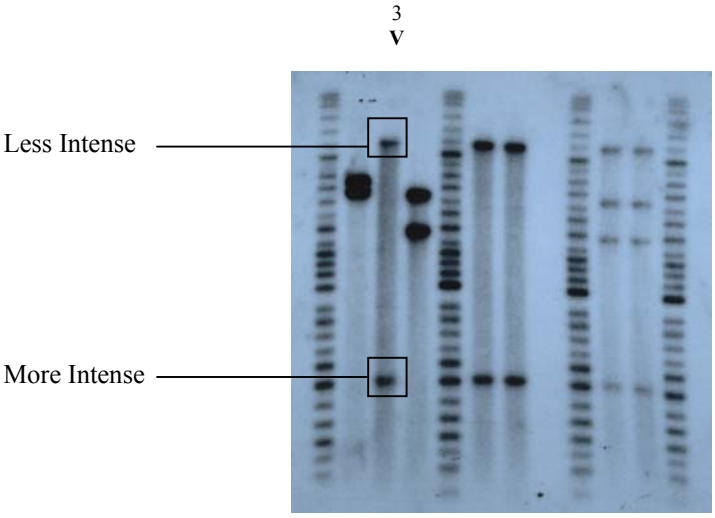

Fig. 20. ***D1 Autorad.***
NOTE: Intensity disparity between bands within lane 3.

(5) defendant's bands on the D1 autorad:

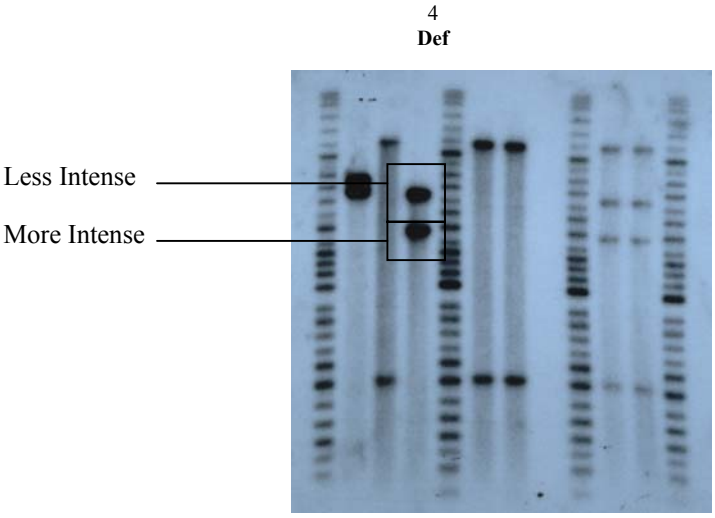

Fig. 21. ***D1 Autorad.***
NOTE: Intensity disparity between bands within lane 4.

Furthermore, the comparison *between* autorads that prosecution witness Adams testified showed a correlation between DNA quantity and band intensity (see fig. 14, *ante*) does not necessarily find further support in the evidence. For example, the victim's bands on the D2 autorad were far more intense than the victim's bands on the D1 and D4

autorads, yet the D2 victim's bands were not expected to contain twice as much DNA as the D1 and D4 victim's bands. (Fig. 22.)

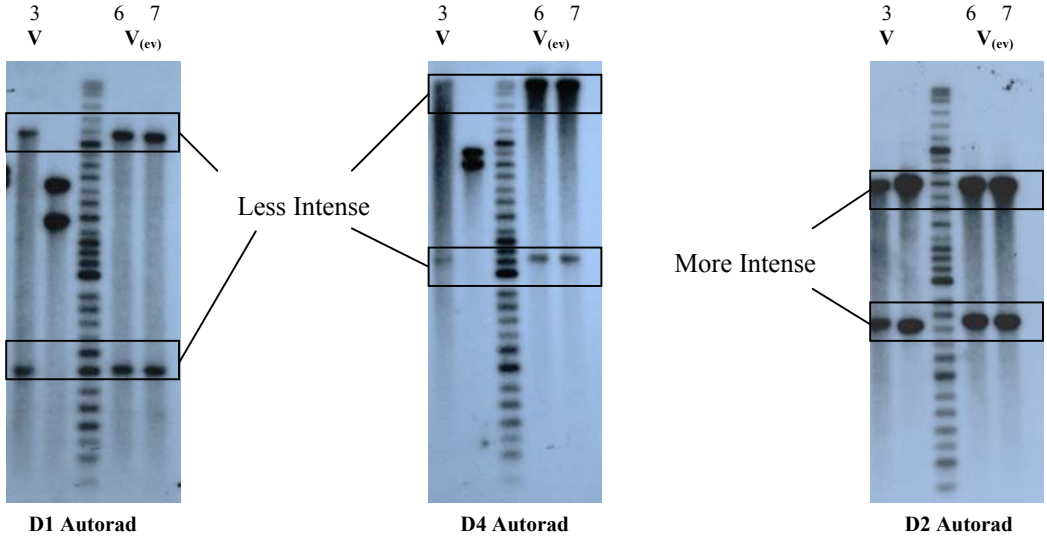

Fig. 22. ***Band Intensity Comparison Between Victim's Bands on Different Autorads.***
NOTE: The D2 victim's bands were more intense than most of the corresponding victim's bands on the D1 and D4 autorads, but there was no evidence the D2 bands contained significantly more DNA than the bands on the other autorads.

The point is that Adams's theory, which was apparently based only on the comparison of the two perpetrator/victim lanes between the autorads, did not necessarily hold true for comparisons of the other five lanes.[70]

We note that NRCI states: "Mixed samples can be very difficult to interpret, because the components can be present in different quantities and states of degradation. It is important to examine the results of multiple RFLPs, as a consistency check. Typically, it will be impossible to distinguish the individual genotypes of each contributor." (NRCI, *supra*, at p. 59.) "Mixed samples are a reality of the forensic world

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70 The intensity of the D2 autorad bands could possibly have been affected by the fact that the D2 probe was the first probe hybridized to the membrane. Sequential probing of a membrane gradually washes some of the DNA from the membrane, and thus later hybridizations may produce less intense results than earlier ones. It appears that the D2 probe was hybridized to the membrane first, followed by D17 (which was inconclusive), then D1, and finally D4. Of course, may be many other factors that influence band intensity differences between autorads.

that must be accommodated in interpretation and reconstruction. As a rule, mixed samples must be interpreted with great caution…. Interpretations based on quantity can be particularly problematic -- e.g., if one saw two alleles of strong intensity and two of weak intensity, it would be improper to assign the first pair to one contributor and the second pair to a second contributor, unless it had been firmly established that the system was quantitatively faithful under the conditions used." (*Id.* at p. 66.) NRCII states: "In some cases, it might be possible to distinguish the genetic profiles of the contributors to a mixture from differences in intensities of bands in an RFLP pattern or dots in a dot-blot typing …." (NRCII, *supra*, at p. 129.) Modern Scientific Evidence: The Law and Science of Expert Testimony (2001) (hereafter Modern Scientific Evidence) states: "Studies in which DNA from different individuals is combined in differing proportions show that the intensity of the bands reflects the proportions of the mixture. Thus, if bands in a crime-scene sample have different intensities, it may be possible to assign alleles to major and minor contributors. However, if the bands are present in roughly equal proportions, this allocation cannot be made, and the statistical interpretation of the observed results must include all possible combinations." (*Id.* at § 25-2.4.3, fn. 93.)

