JAY JAFFE
State Bar #53812
433 North Camden Dr., Suite 1200
Beverly Hills, Calif. 90210
(310) 275-2333

WILLIAM C. THOMPSON
State Bar # 104967
6 Dickens Court
Irvine, Calif. 92715
(714) 856-2917

Attorneys for Defendant
SAMMY MARSHALL

SUPERIOR COURT OF THE STATE OF CALIFORNIA
FOR THE COUNTY OF LOS ANGELES

THE PEOPLE OF THE STATE OF CALIFORNIA, Plaintiff, v. SAMMY MARSHALL Defendant.	No. BA 069796 **Motion to Exclude DNA Evidence** In Department 115, Los Angeles County Superior Court

TO THE CLERK OF THE ABOVE-ENTITLED COURT AND TO THE DISTRICT ATTORNEY OF THE COUNTY OF LOS ANGELES:

Defendant, SAMMY MARSHALL, by and through counsel, hereby moves this Honorable Court for an order providing that:

I. Pursuant to the rule in People v. Kelly (1976) 17 Cal.3d 24, 130 Cal.Rptr 144. governing the admissibility of scientific evidence, the results of forensic DNA testing that

purport to incriminate Mr. Marshall be excluded from evidence on grounds that Genetic Design, the laboratory that performed DNA analysis in this case, failed to follow correct scientific procedures. The issues in controversy include:

A. The appropriateness of the method used to score and interpret the results of RFLP analysis in this case, particularly the scoring of "faint bands" that allegedly incriminate defendant Marshall.

B. The appropriateness of the data base used to generate estimates of the frequency of DNA profiles in this case: Genetic Design used a secret, proprietary data base which the company has refused to make available to defendant (in defiance of this court's discovery order), which Genetic Design has never made available to the scientific community, and which therefore cannot be checked to verify its appropriateness for forensic DNA analysis.

C. The use of frequency estimation procedures that misstate the likelihood of a coincidental match because they fail to take into account that the evidentiary samples are mixtures of DNA from multiple contributors.

D. The failure of the laboratory to make valid estimates of its rate of false positive laboratory errors.

E. The failure of the laboratory to take adequate steps for quality assurance and quality control, including (a) the failure of the laboratory to seek or obtain accreditation; and (b) the failure of the laboratory to participate in an adequate program of external proficiency testing.

F. The failure of the laboratory to follow the method recommended by the National Research Counsel for computing the statistical significance of a DNA match.

II. That the DNA statistical estimates computed by Genetic Design in this case be excluded pursuant to the rule of People v. Cella (1983) 139 Cal.App. 3d 391, 188 Cal.Rptr. 675, on grounds that these statistics fail to quantify all crucial variables. The issues in controversy include the failure of Genetic Design's statistical estimates to quantify or take into account several variables that are crucial to the value of the DNA evidence in this case, including: a) the possibility of laboratory error; b) the uncertainty

introduced by the need to interpret "faint bands;" c) that the evidentiary samples may be mixtures of DNA from multiple contributors.

III. That pursuant to California Evidence Code Section 352, Genetic Design's DNA statistical estimates should not be presented to the jury in this case because they are biased against the defendant in ways that will be very difficult to explain to a lay jury and therefore are unfairly prejudicial, confusing and misleading. The proffered statistics overstate the value of DNA evidence by :

A. Failing to incorporate or include quantitative estimates of laboratory error rate.

B. Failing to take into account the uncertainty introduced into the analysis by the faintness of the bands that allegedly incriminate defendant Marshall.

C. Failing to take into account the greater likelihood of a coincidental match when a suspect's DNA profile is compared to a mixed DNA sample.

IV. That the Court take judicial notice of the scientific and legal articles and transcripts upon which the attached memorandum of points and authorities is based. These materials are assembled in the binder enclosed herewith and organized therein alphabetically by last name of the author.

Dated: October 10, 1995

Respectfully submitted,

William C. Thompson

MEMORANDUM OF POINTS AND AUTHORITIES IN SUPPORT OF DEFENDANT'S MOTION TO EXCLUDE DNA EVIDENCE

I. INTRODUCTION

The prosecution seeks to introduce the results of a DNA test performed by Genetic Design, a private, commercial laboratory in North Carolina, using a method known as restriction fragment length polymorphism analysis (RFLP analysis). Defendant concedes that RFLP analysis, when properly performed, is a generally accepted method for forensic DNA testing that can pass muster under the standard of People v. Kelly (1976) 17 Cal.3d 24, 130 Cal.Rptr. 144.[1] Defendant contends, however, that Genetic Design failed to follow correct scientific procedures for performing RFLP analysis in this

---

[1] California appellate decisions on the admissibility of forensic RFLP analysis have reached mixed results, although the recent trend favors admissibility, at least where the laboratory complied with the recommendations of the National Research Council for computing statistical estimates. See, People v. Axell (1991) 235 Cal.App.3d 836 (Cellmark RFLP test passes muster under Kelly/Frye); People v. Barney (1992) 8 Cal.App.4th 798, 10 Cal.Rptr.2d 731 (Cellmark and FBI RFLP tests fail to meet Kelly/Frye standard due to scientific dispute over statistical method); People v. Wallace (1993) 14 Cal.App.4th 651 (dispute over statistical method continues and precludes admissibility); People v. Taylor (1995) 33 Cal.App.4th 262, 40 Cal.Rptr.2d 132 (RFLP evidence admissible where statistics are computed in accordance with the method recommended by the National Research Council); People v. Amundson (1995) 34 Cal.App.4th 1151, 41 Cal.Rptr.2d 127 (Cellmark RFLP test admissible under Kelly; concerns raised in Barney have been answered).

