EDMUND G. BROWN JR.

Attorney General of the State of California

1. DANER. GILLETTE

Chief Assistant Attorney General

1. GERALD A. ENGLER

Senior Assistant Attorney General

1. JOYCE BLAIR

Supervising Deputy Attorney General

1. MICHAEL CHAMBERLAIN Deputy Attorney General
2. State Bar No. 185620

455 Golden Gate Avenue, Suite 11000

1. San Francisco, CA 94102-7004 Telephone: (415) 703-5892

8 Fax: (415) 703-1234

Attorneys for Real Party In Interest

9

1. SUPERIOR COURT OF CALIFORNIA
2. COUNTY OF SAN FRANCISCO 12

**THE PEOPLE OF THE STATE OF CALIFORNIA,**

Plaintiff,

v.

**LANCE FORD,**

Defendant.

13 Case No:

MCN2151192

14 SCN 196780

1. NOTICE OF OBJECTION

**AND MOTION TO QUASH**

1. **SUBPOENA DUCES TECUM;**

**OBJECTION AND MOTION**

1. **TO QUASH; POINTS AND**

**AUTHORITIES**

18

Date:

19 Time:

Dept:

20

21

August 18, 2008

9:00 a.m.

25

NOTICE OF OBJECTION AND MOTION TO QUASH SUBPOENA DUCES TECUM;

1. **OBJECTION AND MOTION TO QUASH**
2. PLEASE TAKE NOTICE that at 9:00 a.m. on August 18, 2008, in Department 25 of
3. the above-entitled court, or as soon thereafter as the matter may be heard, the California
4. Department of Justice ("DOJ") will object to, move, and hereby requests an order quashing item
5. numbers 1, 2, 3, and 6 of defendant Ford's subpoena duces tecum ("SOT") issued July 29, 2008,
6. to the DOJ's Richmond DNA Laboratory.
7. This motion is based upon this Notice of Motion, the attached Memorandum of Points



•

and Authorities, any and all pleadings and papers on file in this matter, and any arguments

* 1. offered to the Court on this subject.
	2. WHEREFORE the California Department of Justice respectfully requests that items
	3. numbers 1, 2, 3, and 6 of defendant's SDT be quashed. 5
1. INTRODUCTION AND SUMMARY OF POSITION
2. Defendant Ford is charged with special circumstances murder and rape. The crime
3. took place in San Francisco in 1982. In 2004, a DNA "cold hit" in the Oregon state DNA
4. database identified defendant as the perpetrator. Consequently, California's offender DNA
5. Database played no role in the case.
6. Nonetheless, on July 29, 2008, defendant Ford issued a subpoena duces tecum to the
7. California Department of Justice seeking, among other items, more than one million statutorily
8. confidential and privileged offender DNA profiles maintained in California's DNA Database.
9. (Exh. 1, SDT.) In support of this demand, and despite having unsuccessfully litigated the issue
10. previously in other San Francisco cases, counsel for defendant asserts only that this massive
11. amount of information is "material, necessary, and essential for the defense" of the case. (Exh. 1,
12. Deel. of Counsel.) No justification or rationale is provided..!L
13. The SDT demands that DOJ produce eight collections of material. (Exh. 1, Deel. of
14. Counsel at pp. 2-4 [although no page numbers provided in actual document].) DOJ's responses 20

21 1. This is not a novel issue. Criminal defendants have issued similar SDTs or made discovery requests to DOJ seeking a copy of the California offender DNA Database in a number of cases, and each time the trial court has quashed the SDT or denied the motion to compel discovery.