f. Risk of Overlooking First-Prong Issues

Venegas stressed the risk of mistaking third-prong issues for first-prong issues, but we are also apprehensive of the converse problem -- mistaking first-prong issues for third-prong issues. First, courts may overlook the distinctness of a new procedure, believing it is merely an immaterial variation on an already accepted procedure (i.e., it is the same procedure). Second, courts may assume that a truly distinct procedure is merely one method for performing a more general, already accepted procedure (i.e., it is an implemental procedure). In both cases, the trial court, believing the procedure has already been deemed accepted, will erroneously perform only a third-prong analysis. Although both the first-prong and third-prong tests go to admissibility, the standards for

admissibility and, perhaps more importantly, the standards of review are different for the two tests.

1. Same Procedure

Venegas determined that an already accepted procedure serves as precedent for the acceptance of another procedure unless the defendant can prove that the other procedure is materially distinct. For example, if the prosecution presents RFLP autorads produced by the FBI, *Axell* serves as precedent for the general acceptance of the RFLP procedure to produce those autorads unless the defendant shows that differences in the FBI's procedure make it materially distinct from the procedure deemed accepted by *Axell*. (*People v. Venegas, supra*, 18 Cal.4th at pp. 53-54.) There is in effect a presumption that the procedures are the same, and the defendant bears the burden of demonstrating they are not.

If the defendant shows the differences are significant enough to render the procedure materially distinct from the already accepted procedure, the procedure must be analyzed under *Kelly*'s first prong. If, on the other hand, the defendant does not show the differences make the procedure materially distinct from the already accepted procedure, then the procedures are the same and the differences go to whether the proper procedure was followed in the particular case. (*People v. Venegas, supra*, 18 Cal.4th at p. 78.) If the differences amount to a failure to follow proper procedure, the evidence is inadmissible under *Kelly*'s third prong.

There is an obvious danger that courts may neglect or misunderstand which differences nudge a procedure into material distinctness. How different must a procedure be to qualify as distinct? In the continuum of what can be defined as differences in procedure, there inevitably comes a point at which the differences are dramatic enough to transform the procedure into a distinct procedure. A court that fails to recognize this transformation will conduct an inappropriate third-prong analysis where a first-prong analysis is required.

2. Implemental Procedure

A second risk is that courts may construe a truly distinct procedure as merely one of a number of alternative methods for implementing or accomplishing a more general, already accepted procedure -- for instance, band-intensity analysis as one method of accomplishing autorad analysis. When an accepted procedure is stated in broad terms as a general principle or step, courts may be tempted to assume that the acceptance of that procedure carries on its coat-tails all the methods of accomplishing it, and to assume that those methods comply with the general principle or step purely because they accomplish it. However, every conceivable procedure accomplishes a more general principle or step, and courts, liberated by this logic, could find that hundreds of highly sophisticated procedures are simply different methods of performing a single accepted procedure -- and again *Kelly*'s first prong would be handily eviscerated. Although these procedures would still be required to survive the scrutiny of *Kelly*'s third prong, every procedure could satisfy the test under this perversion since every procedure could be said to comply with the general principle or step.

Courts therefore must be aware that acceptance of a general scientific principle or procedure does not automatically confer a passive surrogate acceptance on every technical method for implementing or interpreting that principle or procedure. Every distinct procedure, whether general or technical, must pass the first-prong test.[71]

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[71] On rehearing, the People argue that procedure and interpretation are "coextensive" in the case of DNA evidence, and that general acceptance of the procedure as a whole includes general acceptance of the interpretation necessary to give the procedure meaning. But, as our previous discussion points out (see part V.C.3.c., *ante*), *Venegas* and other courts have addressed the general acceptance of *each basic step of RFLP*, not the entire procedure as a whole.

3. Appellate Error

Of course, if the appellate court also overlooks a first-prong issue, it compounds the trial court's error. For example, the trial court, erroneously applying the third prong, may find the evidence admissible because it believes the procedure was in compliance with the accepted procedure. On review, the appellate court can rectify the mistake only if it recognizes that the first-prong test should have been applied originally. If, however, the appellate court labors under the same misconception as the trial court, the appellate court applies an abuse of discretion standard, and affirms the trial court's ruling if there is evidence to support it. (*People v. Venegas, supra*, 18 Cal.4th at p. 91) Thus, the evidence slips by, its reliability unscrutinized. Only if the evidence fails to support the ruling will the appellate court reverse. Similarly, if the trial court correctly applies the first prong but incorrectly determines that the procedure is generally accepted, the mistake goes uncorrected if the appellate court believes the issue is strictly a third-prong issue and reviews it as such.

Assume, for example, that we erroneously believed band-intensity analysis was a third-prong issue. We would review the trial court's finding that correct procedures were followed for abuse of discretion.[72] Under that test, we could reverse only if we concluded the trial court's finding was arbitrary, capricious, absurd, or outside the bounds of reason. (*People v. Coddington, supra,* 23 Cal.4th at pp. 587-588; *People v. Garcia, supra,* 20 Cal.4th at p. 503.) Looking to the evidence, we would see that the prosecution

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[72] In this case, we presume the trial court applied both first-prong and third-prong tests to band-intensity analysis. Although the court's ruling did not mention band-intensity analysis, the court found there was general acceptance of the FBI's procedure and held the evidence admissible. We presume all findings necessary to support the trial court's ruling. (*Denham v. Superior Court* (1970) 2 Cal.3d 557, 564 ["[a]ll intendments and presumptions are indulged to support [the judgment or order] on matters as to which the record is silent...."].)

presented testimony that band-intensity analysis can and did reveal the perpetrator's alleles from a superimposed mixture. In opposition, we would find defense testimony that band-intensity analysis could not be relied upon for this purpose. If that evidence demonstrated to us the lack of correlation between band intensity and DNA quantity, even though the trial court was apparently unconvinced by the evidence, we would conclude band-intensity analysis was not proper procedure because the autorads contained several instances of its failure (where approximately equal amounts of DNA did not produce approximately equal band intensities). We would conclude the defense presented evidence that the proper procedures were not followed in this case, and the prosecution's evidence in opposition to the defense testimony was insubstantial and founded on assumptions proved invalid by the evidence. For these reasons, we would hold the trial court's reliance on this evidence unreasonable and an abuse of discretion. Although in this scenario we, like the trial court, would fail to recognize the issue as a first-prong issue, we would nevertheless (but only fortuitously) find the evidence inadmissible under the third prong.