On March 16, 1995, the California Supreme Court granted a petition for review in People v. Venegas (1995) 31 Cal.App.4th 856. On the same day, the Supreme Court issued "grant and hold" orders (See California Rules of Court, Rule 29.2 (c)) in the cases of People v. Soto (1994) 30 Cal.App.4th 340, and People v. Wilds (1995) 31 Cal.App.4th 636. On July 20, 1995, the Supreme Court granted review in People v. Marlow (1995) 41 Cal.Rptr.2d 5 (Cal.App. 6 Dist.). Consequently, Venegas, Soto, Wilds, and Marlow cannot be cited as legal authority. See California Rules of Court, Rule 976(d)("Unless otherwise ordered by the Supreme Court, no opinion superseded by a grant of review, rehearing, or other action shall be published.") and Rule 977(a)("An opinion that is not ordered published shall not be cited or relied on by a court or a party in any other action or proceeding...).

case, and that the test results must therefore be excluded under the so-called "third prong" of Kelly.

> The California Supreme Court held in Kelly that, in addition to establishing the reliability (i.e., general acceptance) of a new scientific technique and the qualifications of expert witnesses, "the proponent of the evidence must demonstrate that correct scientific procedures were used in the particular case [Citations.]" (People v. Kelly, supra, 17 Cal.3d at p. 30.) This latter point is sometimes called the "third prong" of Kelly-Frye.
>
> People v. Barney (1992) 8 Cal.App.4th 798, 10 Cal.Rptr.2d 731, 746

The need for a pretrial hearing to establish that a DNA laboratory followed correct procedures was first recognized in People v. Axell (1991) 235 Cal.App.3d 836,[2] and has been reaffirmed by subsequent cases. Barney explained the need for a third-prong hearing as "a matter of simple common sense." 10 Cal.Rptr. at 747. "If it is not established that correct scientific procedures were used in the particular case, it cannot be known whether the test that was actually conducted is the one that has achieved general scientific acceptance." Id. Moreover, the purpose of the Kelly/Frye rule (i.e., assuring that scientific evidence is reliable) is thwarted if the methods used by a DNA laboratory in a given case differ from those used when the test passed muster under Kelly.

> Kelly/Frye resolves not just that a technique is reliable but also that the manner in which the technique is performed assures its reliability. Therefore, the procedure by which the technique or process is performed is part of the Kelly/Frye

---

[2] "Due to the complexity of the DNA multisystem identification tests and the powerful impact that this evidence may have on a jury, satisfying Frye alone is insufficient to place this type of evidence before a jury without a preliminary critical examination of the actual testing procedures performed. [Citations.]
... we adhere to the traditional view that the third prong of the Kelly test is also the subject of a pretrial hearing on the question of admissibility."
People v. Axell, supra, at p. 862.

> evaluation. If someone performs the test in a manner distinct from the procedures used when the test has successfully undergone Kelly/Frye scrutiny, that different procedure must itself assure reliability.

People v. Pizarro (1992) 10 Cal.App.4th 57, 12 Cal.Rptr.2d 436, 449

Defendant contends that Genetic Design deviated from accepted procedures for forensic RFLP analysis in several crucial respects (which will be elaborated below) and that, as a result, the findings that purportedly incriminate Mr. Marshall are unreliable and would not be generally accepted by the scientific community, and must therefore be excluded under Kelly.

Defendant also challenges the admissibility of the statistical estimate computed by Genetic Design to show the significance of the "DNA match" between defendant Marshall and an evidentiary sample in this case. This statistic fails to take into account a number of important variables that affect the value of the DNA match in this case and is therefore misleading and prejudicial. As will be explained below, the statistical evidence should be excluded under the standard of People v. Cella (1983) 139 Cal.App. 3d 391, 188 Cal.Rptr. 675 and under Evidence Code Section 352.

II. THE "FAINT BAND" PROBLEM

The key evidence against defendant Sammy Marshall in this case is derived from a DNA test that was performed and interpreted by Mr. Michael DeGuglielmo, a technician[3]

[3] Mr. DeGuglielmo does not have a Ph.D. Should he be called to testify, the defense will challenge his expertise in areas of science relevant to forensic DNA testing (i.e., molecular biology, population genetics, statistics).

employed by Genetic Design Corporation, an unaccredited[4] private forensic laboratory in Greensboro, North Carolina. According to Mr. DeGuglielmo, his test (which employed RFLP analysis) shows a DNA banding pattern in the "vaginal aspirate" of the rape victim that is consistent with Mr. Marshall's DNA banding pattern; this pattern is estimated to occur with a frequency of only one in 641 million. On its face, this DNA evidence appears to provide powerful proof of Marshall's guilt.

With DNA evidence, however, appearances can be deceiving. At the request of defense counsel, two Ph.D.-level experts have reviewed DeGuglielmo's work by examining copies of the test results disclosed by the prosecution, including copies of x-ray plates, known as autorads, that show the "DNA banding pattern" of each sample. The two experts, Professor William Shields of the State University of New York, Syracuse, and Professor Aimee Bakken of the University of Washington, independently reached the same conclusion: the DNA test does **not** incriminate Mr. Marshall. The professors could not see a "DNA banding pattern" in the vaginal aspirate that corresponds to Marshall's pattern. When Professor Bakken "scored" these autorad copies, using a BioImage machine (the same type of computer-assisted imaging device used by Mr. DeGuglielmo), the machine found a different "DNA banding pattern" in the vaginal aspirate than had been reported by DeGuglielmo. Based on these findings, the experts concluded that, with respect to Mr. Marshall, the results of the DNA test are either inconclusive or exculpatory.