22

1. (See, e.g., *People v. Eric Ardoin* (San Francisco Superior Court No. SCN 196690-3, Sept. 20, 2006);

*People v. David Perryman* (San Francisco Superior Court No. SCN 198604, Nov. 16, 2006); *People*

1. *v. John Davis* (San Francisco Superior Court No. SCN 190226, Nov. 21, 2006 [Morgan, J.]); *People*

*v. Ivan Hill* (Los Angeles Superior Court No. KA064034, Feb. 24, 2005); *People v. Wayne Smith*

1. (Los Angeles Superior Court No. BA255390, Sept. 26, 2006); *People v. Timothy Brown* (Santa Clara
2. Superior Court No. CC643081, July 11, 2008).) The California Court of Appeal denied a defense petition for writ of mandate following the trial court's decision to quash the defense SDT in the
3. *Davis* case, *supra. (Davis et al. v. Superior Court* (Case No. Al 16603, March 8, 2007 [[http://appellatecases.courtinfo.ca.gov/search/case/disposition.cfm?dist=l](http://appellatecases.courtinfo.ca.gov/search/case/disposition.cfm?dist=l) &doc\_id=417941 &doc

28 \_no=Al 16603].)

 2

Nnti"P "",1 nhiP<'tinn ;,,nrl Mntion to Omtsh Suhnoena Duces Tecum: Obiection and Motion to Ouash: P's & A's

to defendant's demands are as follows:

* 1. Items I, 2, 3, and 6 [records of matching and partially-matching DNA profiles in the State's
	2. DNA Database, and in the alternative, a copy of every profile in the Database]
	3. DOJ objects to items 1, 2, 3, and 6 in their entirety, and respectfully requests that they
	4. be quashed.li As will be discussed in detail in Sections II-VII, below, complying with request
	5. numbers 1, 2, 3, or 6 ("[i]n the alternative") would entail the illegal disclosure of confidential
	6. genetic profiles - potentially more than a million - maintained by DOJ in California's offender
	7. DNA Database. Providing the contents of the Database would violate an absolute privilege of
	8. nondisclosure held and asserted by DOJ pursuant to Evidence Code section 1040(b)(1), and
	9. would contravene clear and controlling statutory confidentiality mandates, both state and federal,
	10. protecting that information (Pen. Code,§ 299.S(h), 42 U.S.C. § 14132(b)).
	11. In any event, there is no credible rationale for obtaining information from California's
	12. DNA Database in order to assess the accuracy of the cold hit identification in this case, which
	13. took place in Oregon's database. Finally, arguments suggesting that California's Database is
	14. "necessary'' in order to let defense experts conduct research into the validity of long-accepted
	15. DNA profile rarity statistics similarly fail as a matter of actual science reflected in published
	16. literature, and given the availability of alternative, non-privileged, data sources.
	17. Item 4 [records of adventitious Database hits to innocent subjects]
	18. *DOI* does not object, but possesses no responsive materials. No records exist
	19. indicating that the properly identified subject of a database match could not have been the
	20. perpetrator of the crime because of an adventitious match to a third party who coincidentally

22

23

24

2. Note that number 6, which seeks a copy of well over one million offender DNA profiles

1. maintained in the State's offender DNA Database ("the Database"; Pen. Code, § 295 et seq.) is
2. phrased as an "alternative" to (DOJ presumes) numbers 1, 2, and 3, which seek hypothetical matches and partial matches between pairs of DNA profiles in the Database not related to the current
3. prosecution. DOJ does not imply that any documents satisfying request numbers 1, 2, or 3 exist. The legal and factual arguments offered herein do not depend upon the existence of the documents
4. described.

 3

Notice and Objection and Motion to Quash Subpoena Duces Tecum; Objection and Motion to Quash; P's & A's

shares the perpetrator's DNA profile, except for identical twin situations.l! Situations may occur,