In an alternative scenario, assume there was no such evidence; the *only* evidence on the issue was the two opposing expert views. Nothing in the evidence would suggest to us that the trial court was unreasonable in finding that band intensity was proper procedure for determining DNA quantity and discerning superimposed bands, and we would be compelled to find that the trial court reasonably relied on the prosecution testimony that band-intensity analysis was proper procedure. The unreasonableness of that reliance would not be apparent to either the trial court or this court. We would have neither the suspicion nor the authority to find an abuse of discretion, and we would uphold the admissibility of the evidence.

This second scenario emphasizes why the first-prong analysis is so critical to the screening of scientific evidence. Without first-prong inspection, unreliable evidence can be admitted into the trial and survive appellate review. The first prong not only presents a

more rigorous standard for admission in the trial court, but it also allows the reviewing court an opportunity to independently evaluate and ensure the reliability of the evidence. In the first scenario, as in the present case, the procedure's unreliability might have been apparent from the evidence. But in the many cases where it is not, the admission of such unreliable evidence would be affirmed by the appellate court, unaware of its unreliability and powerless to rectify its improper use.

In *State v. Harvey* (1997) 699 A.2d 596, the defendant challenged the reliability of a somewhat similar procedure, dot-intensity analysis, to analyze a mixed DNA sample on a dot blot (not an autorad). The majority concluded dot-intensity analysis was generally accepted (*id.* at pp. 624-629), but the dissenting judge articulated some of our concerns, as follows:

> "The principal disagreement that I have with the majority concerns the general acceptance of dot-intensity testing. Dot-intensity analysis was the essential evidence relied upon by the State to demonstrate that defendant was in all likelihood the actual person whose blood contributed to the mixed sample found at the scene. The majority properly, if reluctantly, recognizes that dot-intensity testing, as a scientific method, must meet the standard of general acceptance even if DQ-Alpha and polymarker testing are themselves found to be generally accepted scientific tests. The majority, however, misconstrues the distinctive and distinguishing features of dot-intensity testing as a method of analyzing DNA, denigrates many of defendant's challenges to the testing as not going to the reliability of the procedure, but rather only to its weight, and then, on an embarrassingly deficient record, summarily concludes that the novel scientific procedure passes muster under our long-standing precedent. Dot-intensity analysis as used here -- a procedure never before used in any court case, successfully documented in any laboratory, or validated in any scientific study or published literature -- has not been shown to be an established and reliable procedure. Further, no foundation for dot-intensity analysis exists in the record, and the results obtained clearly show that such evidence is grossly unreliable. Finally, the analysis rests on a combination of assumptions that renders the evidence so unpersuasive and speculative that it is inadmissible under New Jersey Rule of Evidence 402." (*State v. Harvey, supra*, 699 A.2d at p. 658, Handler, J. diss. opn.)

"The polymarker and DQ-Alpha testing kits were designed solely to determine the presence or absence of certain alleles. Dot-intensity analysis, however, purports to determine more. It purports to quantify the alleles that are present and thereby to identify the specific alleles contributed by each donor to the DNA mixture. The majority only grudgingly rejects the State's argument that dot-intensity analysis is nothing new and that no independent basis for its admission need be established. Without discussion, it recognizes, without really appreciating, that that difference requires an independent foundation for admissibility. [Citation.] Notwithstanding its concession, the majority then erroneously devalues and mischaracterizes defendant's challenges to the evidence -- challenges to its competency -- as merely going to Cellmark's performance of the polymarker test ….[73] [Citation.] That conclusion derives from a distortion of defendant's claims and from a serious misunderstanding of the distinctive nature and purposes of dot-intensity analysis." (*Id.* at pp. 658-659.)

"The issue here is not whether the reverse dot-blots obtained on the polymarker strips can reveal the presence of alleles in the mixture -- they can. At issue is whether an interpretation made of those strips that goes beyond what results that the strips were designed to show -- the presence of alleles -- is generally accepted as scientific evidence. [Citation.] Thus, unlike 'an expert's ability to perceive an abnormality on an x-ray,' which concededly 'is a matter within the province of the jury,' [citation] here we must decide, by analogy, whether a doctor's interpretation of an x-ray can be admitted without restrictions when he testifies to a condition that the x-ray was not designed to reveal. Therefore, while a doctor's diagnosis of a broken bone from an x-ray may be admissible because it is based on a generally accepted interpretation of a generally accepted test, the doctor's diagnosis of cancer from that same x-ray ought not to be admitted unless and until the doctor can establish that such a diagnosis from an x-ray is generally accepted." (*Id.* at pp. 659-660, fn. omitted.)

"Not only do the results obtained here establish the gross unreliability of this evidence, but the entire practice of visualizing and weighing dot intensities to determine the makeup of a mixture is unavoidably subjective. A subjective test, especially one that is immune from later challenge, should not be admissible evidence in these

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73 Apparently, under the New Jersey court's three-prong test, the third prong goes to weight, not admissibility as it does in California.

> circumstances. The standard for the admissibility of scientific evidence is designed to ensure that the testing procedure 'relies primarily upon objective factors for reaching a conclusion, with subjective factors playing only a minimal role in the analysis.' [Citation.]" (*Id.* at p. 670.)
>
> " … A full hearing on the assumptions and the entire validity of the dot-intensity analysis should have been held. That hearing was necessary to explore the inconsistencies in both the State's experts' comments and in the actual results obtained. The uncritical admission of this evidence … without even remotely establishing its validity is an egregious wrong." (*Id.* at p. 672.)

g. Pizarro's Case

In this case, a Kelly hearing on band-intensity analysis would have helped ensure against presentation of unreliable scientific evidence. If the trial court had found band-intensity analysis unaccepted or improperly performed, it would have excluded the D2 autorad evidence and the frequency of that locus would not have been multiplied into the overall profile frequency. If, on the other hand, the trial court had found band-intensity analysis accepted and properly performed, it would have admitted the D2 autorad evidence and the D2 genotype would have been used to declare defendant a match and its frequency would have been included in the overall profile frequency, as in fact occurred. But, even in that situation, the Kelly hearing would have served another important but often overlooked purpose -- it would have defined and focused the scientific and legal issues for the attorneys and the trial court, affecting the manner in which evidence would have been presented at trial. The thorough examination required for a Kelly hearing would have resulted in a greater understanding of these issues and would have promoted challenges to the evidence. The trial court's Kelly ruling of admissibility would not have precluded the defense from challenging band-intensity analysis and the D2 autorad results before the jury at trial. Defense counsel would have presented experts to challenge the procedure and to explain to the jury that, if band-intensity analysis is in fact not reliable or was in fact not properly performed in this case, then two of the three possible interpretations of the D2 autorad would actually exonerate defendant. This

information would have allowed the jurors to better weigh the value of the evidence. In this case, the jurors heard nothing regarding band-intensity analysis and the possible interpretations of the D2 autorad evidence; they were simply given the overall profile frequency.

Although we have the prerogative to independently consider and render a decision on whether band-intensity analysis has gained general acceptance in the relevant scientific community, we decline to do so pending full and complete litigation of that issue, assisted by live expert witnesses, in the trial court. (*People v. Leahy, supra*, 8 Cal.4th at pp. 609-610; see also *Cramer v. Morrison* (1979) 88 Cal.App.3d 873, 888 [general acceptance of HLA paternity testing].)