---

[4] The only recognized system of accreditation for forensic DNA laboratories is administered by the American Society of Crime Laboratory Directors (ASCLD). A number of state and county crime laboratories, and at least one private laboratory (Cellmark Diagnostics), have received ASCLD accreditation. Genetic Design has not.

(See declarations of Professors Shields and Bakken, attached to defendant's Points and Authorities in support of his Motion for Appointment of Expert and Defense Access to Laboratory).

What accounts for the contradiction between the conclusions of defendant's Ph.D.-level experts and those of Genetic Design's technician, Mr. DeGuglielmo? Defendant contends that DeGuglielmo reached the wrong conclusion because he failed to follow correct scientific procedures for analyzing DNA evidence. Specifically, DeGuglielmo failed to use objective procedures for "scoring" the autorads. Although he used a computer-assisted imaging device to "score" the autorads, defense counsel believe that he overrode the device's findings and substituted his own subjective interpretation of the autorads and did so in a manner that caused him (perhaps unwittingly) to be biased in favor of an incriminating result. Additionally, defendant contends that the BioImage machine is unreliable for scoring bands as faint as those that allegedly incriminate Mr. Marshall

The extreme faintness of the "incriminating bands" is one factor that distinguishes this case from previous cases in which RFLP analysis was found admissible. In previous cases where DNA evidence was admitted, the critical bands were so dark and clear that there was no dispute about their presence. The reliability of the procedure for "scoring" these bands (i.e., for detecting their presence) was not even an issue. In this case, however, the critical bands are so faint that they are difficult to see (if they are present at all). Consequently, the reliability of the methods used to score these bands will be a central issue.

Defendant will present evidence that subjective interpretation of autorads is not an accepted scientific procedure for performing RFLP analysis, that it is scientifically incorrect, and that it produces a severe bias against the defendant. See, E. Lander, DNA Fingerprinting On Trial, Nature 339:501-05 (1989)(in binder); W.C. Thompson, Subjective Interpretation, Laboratory Error and the Value of Forensic DNA Evidence: Three Case Studies, Genetica 96:153-68 (1995) (in binder). Defendant's evidence will prove that the accepted procedure requires an objective and reliable scoring method. See National Research Council, DNA Technology in Forensic Science (1992), at p. 53. If Genetic Design failed to use an objective method, or used a method that is unreliable, then it failed to employ correct scientific procedures within the meaning of Kelly and the DNA evidence that incriminates Mr. Marshall must be excluded.

The use of subjective and/or unreliable procedures to score faint bands also renders the DNA evidence inadmissible under Evidence Code Section 352. Defendant will offer evidence that subjective scoring of bands can greatly reduce the probative value of DNA evidence, and can do so in ways that are likely to be difficult to explain to lay jurors. Consequently, the value of subjectively scored DNA evidence may be far less than the jury would assume, creating an unfair prejudice and bias against defendant.

III. THE SECRET DATA BASE

To come up with the impressive figure of one in 641 million, Genetic Design used its own proprietary data base.[5] Genetic Design has refused to provide defendant a copy of

[5] For background information on the nature of a data base or the way in which a data base is used to derive estimates of the frequency of DNA profiles, see W.C. Thompson,

the raw data in this data base, despite repeated discovery requests. Genetic Design has also defied an order of this court's order of August 21, 1995 which which requires production of copies of "all data that Genetic Design has sent to outside consultants for the purpose of Hardy-Weinberg/linkage studies..." and specifies that "[t]he data is to be provided in the same form that it was provided to outside consultants (i.e., on computer diskettes)." (Item #3). Without access to the raw data, defendant's experts cannot perform basic checks on the validity of the data base, such as checks for Hardy-Weinberg equilibrium.

It is not acceptable in the scientific community to rely on a secret, proprietary data base to compute statistics that are presented in evidence in a criminal case.

> Any population databank used to support forensic DNA typing should be openly available for reasonable scientific inspection. Presenting scientific conclusions in a criminal court is at least as serious as presenting scientific conclusions in an academic paper. According to long-standing and wise scientific tradition, the data underlying an important scientific conclusion must be freely available, so that others can evaluate the results and publish their own findings, whether in support or in disagreement. There is no excuse for secrecy concerning the raw data. Protective orders are inappropriate, except for those protecting individual's names and other identifying information, even for data that have not yet been published or for data claimed to be proprietary. If scientific evidence is not yet ready for both scientific scrutiny and public re-evaluation by others, it is not yet ready for court.

National Research Council, DNA Technology in Forensic Science, 1992 (hereinafter "NRC Report"), at p. 93-94.

In previous California cases where RFLP evidence has been found admissible, the laboratory made its data base available to opposing experts for analysis and study. Both Cellmark and the FBI have made their raw population data available in computer-readable

---

Evaluating the Admissibility of New Genetic Identification Tests: Lessons from the "DNA War" 84 J.Crim.L. & Criminol. 22 (1993)(hereinafter, "Lessons"), at p. 65-70 (in binder).

form to opposing parties in litigation. Defense counsel is informed by other defense lawyers, and by scientists familiar with the issue, that Genetic Design has never made its data base available to opposing experts.