1. however, in which an uploaded forensic unknown profile is not probative of guilt given the
2. circumstances of the case. An example might be a situation where the match and subsequent
3. identification were correct but the subject of the match was cleared by further investigation. DOJ
4. assumes that this situation is not within the intended scope of the SOT.
5. Item 5 [Database manuals and procedures]
6. This request was withdrawn by defense counsel pursuant to informal communications
7. with counsel for DOJ.
8. Item 7 [kinship analysis of DNA Database]
9. DOJ does not object, but no responsive materials exist. DOJ has never collected data
10. concerning actual kinship patterns or occurrences in the State's offender DNA Database. As part
11. of DOJ's ongoing evaluation and development of familial search protocols, however, DOJ is
12. currently conducting studies to evaluate the efficiency of search programs that include kinship
13. analysis as an element. DOJ is in the process of accumulating and evaluating data in these
14. uncompleted studies.
15. Item 8 [requests by outside experts to obtain offender Database for research]
16. DOJ does not object, but no responsive materials exist. Outside ofrequests (such as
17. this one) made in the context of criminal proceedings, DOJ has not received requests or written
18. proposals for the DNA profile database directly from outside scientists.

20

21

22

23

24

25

26

1. 3. Information about matches to sets of identical twins is confidential and not subject to disclosure for the same reasons that will be set forth with respect to request numbers l, 2, 3, and 6,
2. below.

 4

Nntire anct Ohiectinn and Motion to Ouash Subooena Durr.s Ter11m· Ohiection anct Mntinn tn Omish· P's *Iv* A's

MEMORANDUM OF POINTS AND AUTHORITIES

* 1. I.
	2. LEGAL STANDARD
	3. A third party in a criminal matter may move to quash an SDT, and is entitled to "the
	4. opportunity, through its legal representative, to lodge objections and set forth any claims of
	5. privilege against disclosure of the material ...." *(People v. Superior Court (Barrett)* (2000) 80
	6. Cal.App.4th 1305, 1320.) If such objections are made, "the party seeking the information must
	7. make a plausible justification or a good cause showing of need therefor." *(Alford v. Superior*
	8. *Court* (2003) 29 Cal.4th 1033, 1045; see also *People v. Superior Court (Barrett)* (2000) 80 1O Cal.App.4th 1305, 1320 & fn. 7.) Stated differently, should the recipient of an SDT move to
1. quash, the defendant assumes the burden of demonstrating that the materials sought are relevant
2. to the defense of his case. *(Barrett, supra,* 80 Cal.App.4th at p. 1320 ["Assuming CDC moved to
3. quash a subpoena duces tecum by Barrett, the burden would be on Barrett to demonstrate the
4. materials he seeks are relevant."].) In so holding, *Barrett* cited *United States v. Valenzuela-*
5. *Bernal* (1982) 458 U.S. 858, for the proposition that a showing of relevance, at a minimum,
6. requires a "plausible showing" of how the information requested would be "both material and
7. favorable to his defense." (458 U.S. at p. 867.)
8. Further, "[a] subpoena duces tecum that makes a blanket demand for ... documents
9. and amounts to nothing more than a fishing expedition is subject to being quashed." *(Ibid.)* Of
10. course, a defendant is entitled only to unprivileged materials. (*Vela v. Superior Court* (1989) 208
11. Cal.App.3d 141, 148 ["An accused is entitled to any "'pretrial knowledge of any *unprivileged*
12. evidence, or information that might lead to the discovery of evidence, if it appears reasonable
13. that such knowledge will assist him in preparing his defense...."[Citation.]' [Citations.]",
14. italics added].)

###### II.

1. THE DNA DATABASE IS PROTECTED BY THE ABSOLUTE PRIVILEGE OF NONDISCLOSURE SET FORTH IN EVIDENCE CODE

27 **SECTION 1040(8)(1)**

28 Ordering DOJ to provide any offender DNA profile other than defendant's, let alone

 5

1. providing over a million such profiles, would infringe upon an absolute privilege of
2. confidentiality and nondisclosure held and asserted pursuant to Evidence Code section
3. 1040(b)(1). Section 1040(b)(1) provides that:
4. A public entity has a privilege to refuse to disclose official information, and to prevent another from disclosing official information, if the privilege is claimed by a person
5. authorized by the public entity to do so and: (1) Disclosure is forbidden by an act of the Congress of the United States or a statute of this state ....