D. CONCLUSION

The prosecution failed to carry its burden of demonstrating that the FBI used proper scientific procedure to determine the perpetrator's D2 genotype. Reference to defendant's genotype to prove the perpetrator's genotype was improper, and use of band-intensity analysis to prove the perpetrator's genotype required *Kelly* first-prong scrutiny of that method. Thus, the FBI's method of discerning the perpetrator's D2 genotype constituted improper procedure under *Kelly*'s third prong.

Use of that improperly discerned genotype to declare defendant a match at the D2 locus and to calculate the profile frequency was also improper procedure under *Kelly*'s third prong. The D2 genotype, which was offered to prove a match with defendant, in essence had a two-out-of-three chance of exonerating defendant, and inclusion of the D2 genotype in the statistical calculation made the perpetrator's profile rarer and defendant's possession of it more incriminating.[74] Simply put, because the perpetrator's D2 genotype

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[74] The documents the People seek to introduce as new evidence on appeal seem to suggest that the profile frequency, without the D2 genotype, would have been 1 in 2,452 rather than 1 in 256,994 -- a 100-fold increase in the frequency of the perpetrator's profile

was not discernible by a proper method, it should not have been used to declare the defendant a match or to calculate the profile frequency and such use constituted improper scientific procedure under *Kelly*'s third prong and section 405. It was error going directly to the reliability of the DNA evidence.

Furthermore, the DNA evidence -- both the match and the profile frequency -- relied on the perpetrator's genotype as preliminary fact and thus was admitted without adequate foundation under section 403.

On retrial, the autorads may be re-examined by scientists at the FBI or another institution. The trial court must then conduct a thorough *Kelly* hearing, at which the prosecution must establish that the perpetrator's alleles can be discerned reliably from the perpetrator/victim mixture on the D2 autorad. If the method used to discern the perpetrator's alleles has not yet passed first-prong scrutiny, the court must determine the reliability and general scientific acceptance of that method under *Kelly*'s first prong. If the trial court deems the method generally accepted as a reliable method for discerning alleles from a superimposed mixture on an autorad, then the court will hear third-prong testimony regarding whether the mixture on the D2 autorad in this case was properly analyzed and interpreted according to that method. If the method used to discern the alleles in the mixture is not reliable and generally accepted, or if the testing in this case fails to follow proper procedure, then the D2 autorad evidence cannot be used to calculate the profile frequency, which will then be based only on evidence from the other autorads.

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in the population. The People's motion to introduce new evidence on appeal is hereby denied. Such evidence is subject to dispute and is properly a trial issue as opposed to an appellate consideration. We note that nothing in those documents would, if admitted, affect our reversal.

VI. ETHNIC FREQUENCY

Defendant contends that correct scientific procedures were not followed and the requirements of the Evidence Code were not satisfied when the jury was informed that the DNA profile frequency applicable to his case was the probability of finding a matching profile in the *Hispanic* population, although there was insufficient evidence that the perpetrator was Hispanic.

The People assert that defendant's contention must be rejected in light of the conservative nature of the Hispanic database and the fact that frequencies do not vary greatly by ethnicity. The People argue the error is harmless because the profile frequency from the Hispanic database was more common and thus more favorable to defendant than the profile frequencies calculated from other databases.[75] Defendant maintains, however, that the error cannot be harmless because presentation of the Hispanic frequency itself -- regardless of the favorableness of the number -- and the manner in which the evidence was presented led the jury to believe the perpetrator was Hispanic, even though no independent evidence justified the drawing of such an inference.

We conclude that an ethnic profile frequency relies for its relevance on the foundational showing that the perpetrator is a member of the particular ethnicity. (§ 403.) The ethnic frequency is subject to a relevance analysis and is not made relevant simply because it is based on the *defendant's* ethnicity. Although we do not resolve the question of whether there was sufficient evidence to conclude the perpetrator in this case was

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[75] The People also argue that defendant waived this issue by failing to object on relevance grounds at the original trial. However, we placed the preliminary fact question in issue in *Pizarro I* for consideration on remand, and thus the issue was "technically encompassed" in our remand order (*People v. Senior* (1995) 33 Cal.App.4th 531, 535). The People did not petition for rehearing after *Pizarro I*, and following remand both parties briefed and addressed the issue before the trial court. We reject the People's waiver argument and address this issue, which involves a critical aspect of the DNA statistical evidence.

Hispanic, it is clear that the preliminary fact foundation was predicated solely on defendant's ethnicity. We address this issue to reiterate our cautionary comments in *Pizarro I* regarding the serious dangers of unjustifiable reliance on and reference to ethnicity.

For context, we begin with the trial testimony, our comments in *Pizarro I*, and a summary of the *Kelly* hearing on remand.

A. TRIAL TESTIMONY

At trial, there was evidence that the victim was last seen as she approached the area where defendant, who was half Hispanic, had been not long before. This was the extent of the evidence offered to establish that the perpetrator was Hispanic (or half Hispanic).

Adams, who conducted the scientific work in Pizarro's case in 1989, was the sole scientific witness at trial. He testified that "[t]he likelihood of finding another unrelated Hispanic individual" with a profile similar to the perpetrator's and defendant's profiles was approximately 1 in 250,000. His 1990 testimony follows:

> "[PROSECUTOR:] What is your opinion as to the chances of another Hispanic male having the same DNA profile as Mr. Pizarro?
>
> "[ADAMS:] *The likelihood of finding another unrelated Hispanic individual with a similar profile as Mr. Pizarro is one in approximately 250,000.*
>
> "[PROSECUTOR:] *And this would also be the same statistic for the probability of a match of a DNA profile between the [perpetrator's DNA] obtained from the vaginal swab?*
>
> "[ADAMS:] *That is correct.*
>
> "[PROSECUTOR:] Same statistic?
>
> "[ADAMS:] Yes.
>
> "[PROSECUTOR:] And, again, this is only with Hispanic men?
>
> "[ADAMS:] Hispanics, not broken down into gender. [¶] … [¶]

"[PROSECUTOR:] Dr. Adams, we have been talking about the chance for a match within the Hispanic community. Would the statistics for a match within the Caucasian community be different?

"[ADAMS:] Yes, generally there are going to be some differences in the population data from the different populations. So that's why we keep them separate. That's why we have a Caucasian and a Black and a Hispanic, American Indian population because there are differences. [¶] So if I were to compare one person in each of those different populations I would come up -- I'm sure I would come up with somewhat different results because in one population that pattern may be very rare, and another population that same pattern may be very common.

"[PROSECUTOR:] Have you done any of the calculations necessary to determine what the chances are of having matches of this particular DNA profile within the Caucasian community?

"[ADAMS:] Yes.

"[PROSECUTOR:] And what are those statistics?

"[ADAMS:] The statistics in those cases -- in that case comparing the same profile to the Caucasians is much greater. It would be one in 10,000,000.