In light of the National Research Council's commentary on the matter (quoted above) it is clear that the scientific community does not accept statistics computed from secret data bases. Reliance on a secret data base therefore constitutes a deviation from accepted scientific procedure and renders the resulting statistical estimates inadmissible under Kelly.

IV. THE PROBLEM OF LABORATORY ERROR

Evidence of a DNA "match" between two samples is impossible to evaluate without reliable information on the probability that a match would be declared if the samples are from different individuals. Most commentators consider the ability to express this probability to be crucial to the admissibility of DNA-derived evidence: "without being informed of such background statistics, the jury is left to its own speculations." McCormick, Evidence, 655 (Cleary ed.).

The need for background statistics to show the meaning of a DNA match is firmly established in California law. People v. Barney, 10 Cal.Rptr.2d 731, 742 ("The statistical calculation step is the pivotal element of DNA analysis, for the evidence means nothing without a determination of the statistical significance of a match of DNA patterns."); People v. Axell (1991) 235 Cal.App.3d 836, 866 1 Cal.Rptr.2d 411, 430 ("We find that...a match between two DNA samples means little without data on probability...); People v. Wallace (1993) 17 Cal.Rptr.2d 721, n. 3 (without valid statistics DNA evidence is

"meaningless"[6]); accord, Commonwealth v. Curnin, 409 Mass. 218, 526 N.E.2d 440 (1991)("It is apparent from the basis on which we decide the DNA testing issue that we would not permit the admission of test results showing a DNA match (a positive result) without telling the jury anything about the likelihood of that match occurring"); Ex Parte Perry, 586 So.2d 242, 254 (Ala. 1991); State v. Cauthron, 846 P.2d 502 (Wash. 1993)("[t]estimony of a match in DNA samples, without the statistical background or probability estimates, is neither based on a generally accepted scientific theory nor helpful to the trier of fact."); Nelson v. State, 628 A.2d 69 76 (Del. 1993)(trial court's exclusion of match frequency "inherently inconsisitent" with its admission of testimony of a match, because "without the necessary statistical calculations, the evidence of the match was 'meaningless' to the jury."); State v. Brown, 470 N.W.2d 30 (Iowa 1991)("Without statistical evidence, the ultimate results of DNA testing would become a matter of speculation."); State v. Vandebogart, 616 A.2d 483, 494 (N.H. 1992)("A match is virtually meaningless without a statistical probability expressing the frequency with which a match would occur.").

When DNA evidence was first offered in the courtroom, the only statistic considered necessary was the frequency of the matching DNA profile in a reference

---

[6] To say that DNA evidence is "meaningless" without statistical data on match probabilities is not the same as saying that such evidence has no probative value. The problem is not that evidence of a match, by itself, is valueless; the problem is that its value is impossible for the trier of fact to assess in a meaningful manner. Thus, in Wallace, the Court of Appeal suggested that it might be more accurate to state that DNA evidence "'is incomplete without an interpretation of its significance'." 17 Cal.Rptr. at 726 (n. 3)(quoting Barney). Regardless of the semantics, it is clear that without appropriate statistics the trier of fact will find it difficult if not impossible to weigh the DNA evidence.

population. The frequency of the profile is thought to reflect the probability of a coincidental match. If the profile of an evidentiary sample has a frequency of only one in a million in the population, for example, then presumably there is only one chance in a million that the defendant will, by coincidence, happen to match it. When DNA evidence was first offered in the courtroom, it was widely (but mistakenly) assumed that a coincidental match is the only way that DNA profiles of different people would be found to match. Consequently, appellate courts have, to date, required that no statistics other than frequency statistics be presented to juries.

But scientific opinion has recently shifted on the question of what statistics are necessary to evaluate DNA evidence. It is now broadly recognized that a false "match" between samples can occur in two ways.

> Interpretation of DNA typing results depends not only on population genetics, but also on laboratory error. Two samples might show the same DNA pattern for two reasons: two persons have the same genotype at the loci studied, or the laboratory has made an error in sample handling, procedure, or interpretation.

NRC Report, at p. 88

Thus, to evaluate DNA evidence, the jury needs statistics that address the probability of both events that could cause a false match: a coincidental match and a “false positive” laboratory error. To provide statistics that reflect the probability of one event that could cause an innocent person to match, and not the other, would leave the jury to speculate about the meaning of DNA evidence.

> Especially for a technology with high discriminatory power, such as DNA typing, laboratory error rates must be continually estimated in blind proficiency testing and must be disclosed to juries. For example, suppose the chance of a match due to two persons' having the same pattern were 1 in 1,000,000, but the

> laboratory had made one error in 500 tests. The jury should be told both results; both facts are relevant to a jury's determination.

NRC Report, at p. 89.

Other experts have recently echoed this conclusion:

> Statisticians and geneticists involved in the controversy over DNA testing have understandably been fascinated by and mostly written on disputes regarding the statistical and genetic issues that DNA identification raise, but laboratory error places the most serious limits on the evidentiary import of reported DNA matches. If justice is the mutual goal of those involved in the debates over DNA identifications--and I believe it is everyone's concern--the possibility of error must be honestly faced, and it must be incorporated into estimates of the incriminatory power of DNA matches.

Richard Lempert, Comment: Theory and Practice in DNA Fingerprinting, 9 Statistical Science 255, 257 (1994) (in binder).