6

1. The California Supreme Court recognized that Section 1040(b)(1) confers upon its holder "an
2. absolute privilege if disclosure is forbidden by a federal or state statute." *(Shepherd v. Superior*
3. *Court* (1976) 17 Cal.3d 107, 123, overruled in part on other grounds by *People v. Holloway*

10 (2004) 33 Cal.4th 96, 131; *Marylander v. Superior Court* (2000) 81 Cal.App.4th 1119, 1126, fn.

1. 1; *Rubin v. Superior Court* (1987) 190 Cal.App.3d 560, 584.)
2. Among other state and federal statutory confidentiality provisions, California Penal
3. Code section 299.5, subdivision (h), plainly forbids disclosure of an offender DNA profile in
4. response to a subpoena, and thus triggers the absolute privilege asserted here. Section 299.5(h)
5. reads as follows (emphasis added):
6. Except as provided in subdivision (g) and in order to protect the confidentiality and privacy of database and data bank information, the Department of Justice and local
7. public DNA laboratories shall not otherwise be compelled in a criminal or civil proceeding to provide any DNA profile or forensic identification database or data bank
8. information or its computer database program software or structures to any person or party seeking such records or information whether by subpoena or discovery, or other
9. procedural device or inquiry.
10. California's privilege is therefore absolute and cannot be defeated.
11. III.
12. **CALIFORNIA'S DNA DATABASE IS CONFIDENTIAL AND EXPLICITLY EXEMPT FROM DISCLOSURE IN DISCOVERY AND**
13. **BY SUBPOENA**
14. In addition to the absolute privilege discussed above, rigid statutory confidentiality
15. mandates forbid disclosure of DNA Database information as contemplated by defendant's SDT.
16. California's DNA Database is a statutorily-created and confidential law enforcement
17. tool used to link forensic DNA profiles of qualifying offenders to matching DNA profiles from
18. unsolved case evidence nationwide. (See Pen. Code,§ 295 et seq.; *People v. King* (2000) 82

 6

Cal.App.4th 1363; (2002) 98 Cal.App.4th 492.) The State's Database is administered by DOJ,

1. and is part of the FBI's national CODIS ("Combined DNA Index System") crime solving
2. network. Currently, California's offender database contains over 1,089,000 searchable offender
3. profiles.1!
4. Several independent sources, described below, protect the confidentiality of
5. information contained in the Database, and prevent DOJ from releasing any of that information
6. to defendant. These disclosure restrictions are, in tum, a significant factor in maintaining the
7. program's constitutionality. (See *People v. King, supra,* 82 Cal.App.4th at pp. 1377, 1375, fn. 6
8. [recognizing data bank's use limitations as part of the constitutional balancing analysis; *Alfaro v.*
9. *Terhune, supra,* 98 Cal. App.4th at pp. 492, 507-508 ["The extent of the [data bank] intrusion is
10. measured by reference to express limitations on the uses to which the specimens and samples

12 may be put ...."]s;ee also *United States v. Kincade* (9th Cir. 2004) 379 F.3d 813, 837, & fn. 33

1. [observing that statutory confidentiality protections counter defense claim that "soon, if not
2. already, scientists will request access to what would serve as [a] preexisting goldmine of DNA
3. data for their research."].)
4. **A. Penal Code Section 299.5**
5. As discussed, California Penal Code section 299.5 codifies the strict confidentiality of
6. the State's DNA Database Program. It is comprehensive, clear, and controlling: No DNA
7. profile, no data bank or database information, and no database computer program or structure is
8. available to a criminal defendant by way of subpoena or other discovery mechanism. (Pen. Code,
9. § 299.5(h).) The law expressly anticipates that demands for database information would be made
10. by subpoena, and provides that such requests are prohibited as a matter oflaw. Compliance with
11. defendant's SOT would violate the law.
12. California places such a premium on the protection and confidentiality of genetic
13. information that state law sets forth severe criminal and civil sanctions for "any person" who
14. violates the DNA Data Bank Program's strict nondisclosure restrictions: 27

28 4. As of August 2008.