"[PROSECUTOR:] But within the Hispanic group alone it is according to your testimony one in 250,000?

"[ADAMS:] Yes, ma'am.

"[PROSECUTOR:] *What about a situation where someone is half Hispanic and half Caucasian?*

"[ADAMS:] *Well, there is nothing we can do other than to compare them to the two populations and we would use only the smaller of the two in our report.* [Adams referred to the number with the smaller *denominator*.]

"[PROSECUTOR:] Why do you use only the smaller of the two?

"[ADAMS:] We attempt to be as conservative as possible. The smaller number is less detrimental to the defendant." (Italics added.)

B. PIZARRO I OPINION

In *Pizarro I*, to guide the trial court on remand, we explained that admission of evidence of the perpetrator's profile frequency derived from the Hispanic database would

require the trial court's determination of a preliminary fact -- that the perpetrator was Hispanic. Otherwise, the Hispanic database and frequency would not be relevant. We explained in *Pizarro I*:

> "In *People v. Axell*, the unknown assailant left strands of hair at the crime scene.
>
> "'July 28, 1988, Cellmark Diagnostics, a testing laboratory in Germantown, Maryland, received from the district attorney's investigator, whole bloodstains on cotton from the victim and appellant, and roots from 15 hairs recovered from the crime scene. The DNA was extracted from these materials, and Cellmark reported that the banding patterns obtained from the appellant's whole bloodstain matched the DNA banding patterns obtained from the 15 hair roots found at the scene of the murder. Subsequently, Cellmark reported that the frequency of that DNA banding pattern in the Hispanic population is approximately 1 in 6 billion. Appellant is part Hispanic. Simply put, Cellmark's analysis meant that the chance that anyone else but appellant left the unknown hairs at the scene of the crime is 6 billion to 1.' ([*Axell, supra,*] 235 Cal.App.3d 836, 844 ….)
>
> "This statement reveals the problem in the instant case. The selected racial or ethnic data base is predicated on the *suspect's* racial or ethnic background. However, the relevancy of the statistical probability depends on the *perpetrator* being the same racial or ethnic background as the suspect. In other words, examining the defendant's DNA banding pattern and concluding that it has an expected frequency of occurrence of, for example, 1 in 500,000 in a specific racial/ethnic data base would reflect the probability that the suspect committed the crime only if the perpetrator was within that same data base. It is clear that all population groups share common allele patterns according to the theory advanced by the FBI -- it is the frequency with which these patterns appear within different groups which will vary. Nothing in the record supports the conclusion that the banding patterns are race or ethnic specific so that a review of the banding pattern would conclusively establish that the person who left the sample was of a particular racial or ethnic background. Dr. Adams did not testify and, as we understand the evidence, could not testify that the perpetrator in the instant case was Hispanic based solely upon the allele pattern found in the evidence which was left at the crime scene by the perpetrator. What if the perpetrator was/were Black or non-Hispanic Caucasian, etc., and what is the relevancy of the estimated probabilities for these groups if we do not know the race or ethnic background of the perpetrator? It is a bootstrap

argument to assume relevancy of a Black or Hispanic data base simply because the *suspect* falls within that racial or ethnic group. [¶] … [¶]

"Proffered evidence as utilized in section 403 'means evidence, the admissibility or inadmissibility of which is dependent upon the existence or nonexistence of a preliminary fact.' (Evid. Code, § 401.) Here the proffered evidence is the result of statistical analysis which utilizes ratios assigned to particular racial or ethnic databases. '"Relevant evidence" means evidence, including evidence relevant to the credibility of a witness or hearsay declarant, having any tendency in reason to prove or disprove any disputed fact that is of consequence to the determination of the action.' (Evid. Code, § 210.)

"The disputed fact generally is whether the suspect is also the perpetrator. Thus, the evidence is relevant if it tends to prove the suspect is the perpetrator. However, the preliminary fact upon which the relevancy of the proffered evidence depends is the racial/ethnic background of the *perpetrator*, not the suspect. If the only way you can conclude the perpetrator fits a racial/ethnic category is to assume the perpetrator was the same race/ethnic background as the suspect then the reasoning is circular, i.e.: proof of the racial/ethnic background of the perpetrator depends on the racial/ethnic background of the suspect from which we infer a statistical probability that the perpetrator is the suspect. Absent proof sufficient under … section 403 to support the preliminary fact as to the racial/ethnic background of the perpetrator, we see no relevancy to a data base selected because of the racial/ethnic background of the suspect/defendant. The problems created by employing assumed relevancy of the data base are insidious. A jury hears an astronomical figure that not uncommonly depends for its relevance upon the very issue that they have to decide: is the defendant the perpetrator? The same … section 403 problem does not appear, however, if the general population data base, which has been created without regard to race or ethnic background, is utilized.

"We must point out that the probative value of DNA matches using the general population data base may well be substantial. For example, the expected frequency of occurrence in the general population may be one in five thousand or even one in five million. This approach establishes a degree of probability that the suspect is the perpetrator, but it does so without *assuming* the suspect and the perpetrator belong to the same ethnic/racial background. Likewise, evidence sufficient under … section 403 to support the preliminary fact as to the racial/ethnic background of the perpetrator alleviates this problem. We do not presume that evidence sufficient to support a preliminary factfinding in the instant case does or does not exist, our comments are designed to assist the trial court in

assessing the relevancy of the proffered evidence." (*Pizarro I*, *supra,* 10 Cal.App.4th at pp. 92-95, fns. omitted.)

C. KELLY HEARING

At the *Kelly* hearing on remand, Sensabaugh explained that the database population relevant for predicting allele frequency is the "[p]opulation of possible perpetrators [who] are possible sources of [the DNA] sample." He stated:

> "This is the first case I have seen in which only the defendant's racial type is reported. That may or may not have been justified, depending upon the information that was provided to the FBI by the reporting agency."

No evidence beyond that presented at trial was presented at the hearing to establish that the perpetrator was Hispanic. After the hearing, the trial court ruled that the DNA evidence was admissible. In its ruling, the court did not mention any finding on the preliminary fact question, but did conclude that the database used by the FBI was accepted in the scientific community.

D. ANALYSIS

As we explained in *Pizarro I*, the relevance of the Hispanic profile frequency depended on the preliminary fact that the perpetrator was Hispanic.[76] (§ 403.) In the

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[76] The profile frequency estimates how many people in the *relevant* population match the perpetrator's profile. The *relevant* population, as Sensabaugh explained, is the perpetrator's population -- the population to which possible perpetrators belong. (See *People v. Venegas, supra,* 18 Cal.4th at pp. 63-64 ["The question properly addressed by the DNA analysis is therefore this: Given that the suspect's known sample has satisfied the 'match criteria,' what is the probability that a person chosen at random from the relevant population would likewise have a DNA profile matching that of the evidentiary sample?"]; *People v. Soto, supra,* 21 Cal.4th at pp. 512, 518 [calculation should be made from "population or populations to which the perpetrator of the crime might have belonged"]; NRCII, *supra*, at pp. 30, 114, 122, 127.) Scientists often use the relevant *ethnic* population, rather than a more general population, because frequencies are thought to vary between ethnic populations. NRCII explains that profile frequency calculations are subject to uncertainties, one of which is "due … to the possibilit[y] that the database is not representative of the population of interest …." (NRCII, *supra*, at p. 33.) NRCII

physical profile analogy, a Hispanic frequency, which estimates how many Hispanics have black hair, blue eyes, and 5-foot-8-inch stature, is not relevant to prove the rarity of the profile in the perpetrator's population unless the preliminary fact that the *perpetrator* is Hispanic is established. In the absence of sufficient proof, it is entirely possible that the perpetrator is actually a member of a different ethnic population.