Little attention was devoted to the likelihood of false positives when DNA evidence was first introduced in the courtroom because there was a widespread misperception that false positive are impossible in RFLP-based DNA tests.[7] This misperception was generated and sustained by self-serving claims of DNA test promoters that DNA tests are infallible, fail-safe, and error-free.[8] Professor Jonathan Koehler has

---

[7] The courts that decided Axell, Barney, and Wallace appear to have been unaware of the growing belief, among scientists, that laboratory error rates are crucial to the evaluation of DNA evidence. Consider, for example, the following statement from Barney:

> To say that the frequency of Howard's DNA pattern in 1 in 200 million...is tantamount to saying his pattern is totally unique, and thus only he could have been the source of the crime scene blood stains. 8 Cal.App. at 817. (emphasis added)

This statement is coherent only if one assumes, as the court undoubtedly did, that laboratory error is not a factor in determining whether Howard was the source of the bloodstains.

[8] See, People v. Shi Fu Huang, 546 N.Y.S.2d 920 (Co.Ct. 1989)("Dr. Baird testified that it is impossible to get a false positive"); People v. Wesley, 533 N.Y.S.2d 643 (Co.Ct. 1988)("it is impossible under the scientific principles, technology and procedures of DNA Fingerprinting (outside of an identical twin), to get a "false positive" -- i.e., to identify the wrong individual as the contributor of the DNA being tested...Under the undisputed testimony received at the hearing, no "wrong" person, within the established powers of identity for the test, can be identified."); Hicks v. State, 860 S.W.2d 419, Tex.Crim. App. 1993)("According to Caskey, a false positive finding was impossible..."); State v. Cobey,

suggested that DNA test promoters "engaged in a sinister semantic game" in which they were able to issue misleading denials of the possibility that a DNA test could make an "error" by excluding consideration of human error in administering or interpreting the test. J. Koehler, Error and Exaggeration in the Presentation of DNA Evidence at Trial, 34 Jurimetics 21, 24 (1993)(in binder). Needless to say, the effort to to distinguish "human error" from "test error" is pointless and misleading when humans are necessarily involved in administration and interpretation of the test, when occasional human errors are inevitable, and when it is necessary to know the overall rate of error (from whatever cause) to evaluate the test results. "For juries it is of little significance what causes an innocent person to match, what matters is how often such matches might be expected." Laurence Mueller, The Use of DNA Typing in Forensic Science. 3 Accountability in Research 55, 56 (1993) (in binder).; see also Thompson, "Lessons", supra, at p. 92(in binder)..

But the potential for false positives due to laboratory error in DNA testing is now beyond dispute. "Laboratory errors happen, even in the best laboratories and even when the analyst is certain that every precautioun against error was taken." NRC Report, p. 88-89. See also Koehler, DNA Matches and Statistics. 76 Judicature 222, 229 ("[B]ased on the little evidence available to date, a reasonable estimate of the false positive error rate is 1-4 percent.") (in binder).; Koehler, Error and Exaggeration, supra., p. 26 (proficiency

---

559 A.2d 391, 392 (Md.App. 1989)("An Incorrect match is an impossible result"); see also Jonathan J. Koehler, DNA Matches and Statistics: Important Questions, Surprising Answers, 76 Judicature 222 (1993); Koehler, Error and Exaggeration in the Presentation of DNA Evidence at Trial, 34 Jurimetics 21 (1993)(quoting a number of similar statements from transcripts of expert testimony).

testing shows error rate of 1-4%)(in binder); Donald Berry, Comment, 9 Stat. Sci. 252, 253 (1994)("Only the frequency and type of errors are at issue.") (in binder).; R.C. Lewontin, Comment: The Use of DNA Profiles in Forensic Contexts, 9 Stat. Sci. 259 (1994)(discussing sources of error) (in binder).; William C. Thompson, Comment, 9 Stat. Sci. 263, 265 (1994)(discussing data on laboratory error) (in binder).; Cf. Dan L. Burk, DNA Identification: Possibilities and Pitfalls Revisited, 31 Jurimetics 53, 80 ("Bald statements or broad hints that DNA testing is infallible...are not only irresponsible, they border on scientific fraud")(in binder)..

Indeed, most experts now believe that having an accurate estimate of the false positive rate is more important than having an accurate estimate of the probability of a coincidental match because the rate of false positives is likely to be much greater than the rate of coincidental matches, at least for RFLP-based tests.[9] Paul J. Hagerman, DNA Typing in the Forensic Arena, 47 Am.J.Hum.Genet. 876 (high false positive rate makes probability of coincidental match irrelevant) (in binder).; Richard Lempert, Some Caveates Concerning DNA As Criminal Identification Evidence: With Thanks to the Reverend Bayes. 13 Cardozo L.Rev 303, 325 (the probability of a coincidental match between people who have the same DNA profile "is usually dwarfed by the probability of a false positive error")(in binder).; Mueller, The Use of DNA Typing in Forensic Science, supra, p. 58 (exact probability of a coincidental match "should hardly matter" to jury given much greater likelihood of false positive) (in binder).

[9] By analogy, if one needed to estimate the amount of money a man was carrying, it would typically be more important to have an accurate information on the number and

Consequently, defendant takes the position that DNA evidence cannot now be admitted unless it is accompanied by a scientifically valid and acceptable estimate of the statistical probability of a false positive error. The error rate issue is not merely a matter of the weight of DNA evidence. For reasons stated below, this issue goes to the admissibility of DNA evidence.

A. Evidence of a DNA Match Cannot Meaningfully Be Evaluated Without Knowing the Likelihood of a False Match Due to Laboratory Error and Must Therefore Be Excluded

A central premise of California appellate cases is that evidence of a DNA match is inadmissible unless accompanied by statistics that can tell the trier of fact what the match means. Axell, Barney, Pizarro and Wallace all recognize this principle. Now that the scientific community has recognized that error rates must be taken into account in order to make a meaningful evaluation of DNA evidence, the logic of those cases requires that juries be given statistics on the probability of laboratory error; without such statistics, evidence of a DNA match is inadmissible because it is impossible to evaluate.