 7

Any person who knowingly uses an offender specimen sample or DNA profile collected pursuant to this chapter for other than criminal identification or exclusion

1. purposes, or for other than the identification of missing persons, or who knowingly discloses DNA or other forensic identification information developed pursuant to this
2. section to an unauthorized individual or agency, for other than criminal identification or exclusion purposes, or for the identification of missing persons, in violation of this
3. chapter, shall be punished by imprisonment in a county jail not exceeding one year or by imprisonment in the state prison.

5

## \* \* \*

1. If any employee of the Department of Justice knowingly uses a specimen, sample, or

DNA profile collected pursuant to this chapter for other than criminal identification or

1. exclusion purposes, or knowingly discloses DNA or other forensic identification information developed pursuant to this section to an unauthorized individual or agency,
2. for other than criminal identification or exclusion purposes or for other than the identification of missing persons, in violation of this chapter, the department shall be
3. liable in civil damages to the donor of the DNA identification information in the amount of five thousand dollars($ 5,000) for each violation, plus attorney's fees and
4. costs. In the event of multiple disclosures, the total damages available to the donor of the DNA is limited to fifty thousand dollars ($50,000) plus attorney's fees and costs.

11

12 (Pen. Code,§ 299.5(i)(l)(A), (i)(2)(A); italics added.)

1. Compliance with defendant's SDT would circumvent this statutory scheme. There is
2. no legal authorization for the Database to be converted into an openly available pool of genetic
3. information for defense teams to trawl through in the name of "research" or other objectives.
4. Were this the case, the statutory definition of the Data Bank Program as a pragmatic, narrowly
5. defined, and exclusive "law enforcement tool" (Pen. Code, § 295(b)(3)) would be rendered
6. obsolete.

19 **B. 42 U.S.C. § 14132**

1. Because California uploads the contents of its offender DNA database into the National
2. DNA Index System ("NDIS"), the State is subject to strict and inflexible federal disclosure
3. restrictions as well. Federal law provides as follows:
4. The [National DNA Index System] shall include only information on DNA identification records and DNA analyses that are ...
5. (3) maintained by Federal, State, and local criminal justice agencies ... pursuant to rules that allow disclosure of stored DNA samples and DNA analyses only
6. (A) to criminal justice agencies for law enforcement identification purposes;

(B) in judicial proceedings, if otherwise admissible pursuant to applicable statutes

1. or rules;

(C) for criminal defense purposes, to a defendant, who shall have access to samples

1. and analyses performed in connection with the case in which such defendant is charged; or
2. (D) if personally identifiable information is removed, for a population statistics

 8

database, for identification research and protocol development purposes, or for quality control purposes.

2

* 1. 42 U.S.C. § 14132(b).) As subdivision (3)(C) makes clear, the only database records that may be
	2. provided to a criminal defendant "for criminal defense purposes" are those relating to the DNA
	3. analysis done in conjunction with that particular case. (See also Privacy Act of 1974; New
	4. System of Records, 61 Fed. Reg. 37496 (July 18, 1996).)
	5. Moreover, the federal government has made clear that all personal identification
	6. information found in NDIS is subject to these confidentiality protections, including "operational
	7. identifiers such as the Specimen No., Criminal Justice Agency Identifier, and DNA Personnel
	8. identifier, "because" the identity of an individual could, under some circumstances, be
	9. ascertained with the disclosure of such numbers " *(Ibid.)*
	10. Federal law thus parallels California law. (See Pen. Code,§ 299.5(g) [only a
	11. defendant's DNA profile and associated information is available as discovery].) And, as Section
	12. 14132 and its interpreting regulations demonstrate, only state DNA information that is protected
	13. according to enumerated confidentiality standards is eligible for inclusion in the National DNA
	14. Index System.
	15. The potential sanctions for violating these federal mandates are severe. They include
	16. expulsion from the national CODIS network: "Access to the index established by this section is
	17. subject to cancellation if the quality control and privacy requirements described in subsection (b)
	18. [of Section 14132] are not met." (42 U.S.C. § 14132(c), italics added; see also Privacy Act of
	19. 1974; New System of Records, 61 Fed. Reg. 37497 (July 18, 1996) ["[C]riminaljustice agencies
	20. with direct access to NDIS must agree to adhere to national quality assurance standards for DNA
	21. testing, undergo semi-annual external proficiency testing, and restrict access to DNA samples
	22. and data. The NDIS will not accept DNA analyses from those agencies and/or DNA personnel
	23. who fail to comply with these standards and restrictions; and the NDIS Custodian is authorized
	24. to restrict access to and delete any DNA records previously entered into the system."].)
	25. Therefore, the continuing ability of California to submit offender and forensic DNA
	26. profiles to the National DNA Index System for searches against other states' data may depend in