In this case, the record suggests that the FBI ascertained the perpetrator's ethnicity by referring to *defendant's* ethnicity, and that the prosecution presented the Hispanic frequency because *defendant* was Hispanic. For example, trial testimony regarding which database to choose when "someone is half Hispanic and half Caucasian" plainly referred to defendant.[77] The prosecution *informed* the jury that the relevant population was Hispanic and that the Hispanic database was chosen based on defendant's ethnicity. The prosecution thus communicated its assumption that defendant was the perpetrator and effectively instructed the jury to presume that because defendant was Hispanic, the perpetrator was also Hispanic. This communication potentially lightened the prosecution's burden of proving defendant's identity as the perpetrator. Furthermore, if there was insufficient independent proof to establish the perpetrator's Hispanic ethnicity, reliance on defendant's ethnicity added an unproved trait to the perpetrator's description,[78] and served as inadequate foundation for the Hispanic frequency, which was irrelevant and inadmissible.

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continues to say that if the database from the wrong racial group is used, the error may be larger than 10-fold in either direction, which "argues for the use of the correct racial database if that can be ascertained …." (*Id.* at p. 34.)

[77] Adams explained that when "someone" is half Hispanic and half Caucasian, there is no half Hispanic and half Caucasian database to use; instead, the frequency is calculated using both databases, then the database producing the less detrimental frequency is used. Here, that was the Hispanic database.

[78] Although the ethnic evidence was probably not offered as match evidence, it did have that effect -- showing that the perpetrator and defendant were both Hispanic and

On rehearing, the People argue to the contrary, asserting that an ethnic frequency based on the defendant's ethnicity is relevant for two reasons. First, they contend it is relevant because it assists the jury in assessing the rarity of the profile. We disagree. Such a frequency only tells the jury the rarity of the perpetrator's profile in the *defendant's* population -- a population to which the *perpetrator* has not been shown to belong. The calculation *assumes* the perpetrator, like the defendant, is Hispanic; but if the perpetrator is not, the frequency is irrelevant and does not assist the jury in any way. For example, the jury is not assisted by knowing how many Hispanics possess the perpetrator's traits if the perpetrator is actually Asian.

Second, the People claim a frequency based on the defendant's ethnicity is relevant because it simply includes the defendant within the class of possible perpetrators, in the same way a finding that the defendant matches the perpetrator's blood type includes the defendant in the class of possible perpetrators. Again, we disagree. The procedural step that simply includes defendant within the class of possible perpetrators is the determination that the defendant's profile *matches* the perpetrator's profile, like the determination that the defendant's blood type matches the perpetrator's blood type. These are the findings that render the defendant a possible perpetrator and include him in that class. (See *People v. Venegas, supra,* 18 Cal.4th at p. 63 [a finding that profiles match "places the suspect within a class of persons from whom the sample could have originated"].)

By comparison, the procedure we address here is the subsequent determination of the *frequency* or *rarity* of the perpetrator's profile or blood type in the relevant population -- to provide meaning to the match. The match includes the defendant in the class; the

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therefore resembled each other as to one more trait. Again, this evidence was irrelevant to prove a match unless the preliminary fact of the perpetrator's ethnicity was established.

frequency calculation estimates the size of that class so that membership in it has meaning. The fewer the members, the more incriminating the membership.

The appropriation of the defendant's trait into the perpetrator's profile changes the description of the possible perpetrators, who are now described according to the defendant rather than the perpetrator. This spuriously redefined class is no longer the perpetrator's population, but the defendant's, and inclusion of the defendant in this class simply includes him in his *own* class. Thus, defendant's own Hispanic ethnicity could not properly include him in the class of possible perpetrators unless all possible perpetrators were Hispanic, a determination which relied on proof that the actual perpetrator was Hispanic.

In sum, we do not take issue with procedural steps that simply include the defendant in the class of possible perpetrators, if that is indeed what they do. Our concern is with procedural steps that add to the perpetrator's profile a trait (here, defendant's ethnicity; in the previous issue, defendant's genotype) that the perpetrator has not been shown to possess, and then judge the rarity of possible perpetrators according to that unjustifiable, irrelevant trait.[79]

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[79] We note that several commentators have disapproved or discouraged the practice of referring to the defendant's ethnicity. NRCII states: "If the race of the person who left the evidence-sample DNA is known, the database for the person's race should be used; if the race is not known, calculations for all racial groups to which possible suspects belong should be made." (NRCII, *supra*, at p. 122 [Recommendation 4.1].) "In the great majority of cases, very little is known about the person who left the DNA evidence …. It might be known that the DNA came from a white person, in which case the white database is appropriate. If the race is not known … , the calculations can be made with each of the appropriate databases and these presented to the court. Alternatively, if a single number is preferred, one might present the calculations for the major racial group that gives the largest probability of a match." (*Id.* at pp. 113-114.) "Usually, the subgroup to which the suspect belongs is irrelevant, since we want to calculate the probability of a match on the assumption that the suspect is innocent and the evidence DNA was left by someone else." (*Id.* at p. 29.) Another commentator states: "To calculate a match proportion, laboratories need a reference population. The standard is to