It would be absurd for courts to insist on valid quantitative estimates of the probability of a coincidental match, without also requiring valid estimates of the rate of false positives due to laboratory error, when the scientific community has determined that the latter is more important than the former to a rational evaluation of DNA evidence. If DNA evidence is "meaningless" without statistical estimates of the probability of a

---

denomination of bills in his wallet than on the number and denomination of coins in his pocket because the coins would represent only a small portion of his total money.

coincidental match, it is also "meaningless" without statistical estimates of the probability of a false positive.

This conclusion does not depend on the general acceptance standard of Kelly. It is a fundamental rule of law, established by Axell, Barney, Pizarro and Wallace, that evidence of a DNA match is inadmissible in the absence of statistics that can give meaning to the "match."

Defendant contends that, unlike other laboratories, Genetic Design has done inadequate research to determine its error rate and therefore that no valid estimates of the probability of a false match can be made.

B. The Scientific Acceptability of DNA Evidence Depends On Having a Valid Error Rate Estimates.

Although the conclusion that DNA evidence is inadmissible without valid error rate statistics can be reached without reference to the general acceptance test of Kelly, defendant contends that this conclusion is also compelled by Kelly. In other words, Kelly provides a second, independent grounds for rejecting DNA evidence in the absence of valid error rate estimates. According to current scientific opinion on the matter, DNA evidence is not acceptable without valid error rate estimates. Consequently, a laboratory that performs a DNA test but fails to determine its error rate in a correct manner is not following the accepted procedure.

Professor Eric Lander, one of the earliest and most influential scientific commentator on DNA evidence, and an author of the influential report of the National Research Council on forensic DNA evidence, explained the matter succinctly:

> ...it is simply crazy and scientifically unacceptable to agonize over the exact population frequencies, which might be one in a million, or one in a hundred thousand, or one in ten thousand for the frequency of a genotype in a population, and yet not have actual data for the accuracy, the proficiency of a laboratory's handling of samples....[T]he scientific acceptability of DNA evidence depends on the proficiency of a laboratory being tested such that one can know what the error rate is likely to be, or at least have an upper bound on that error rate.

Prof. Eric Lander, Testimony as a Court's Witness in U.S. v. Porter, District of Columbia Crim. docket 3F-6277-89, p. 46 July 28, 1994 (hereinafter "Lander testimony")(in binder).

The NRC Report recommends that jurors be given two numbers, one indicating the frequency of matching genotypes and the other indicating the rate of laboratory error. "The jury should be told both results; both facts are relevant to a jury's determination." NRC Report, p. 89.

Some experts have gone so far as to suggest that jurors be told only the false positive rate; they reason that the probability of a false positive is so much greater than the probability of a coincidental match (at least for multi-locus RFLP matches) that the latter probability has little bearing on the value of the evidence. For example, if the probability of a false match due to laboratory error were .01 (one chance in 100) and the probability of a coincidental match were .000001 (one chance in one million), then the overall probability of a match between samples from different people would be approximately .010001, a number that conveniently rounds off to .01 (one in 100). So why not just tell jurors the false positive rate and avoid the risk that they will be confused or unduly swayed by an impressive number (one in one million) that has little meaning or value relative to the false positive rate?

> The rate of false positives defines a practical lower bound on the probability of a match, and probability estimates based on population data that are smaller than the false-positive rate should be disregarded.

R.C. Lewontin & Daniel Hartl, Population Genetics in Forensic DNA Typing, 254 Science 1745, 1749 (1991) (in binder).

Professor Richard Lempert specifically cites the danger of confusion and prejudice as a reason for presenting only the error rate statistic in cases where the probability of a false positive greatly exceeds the probability of a coincidental match.

> ...jurors provided with a laboratory's false positive rate and with information about the likelihood, assuming no testing error, of a match if the evidence DNA was not the defendant's, are likely to be hopelessly confused about the weight to accord the testimony because ordinary people are not very good at working with conditional probabilities. Thus, jurors ordinarily should receive only the laboratory's false positive rate as an estimate of the likelihood that the evidence DNA did not come from the defendant.

Lempert, "Caveats" supra, p. 325(in binder)..

Consequently, to meet the foundational requirement established by the third-prong of Kelly (correct scientific procedures were followed), the prosecution will need to proffer an estimate of Genetic Design's error rate and will need to show that it was determined in a scientifically correct manner.

C. Without Valid Error Rate Estimates, the Frequency Statistics Are a Misleading Partial Quantification of the Value of DNA Evidence That Must Be Excluded Under People v. Cella and Evidence Code Section 352.

There are two variables that determine the value of a DNA match. One variable is the probability of a coincidental match, the other is the probability of a false positive due to lab error. Most scientists now think the latter probability is the more important of the two, particularly for RFLP-based DNA tests. The legal issue that arises from this scientific insight can be stated simply: Is it permissible to present to the jury quantitative estimates of one variable that affects the value of a piece of evidence (the less important

one) without also giving the jury quantitative estimates of the other variable (the more important one)? The answer, under California law, is clearly no. "If mathematical probabilities are to be of any use in the courtroom setting, all crucial variables must be quantified exactly." People v. Cella (1983) 139 Cal.App.3d 391, 405, 188 Cal.Rptr. 675, 684.