 9

i,.,1, ; ,. 0 *"r1* n h; 0 ,\_, ; ,..,.., ,,..,,1 Mntinn tn n,rn h S11hnnr.m1 Duces Tecum: Ohiection and Motion to Quash; P's & A's

part upon California's strict observation of the federal confidentiality standards articulated above.

* + 1. Expulsion from CODIS would jeopardize California's ability to solve suspectless crime, which it
		2. does at average rate of more than 150 "cold hits" per month.
		3. IV.
		4. **THE STATUTORY CONFIDENTIALITY OF DATABASE INFORMATION IS NOT OVERCOME BY DUE PROCESS**
		5. **CONSIDERATIONS**
		6. Any claim that defendant's due process rights overcome DOJ's statutory privilege
		7. lacks merit.
		8. The Due Process Clause right to pretrial discovery is otherwise known as the *"Brady"*
		9. obligation, in reference to *Brady v. Maryland* (1963) 373 US. 87. The Supreme Court in *Brady*
		10. held that "the suppression by the prosecution of evidence favorable to an accused upon request
		11. violates due process where the evidence is material either to guilt or to punishment, irrespective
		12. of the good faith or bad faith of the prosecution." *(Id.* at p. 87.) "Material" evidence, in tum, is
		13. defined as follows: "The evidence is material only if there is a reasonable probability that, had
		14. the evidence been disclosed to the defense, the result of the proceeding would have been
		15. different. A 'reasonable probability' is a probability sufficient to undermine confidence in the
		16. outcome." *(United States v. Bagley* (1985) 473 U.S. 667, 682.)
		17. By its very formulation, the *Brady* standard for disclosure is not met when the
		18. defendant relies on pure speculation to demonstrate its relevance. (See, e.g., *Hughes v. Johnson*
		19. (5th Cir. 1999) 191 F.3d 607, 629-630 [denying *Brady* claim as "purely speculative"].)
		20. Nonetheless, speculation is the only possible basis for defendant's SDT. The Database was not
		21. designed for, and has never been used, as a mechanism for testing long-settled principles of
		22. population genetics. As will be discussed below, and as reflected in the scientific literature
		23. attached as Exhibit 2 and Exhibit 3, law enforcement databases are particularly ill-suited as
		24. sources of population genetics research data.
		25. Accordingly, DOJ possesses an absolute and inviolable privilege of nondisclosure with
		26. respect to all offender DNA database information not related to defendant himself. That
		27. privilege is not overcome by speculative claims of due process, because there is no indication

 10

that the information being requested is exculpatory or impeaching within the meaning of *Brady v.*

1. *Maryland, supra.*
2. V.
3. **DOJ'S ABSOLUTE PRIVILEGE IS NOT OVERCOME BY CONFRONTATION CLAUSE CONSIDERATIONS**

5

1. Defendant may also claim that his right to confront and cross-examine requires disclosure of
2. the State's offender database. He would be incorrect. Both the United States Supreme Court and
3. the California Supreme Court have determined that the federal Confrontation Clause does not
4. apply to pretrial discovery, nor does it create a constitutionally compelled rule of pretrial
5. discovery.
6. A plurality of the Court in *Pennsylvania v. Ritchie* (1987) 480 U.S. 39, held that the
7. state did not violate the Confrontation Clause by refusing to disclose privileged child welfare
8. agency records in response to a defendant's SDT. In doing so, the Court differentiated between
9. restricting a defendant's reliance on information he possesses to impeach a witness, and
10. preventing a defendant from gaining access to such information:
11. The Pennsylvania Supreme Court apparently interpreted our decision in *Davis* to mean that a statutory privilege cannot be maintained when a defendant asserts a need, prior to
12. trial, for the protected information that might be used at trial to impeach or otherwise undermine a witness' testimony.....