use the race of the suspect …. This makes no sense. A match proportion is calculated assuming the suspect is *innocent.* So the appropriate reference is the race of the criminal, assuming the criminal is *not* the suspect." (Berry, *Statistical Issues in DNA Identification* in DNA On Trial: Genetic Identification and Criminal Justice (Billings edit., 1992) p. 106 (hereafter Billings.) The FBI's Worldwide Study explains: "The relative rarity of a DNA pattern in a suspect's ethnic subgroup, which might be of some academic interest, is not particularly relevant in the legal setting. To use the specific ethnic background of the suspect (which may be impossible to define) would presuppose that he or she is the true perpetrator. However, if the true perpetrator were known *a priori*, there would be no need for statistical estimates. Furthermore, if a particular subgroup were chosen as the reference database, for the majority of cases this would insinuate that a member of one subgroup is a more likely source of the crime scene evidence. Since the ethnicity of those people who are potential perpetrators rarely, if ever, is known, statistical estimates must be based on some sort of general population database. [¶] [T]he ethnic background of the suspect is not germane to selecting a reference database." (FBI Worldwide Study, Overview (1993) at p. 1.) Another source states: "[T]he suspect is presumed innocent, so the suspect's claim of not contributing the [DNA sample found at the crime scene] is presumptively valid…. [¶] … The relative rareness of the DNA profile in the suspect's ethnic subgroup (or in any ethnic subgroup, for that matter) is not legally relevant …. It does not tell the jury anything about the likelihood that someone other than the suspect could have, in fact, left the sample at the crime scene. Instead, it only tells the jury the likelihood that someone in the suspect's ethnic subgroup could have left the crime scene sample. This has no bearing on the question of guilt or innocence in the typical criminal case. The relative rareness of the pattern in some general population of potential perpetrators, on the other hand, does help the jury assess the likelihood that someone other than the defendant could have left the crime scene sample, and this has a direct bearing on the question of guilt or innocence." (Budowle, et al., *Reliability of Forensic DNA-typing Statistics* in Billings, *supra*, at pp. 81-82.) And another explains: "In most cases … only a single suspect is tested, and without eye-witness or other reliable evidence, not even the race of the criminal is known.… [M]atching probabilities depend on the underlying allele and genotype frequencies (and therefore population), and if there is a considerable ethnic variability, the choice of the database used to evaluate a match is an ethically significant action. One and the same sample DNA profile may be rare in one population, and therefore incriminate the suspect, but may be orders of magnitude more common in another. [¶] Morton [Morton, N.E. (1993) Eur. J. Hum. Genet., 1, 172] has rightly pointed out that the ethnic origin of the suspect is usually irrelevant … , and that the choice of the reference population should not be the expert's major concern. Since match probabilities are calculated under the assumption of *innocence*, the only argument for using allele frequencies from the suspect's population would be courtesy. There are good reasons to assume that under

The People also point to the numerical *benefit* a defendant may gain when his own ethnic population is used. (See, e.g., *People v. Axell, supra*, 235 Cal.App.3d at pp. 865-866 [court explained that Hispanic database had been correctly used since the defendant identified herself as Hispanic]; Krawczak, *supra*, at p. 80 ["There are good reasons to assume that under ethnic heterogeneity the suspect's profile is more frequent in his own population than in many (if not most) others"].) The People contend that the Hispanic frequency presented to the jury in this case was conservative and beneficial to defendant in comparison to frequencies calculated from other ethnic populations. This argument's flaw, however, is that it is not an *evidentiary* argument. It fails to recognize that only relevant evidence is admissible, and that the proffered evidence was relevant only if the preliminary fact was proved by sufficient evidence (§§ 350, 403). If it was not, the Hispanic frequency simply was not relevant; no amount of potential or actual numerical benefit to defendant could transform this irrelevant inadmissible evidence into relevant admissible evidence.[80]

The People argue on rehearing that the calculation and presentation of several frequencies derived from various ethnic databases is a satisfactory and commonly used alternative. For example, the jury might be told the perpetrator's genetic profile is found in 1 in 1 million Caucasians, 1 in 2.5 million Blacks, 1 in 10 million Hispanics, and 1 in 5

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ethnic heterogeneity the suspect's profile is more frequent in his own population than in many (if not most) others." (Krawczak & Schmidtke, DNA Fingerprinting (1998) p. 80 (hereafter Krawczak).)

80 We are nevertheless in no position to engage in a prejudice analysis -- to weigh any numerical benefit against the inferential damage created by the presentation of the evidence because, due to the various errors committed, we do not know if defendant did in fact gain any numerical advantage (and, if so, its extent) from the use of the Hispanic database.

million Asians.[81] The People assert that this practice provides the jury with an accurate range of frequencies over a continuum of ethnic populations, and that all ethnic frequencies are relevant because they tend to prove the significance of the match.[82]

Although presentation of a range of ethnic frequencies may in fact accurately provide the range of all possible frequencies, we see three problems with this practice. First, in the absence of sufficient evidence of the perpetrator's ethnicity, *any* particular

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[81] Despite the People's suggestion to the contrary, such a range of ethnic frequencies was not presented in this case. Only two ethnic frequencies (Hispanic and Caucasian) were mentioned, *expressly* because defendant was half Hispanic and half Caucasian. The Caucasian frequency was not presented as part of a range of ethnic frequencies. (See part VI.A., *ante*.)

[82] We acknowledge that this type of evidence is often admitted without objection. For example, in *Soto*, the prosecution presented frequencies in eight different ethnic populations. (*People v. Soto, supra,* 21 Cal.4th at p. 532.) The Supreme Court noted that "[the criminalist's] use of all these databases in his calculations reflected an objective of finding the probabilities of a random match in databases representing all possible perpetrators. Even though defendant is Hispanic, a possible perpetrator other than defendant could have belonged to some other ethnic group." (*Id.* at p. 532, fn. 27, citing NRCII, *supra*, at p. 122.) Soto's contention on appeal was that use of the unmodified product rule to calculate profile frequencies was not generally accepted by the scientific community. Although the court recognized the criminalist's purpose in using various databases, it did not specifically address the propriety of this method. For this reason, we believe *Soto* does not stand for authority that every ethnic frequency is relevant to prove the rarity of the perpetrator's profile in the perpetrator's population. The court's holding that the unmodified product rule, as applied in that case, had gained general acceptance in the scientific community did not, in our opinion, encompass every other aspect of the scientific procedures mentioned but not addressed by the court (e.g., the fixed bin method, the floating bin method, the use of various databases, etc.).

We also acknowledge that NRCII recognizes the use of this type of evidence (e.g., NRCII, *supra*, at p. 34 [if the correct ethnic database cannot be ascertained, "calculations should be made for all relevant racial groups, i.e., those to which possible suspects belong."]; *id.* at p. 114 [If the race is not known … , the calculations can be made with each of the appropriate databases and these presented to the court."]; *id.* at p. 122 [same]). However, as we explain, we think a second option suggested by NRCII (*ibid.*) is preferable.

ethnic frequency is irrelevant. The problem is again one of preliminary fact -- now occurring multiply and simultaneously. It does not matter how many Hispanics, Caucasians, Blacks, or Native Americans resemble the perpetrator if the perpetrator is actually Asian. If various ethnic frequencies are presented to the jury, each will have been admitted without adequate foundation.

The suggestion that presentation of several ethnic frequencies is appropriate illustrates again the subtle, even unexpected, differences between the scientific and legal approaches to the same problem. Here, science promotes consideration of all possibilities, whereas law restricts consideration to possibilities it deems relevant. A conundrum such as this, bound to arise in scientific cases, can be detected and resolved only through the attentive and respectful contemplation of the two disciplines and the mindful evaluation of their separate and intersecting principles. Inevitably, some scientific principles, although correct in their scientific context, will not survive translation into legal application of relevancy principles.[83]

Second, the improper mention of ethnicity unfairly and unjustifiably encourages the jurors to focus on ethnicity and race -- specifically the ethnicity and race of the defendant, the only suspect before them.