At issue in Cella was the admissibility of a mathematician's estimate of the probability of a "match" in the order of listings on two itemized lists. The mathematician's estimate reflected the probability of a coincidental match occurring due to random chance, assuming that the lists were generated independently. But it failed to take into account other ways (besides coincidence) that the match might have occurred. The failure of the mathematical procedure to take into account all crucial variables rendered it "a prime subject for exclusion under Evidence Code section 352." 139 Cal.App. 405.

To give jurors impressive-sounding numbers reflecting the estimated frequency of a DNA profile, without also quantifying the probability of a false positive, would be gravely prejudicial. Jurors will naturally assume that the number they hear provides a meaningful indication of the value of the DNA match. In the case of an RFLP match, this assumption will be false. The number will in fact be meaningless and misleading to jurors unless they also take into account a more important factor that is not quantified--the probability of a false positive. But they are unlikely to do so.

> The syndrome is a familiar one: If you can't count it it doesn't exist.... Readily quantifiable factors are easier to process--and hence more likely to be recognized and then reflected in the outcome--than are factors that resist ready quantification. The result, despite what turns out to be a spurious appearance of accuracy and completeness, is likely to be significantly warped and hence highly suspect.

Laurence H. Tribe, Trial By Mathematics: Precision and Ritual in the Legal Process, 84 Harv.L.Rev. 1329, 1361-62 (1971).

Some experts have gone so far as to suggest that jurors be told only the false positive rate; they reason that the probability of a false positive is so much greater than the probability of a coincidental match (at least for multi-locus RFLP matches) that the latter probability has little bearing on the value of the evidence. For example, if the probability of a false match due to laboratory error were .01 (one chance in 100) and the probability of a coincidental match were .000001 (one chance in one million), then the overall probability of a match between samples from different people would be approximately .010001, a number that conveniently rounds off to .01 (one in 100). So why not just tell jurors the false positive rate and avoid the risk that they will be confused or unduly swayed by an impressive number (one in one million) that has little meaning or value relative to the false positive rate?

> The rate of false positives defines a practical lower bound on the probability of a match, and probability estimates based on population data that are smaller than the false-positive rate should be disregarded."
> R.C. Lewontin & Daniel Hartl, Population Genetics in Forensic DNA Typing, 254 Science 1745, 1749 (1991) (in binder).

Professor Richard Lempert specifically cites the danger of confusion and prejudice as a reason for presenting only the error rate statistic in cases where the probability of a false positive greatly exceeds the probability of a coincidental match.

> ...jurors provided with a laboratory's false positive rate and with information about the likelihood, assuming no testing error, of a match if the evidence DNA was not the defendant's, are likely to be hopelessly confused about the weight to accord the testimony because ordinary people are not very good at working with conditional probabilities. Thus, jurors ordinarily should receive only the laboratory's false

positive rate as an estimate of the likelihood that the evidence DNA did not come from the defendant.

Lempert, "Caveats" supra, p. 325 (in binder).

Whether jurors should be given both the frequency statistic and the error rate statistic, or just the error rate statistic, will undoubtedly be subject to further debate by experts. It is now clear, however, that giving the jury just the frequency is not an acceptable option. It is misleading, it mischaracterizes the value of the evidence in a manner that is prejudicial to criminal defendants, and it creates a biased perception of the evidence that may be impossible to correct. Consequently, unless valid statistics can be presented on the probability of a false match due to laboratory error, evidence of a DNA match should be excluded under Evidence Code Section 352.

D. Genetic Design Has Yet to Do the Research Needed to Determine Its Error Rate in a Scientifically Acceptable Manner.

Scientific commentary makes it clear that, in order to be accepted as reliable by the scientific community, the method for determining error rate must involve externally administered blind proficiency testing. A blind proficiency test is one in which the analyst is not aware he or she is being tested. The NRC Report declares that "...laboratory error rates must be continually estimated in blind proficiency testing." NRC Report, p. 89. The proficiency tests must be "truly representative of case materials (with respect to sample quality, accompanying description, etc.)." Id. The NRC notes that "[t]ests based on pure blood samples would probably underestimate an error rate." Thus it appears that such tests are not accepted as a reliable way to determine the error rate of a forensic test.

Other commentators agree. For example, Professor Bruce Weir, a frequent prosecution witness, has noted that the NRC Report "makes a strong case" for determining actual error rates through proficiency testing, although he warns that "[e]stablishing rates of false positives and false negatives may not be easy." Weir, supra, p. 11658. Professor Jonathan Koehler declares that "[t]he best way to measure the rate of false positive error associated with a laboratory or an individual technician is through an ongoing series of blind, external proficiency tests conducted under realistic conditions." Koehler, "Error and Exaggeration" supra, p. 28. Others who endorse this position are R.C. Lewontin, supra, p. 260 ("there must be frequent independent and unannounced inspections and tests"); Mueller, supra, p. 57 (noting with approval the NRC's call for blind proficiency tests); Hagerman, supra. (noting importance of proficiency testing to error rate determination).

The NRC Committee emphasized the importance of proficiency testing in a prefatory statement to its report.

> We regard the accreditation and proficiency testing of DNA typing laboratories as essential to the scientific accuracy, reliability, and acceptability of DNA typing evidence in the future. Laboratories involved in forensic DNA typing should move quickly to establish quality assurance programs. After a sufficient time for implementation of quality-assurance programs has passed, courts should view quality control as necessary for general acceptance.

NRC Report, at *x*.