18

If we were to accept this broad interpretation of *Davis,* the effect would be to transform

1. the Confrontation Clause into a constitutionally compelled rule of pretrial discovery. Nothing in the case law supports such a view. The opinions of this Court show that the
2. right to confrontation is a *trial* right, designed to prevent improper restrictions on the types of questions that defense counsel may ask during cross-examination. See
3. *California* v. *Green,* 399 U.S. 149, 157 (1970) ("[It] is this literal right to 'confront' the witness at the time of trial that forms the core of the values furthered by the
4. Confrontation Clause"); *Barber* v. *Page,* 390 U.S. 719, 725 (1968) ("The right to confrontation is basically a trial right"). The ability to question adverse witnesses,
5. however, does not include the power to require the pretrial disclosure of any and all information that might be useful in contradicting unfavorable testimony. Normally the
6. right to confront one's accusers is satisfied if defense counsel receives wide latitude at trial to question witnesses. *Delaware* v. *Fensterer,* 474 U.S., at 20. In short, the
7. Confrontation Clause only guarantees "an *opportunity* for effective cross-examination, not cross-examination that is effective in whatever way, and to whatever extent, the
8. defense might wish." *Id.,* at 20 (emphasis in original).
9. (480 U.S. at pp. 52-53 (footnote omitted), italics added.) Significantly, the defendant in *Ritchie*
10. had sought exculpatory information concerning the primary complaining witness against him,

 11

which would have been far more valuable to the defense than the speculative and collateral

1. information being sought here.
2. The conclusion reached in *Ritchie* was adopted and reiterated by the California
3. Supreme Court in *People v. Hammon* (1997) 15 Cal.4th 1117. In *Hammon,* a criminal defendant
4. also sought disclosure of privileged records by way of SDT, claiming that the Confrontation
5. Clause overrode the assertion of privilege. The court disagreed, and held that the confidential
6. status of the documents was properly maintained:
7. [D]efendant asks us to hold that the Sixth Amendment confers a right to discover privileged psychiatric information before trial. We do not, however, see an adequate
8. justification for taking such a long step in a direction the United States Supreme Court has not gone. Indeed, a persuasive reason exists not to do so. When a defendant

IO proposes to impeach a critical prosecution witness with questions that call for privileged information, the trial court may be called upon, as in *Davis,* to balance the

1. defendant's need for cross-examination and the state policies the privilege is intended to serve. . . . Before trial, the court typically will not have sufficient information to
2. conduct this inquiry; hence, if pretrial disclosure is permitted, a serious risk arises that privileged material will be disclosed unnecessarily.

13

1. (17 Cal.4th at p. 1127; see also *Delaney v. Superior Court* (1990) 50 Cal.3d 785, 805, fn. 18
2. [acknowledging that the Confrontation Clause does not apply to pretrial discovery]; see also
3. *State v. Dykes* (Kan. 1993) 847 P.2d 1214 [defense request to obtain copy ofFBI's DNA
4. database in order to effectively cross-examination of state's expert on DNA statistics was
5. properly denied as speculative, iry-elevant, and immaterial].)
6. In this case, *Ritchie* and *Hammon* are all the more applicable because defendant is not
7. asking DOJ for information that is intended for cross-examination. Rather, to the extent that
8. defendant seeks access to California's offender DNA database in order to permit his own experts
9. to use, study, and analyze the data, he intends to use it during his own case-in-chief. It is well-
10. established, however, that law enforcement need not "obtain evidence, conduct any tests, or
11. 'gather up everything which might eventually prove useful to the defense."' *(People v. Hogan*
12. (1982) 31 Cal.3d 815,851, quoting *People v. Watson* (1977) 75 Cal.App.3d 384, 400.) Certainly
13. citation of the Confrontation Clause - a provision relating exclusively to cross-examination - is
14. inapposite here.