Third, the jury hears unjustifiably damaging evidence because the various ethnic frequencies create a range extending from the most conservative and beneficial to the defendant to the most rare and damning to the defendant. In our example, the evidence against the defendant includes not only the most favorable 1-in-1-million (Caucasian) frequency, but also the most damaging 1-in-10-million (Hispanic) frequency. If the

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83 See, for example, NRCII, *supra*, at page 59 ["We make no attempt to prescribe social or legal policy. Such prescriptions inevitably involve considerations beyond scientific soundness. Nevertheless, we recognize the connection between our scientific assessments and the efforts of the legal system to develop rules for using forensic DNA analyses …."].

perpetrator is actually Caucasian, only the most favorable 1-in-1-million (Caucasian) frequency is relevant, but the jury nevertheless will hear -- and likely focus on -- the more damaging 1-in-10-million figure. If the perpetrator is actually Black, only the 1-in-2.5-million (Black) frequency is relevant, but the jury will hear -- and likely focus on -- the more damaging 1-in-10-million figure. The greater the disparity between the perpetrator's true frequency and the range's most damaging extreme, the greater the prejudice the defendant will suffer from mention of that extreme.[84] Without adequate evidence of the perpetrator's ethnicity, there is no justification for presenting the most damaging frequency.[85]

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[84] This is true even if a range is presented without mention of ethnicity (e.g., the jury is told that the frequency of the profile is between 1 in 1 million people and 1 in 10 million people).

[85] A better option when the perpetrator's ethnicity is not established is presentation of the one most conservative frequency, without mention of ethnicity. In our example, the jury would be told that the perpetrator's genetic profile is found in no more than 1 in 1 million people -- that the profile is at least this rare. This frequency is conservative and makes no assumptions regarding the perpetrator's ethnicity; nor does it direct the jury toward notions of ethnicity or race. NRCII endorses this practice as a viable option. (NRCII, *supra*, at pp. 113-114 ["In the great majority of cases, very little is known about the person who left the DNA evidence …. It might be known that the DNA came from a white person, in which case the white database is appropriate. If the race is not known … , the calculations can be made with each of the appropriate databases and these presented to the court. *Alternatively, if a single number is preferred, one might present the calculations for the major racial group that gives the largest probability of a match*." (Italics added.)].)

On rehearing, the People argue that "giving the jury a single data base statistic with no racial component attached gives the jury *less information* than it would have under the current approach [of presenting several ethnic frequencies]." (Italics added.) But it is precisely this extraneous, potentially irrelevant and prejudicial information given to the jury that makes this method objectionable.

The People also assert on rehearing that NRCII has "resolved" this choice of database issue in favor of "'calculations for all racial groups to which possible suspects belong.'" (Citing NRCII, *supra*, at p. 122.) We do not read NRCII as concluding that this is the one correct practice. NRCII also recognizes use of the one most conservative

frequency, an option we prefer. (NRCII, *supra*, at pp. 113-114.) Furthermore, although NRCII is an extremely helpful scientific and technological resource, it does not have the authority to "resolve" legal issues of relevance. Indeed, NRCII does not claim to make legal conclusions and expressly recognizes the role of courts in determining how best to import science and technology into the trial and in resolving the legal issues that arise in that process.

A second option when the perpetrator's ethnicity is not established is presentation of a single frequency calculated from a general, nonethnic database. Again, this method makes no assumptions regarding the perpetrator's ethnicity and promotes no unwarranted ethnic or racial considerations. If, however, this method is not scientifically valid or results in a frequency that is not considered conservative, it is not a viable option.

In summary, we think prosecutors have three options in presenting profile frequencies: (1) establish that the perpetrator more likely than not belongs to a particular ethnic population, then present only the frequency in that particular ethnic population; (2) present only the most conservative frequency, without mention of ethnicity; or (3) present the frequency in a general, nonethnic population. These options promote the goals of admitting only relevant evidence and eliminating unjustifiable and potentially prejudicial references to ethnicity and race.

In addition, we believe cautious evaluation is appropriate in these cases because of the ambiguous nature of artificially defined ethnicities and the uncertainties connected to use of an ethnic database. The propriety of an ethnic database depends on the accuracy of both its creation and its utilization. These questions, among others, arise: Who determines that a sample person is Hispanic and should be placed in a Hispanic database? What are the criteria for doing so (e.g., the person's appearance, surname, self-description)? (NRCII "recognize[s] that most populations are mixed, that the definitions are to some extent arbitrary, and that they are sometimes more linguistic (e.g. Hispanic) than biological. In fact, people often select their own classification." (NRCII, *supra*, at p. 57.)) Does the Hispanic database contain adequate and proportionate samples of all the various Hispanic populations to which the perpetrator, identified by an eyewitness as Hispanic, could belong? How accurate is the eyewitness's evaluation of the perpetrator's ethnicity (e.g., can an eyewitness mistake a person of Asian, Native American, or Black ethnicity for a person of Hispanic ethnicity)? Is the accuracy of an eyewitness's evaluation affected when the perpetrator is of mixed ethnicity? (As the People recognize, eyewitness testimony regarding the appearance of the perpetrator can be unreliable. This reality lends support to use of options 2 and 3, *ante.*)

VII. CONCLUSION

The scientific issues in this case are straightforward evidentiary issues disguised by technicality. When the evidentiary issues are exposed, it also becomes clear that those issues are plagued by a persistent and insidious tendency to assume the defendant's guilt. The logical and evidentiary infractions in such an exercise are stunning in scope and consequence.

We decline to reconsider our finding in *Pizarro I* that the erroneous admission of the DNA evidence was not harmless (see *People v. Venegas, supra*, 18 Cal.4th at p. 93 [erroneous admission of results of DNA analysis required reversal only if it was reasonably probable verdict would have been more favorable to defendant in absence of error], citing *People v. Watson* (1956) 46 Cal.2d 818, 836), although the People urge us to do so in light of the "overwhelming non-DNA evidence of guilt." In *Pizarro I*, we stated that, despite the prosecution's "strong circumstantial case" against defendant, "the DNA identification evidence clearly 'sealed [his] fate.' Although the jury might have had a reasonable doubt regarding [defendant's] guilt absent the DNA evidence, it is difficult to imagine how the jury could have reached other than a guilty verdict when presented with the evidence that the likelihood of finding someone else with a DNA profile in the Caucasian population was 1 in 10 million and 1 in 250,000 in the Hispanic population. Therefore, it cannot be established that the admission of the evidence constituted harmless error." (*Pizarro I, supra,* 10 Cal.App.4th at p. 90.)

The three autorads (four if the D17 autorad is found to be readable) may now be re-analyzed by the FBI or another appropriate institution.[86] The new profile frequency determined from those autorads, if supported by sufficient foundational evidence, may be presented at trial. (See *People v. Venegas, supra*, 18 Cal.4th at pp. 94-95 [retrial not

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86 We are not aware of whether any portions of the original DNA samples survive.

precluded since erroneously admitted evidence was sufficient to permit finding of guilt beyond a reasonable doubt], citing *Lockhart v. Nelson* (1988) 488 U.S. 33, 40.)

DISPOSITION

The judgment is reversed.

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Ardaiz, P.J.

WE CONCUR:

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Vartabedian, J.

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Harris, J.