In recent testimony, Professor Eric Lander, a member of the NRC committee, explained that the Committee did not wish to call a moratorium on all forensic DNA testing but wanted to see proficiency testing programs set up as soon as possible because the committee members unanimously believed "that proficiency testing is an essential

component of the scientific reliability and acceptability of [DNA] evidence." Lander testimony, supra, at p. 43(in binder). In saying that laboratories should move "quickly" to establish such programs, the Committee chose the term with care "to be faster than with all deliberate speed, for example," p. 80. and to clearly signal courts that failure to do proficiency testing would not be acceptable for long.

Lander also explained the reason the Committee demanded blind proficiency testing: only blind testing gives an adequate measure of the likelihood of error.

> An adequate [method of proficiency testing] must surely be blind. If you know that you are working on test samples rather than case samples, you will, even if you don't intend to, be more careful. Thus, open proficiency testing where the examiner knows that they are being examined, does not provide an adequate measure of proficiency. Blind proficiency testing, where samples are worked in in normal case flow, provides a good measure of that.

Id. at p. 50

In light of these very powerful pronouncements demanding realistic blind proficiency testing, it is clear that there are scientists significant in number and expertise who would accept no less. It would therefore appear impossible for any method or error rate estimation to meet the requirements of Kelly unless it incorporated blind proficiency testing on samples simulating casework.

The defendant will present evidence that Genetic Design has not done sufficient blind proficiency testing on realistic samples to provide a meaningful estimate of its error rate. The true error rate of Genetic Design is unknown and unknowable based on currently available data. Consequently, the value of the DNA evidence it offers is impossible to evaluate and therefore inadmissible.

V. INAPPROPRIATE STATISTICS FOR A MIXED SAMPLE COMPARISON

When a suspect's DNA profile is compared to the DNA profile of an evidentiary sample, the probability of a coincidental match is equal to the frequency of the evidentiary profile. If the DNA profile of a blood stain is found in one person in a million, for example, then there is one chance in a million that the suspect will, by coincidence, happen to have the same profile if he is not the source of the blood stain.

The probability of a coincidental match may be much higher than the frequency of the matching profile, however, when a suspect's DNA profile is compared to a "mixed" evidentiary sample (i.e., a sample containing the DNA of more than one individual). The presence of a second (or third) person's DNA in the evidentiary sample greatly increases the number of ways that an innocent person (i.e., one who is not a source of the evidentiary sample) could "match."

> The population frequency of a particular profile ... understates the probability of a coincidental match in cases where more than one potential match could prove incriminating. In some cases, for example, a defendant is matched to an evidentiary sample that has more than one donor. If the evidence sample contains alleles A, B, C and D, and defendant is genotype AB, he clearly is a possible donor and so will be declared to match. (The additional alleles are consistent with a second donor of genotype CD). In such cases, forensic laboratories all too often present statistics on the frequency of the defendant's genotype. This practice is highly misleading because the defendant's is only one of a number of genotypes that could be said to match. Defendant would also have matched had he had genotypes AC, AD, BC, BD, CD, AA, BB, CC, or DD. Thus, the probability of a coincidental match in such cases may greatly exceed the frequency of defendant's genotype.

William C. Thompson, Evaluating the Admissibility of New Genetic Identification Tests: Lessons From the "DNA War", 84 J.Criminal Law and Criminology 22, 90-91 (1993) (in binder).

In this case, Genetic Design compared defendant Marshall's DNA profile to the profile of a mixed sample (a vaginal swab) containing the DNA of at least two individuals.

The statistic presented by Genetic Design to characterize the "match" was the frequency of defendant Marshall's DNA profile, which is not the probability of a coincidental match with the mixed sample. In this case, the frequency of one in 641 million may grossly understate the probability of a coincidental match.

The discrepancy between the frequency of the defendant's DNA profile and the coincidental match probability increases exponentially with increases in the number of genetic loci that are typed. In the current case, for example, Genetic Design "matched" defendant Marshall to a mixed sample at five genetic loci. If Genetic Design understated the probability of a coincidental match by a factor of 10 at each genetic loci due to its failure to take into account the multiple match possibilities that arise in mixed sample comparisons, then the frequency statistic it computed in this case would understate the true probability of a coincidental match by a factor of $10^5 = 100{,}000$. Although the degree to which Genetic Design actually understated the probability of a coincidental match is difficult to determine exactly, and will be subject to proof, this hypothetical example illustrates that the degree of bias against the defendant is potentially huge.

The statistic computed by Genetic Design to characterize the value of the DNA evidence, vis-a-vie defendant Marshall, should therefore be excluded on several grounds. First, Genetic Design's failure to take into account the higher probability of a coincidental match when performing a mixed sample comparison constitutes failure to follow correct scientific procedures, rendering the resulting statistic inadmissible under the third prong of Kelly. The correct procedure for mixed sample comparisons is set forth in the NRC Report, at p. 59: "If a suspect's pattern is found within the mixed pattern, the appropriate

frequency to assign such a "match" is the sum of the frequencies of all genotypes that are contained within (i.e., that are a subset of) the mixed pattern." Because the "one-in-641 million" frequency was not computed according to the appropriate procedure, it must be excluded under Kelly.

Because this statistic greatly understates the actual probability of a coincidental match, it is also irrelevant and highly prejudicial, and therefore properly excludable under Evidence Code Section 350 and 352.

VI. CONCLUSION

For all of the foregoing reasons, the DNA evidence that incriminates defendant Marshall should be excluded.

Respectfully submitted,

William C. Thompson
Attorney for Sammy Marshall

Date: October 10, 1995