28

 12

Notice and Objection and Motion to Quash Subpoena Duces Tecum; Objection and Motion to Quash; P's & A's

**VI.**

* 1. DEFENDANT'S INQUIRY IS IRRELEVANT
	2. Although defendant asserts only that the entire content of California's DNA Database is
	3. "necessary and essential for the defense," any conceivable actual defense rationale for obtaining
	4. the Database lacks merit. For example, the present case originated from a "cold hit" DNA match
	5. *in Oregon's state DNA database,* not in California's. Any claim that California's Database
	6. contains information relevant to the accurate identification of defendant by Oregon authorities is
	7. thus unfounded.
	8. A more likely rational is that defendant seeks a copy of California's database in order
	9. to let his experts conduct "research" into the validity of long-accepted DNA profile rarity
	10. statistical estimates. That justification would similarly fail. The fundamental reliability of DNA
	11. rarity statistics has been recognized time and time again by appellate courts in California and
	12. nationwide, who have based their decisions on extensive expert testimony and general
	13. acceptance of these statistics by the relevant scientific community. (See, e.g., *People v. Nelson*

15 (2008) 43 Cal.4th 1242, 1259, citing *People v. Soto* (1999) 21 Cal.4th 512, 524-525.)

1. By way of background, DOJ does not use its DNA Database to generate DNA profile
2. statistics in "cold hit" cases. All DNA statistics generated by *DOI* and other government crime
3. laboratories are based on published data tables maintained by the FBI, available to defendant, and
4. thoroughly vetted in peer-reviewed scientific literature over the last 15 years. (See Budowle, et
5. al., Population data on the thirteen CODIS core short tandem repeat loci in African Americans,
6. U.S. Caucasians, Hispanics, Bahamians, Jamaicans, and Trinidadians (Nov. 1999) J. Forensic 22 Sci., Vol. 44, No. 6.)
7. There is no objective, scientific, basis for an assumption that California's offender
8. DNA Database would be an effective tool for conducting empirical research about DNA
9. frequencies in general populations. The Database is a practical tool designed to identify
10. suspects, and was not constructed as a population model for genetic marker frequency 27

28 itself.

1. Although DOJ is forced to speculate given the absence of any theory or detail in the SDT

 13

* + O , ,\_; ,; ,.1 •-·;-.. ·n..hl;:nhnnPno n11rpc TPr1m1· nhiiertinn Anrl Motion to Quash: P's & **A's**

assessments because it contains a significant number of duplicate samples (collected two or more

1. times from the same person, and retained for quality control purposes) as well as certain but
2. undocumented patterns of kinship between offenders from the same family. The latter
3. characteristics would render it impossible to know whether two profiles shared markers
4. randomly or because they represent the same person or because the offenders are, for example,
5. brothers. Interpreting the results of any such examination would thus be fraught with
6. uncertainty.
7. There has been recent speculation by lay reporters in the popular press, as well as by
8. some defense attorneys and defense experts, that data from an atypical search of the Arizona

1O DNA offender database suggest that DNA profiles may not be as rare as their statistics indicate.

1. This speculation is ill-informed and has been soundly rejected by mainstream scientists in
2. published literature. Two such publications are attached to this pleading (Exh. 2; Exh. 3), and
3. conclude that (1) no empirical evidence exists calling into question current statistical
4. methodologies, and (2) law enforcement DNA databases are particularly ill-suited to conducting
5. population genetics research. (Exh. 2, Budowle, Baechtel, & Chakraborty, *Partial matches in*
6. *heterogeneous offender databases do not call into question the validity of random match*
7. *probability calculations* (May 6, 2008) Int. J. Legal Med; Exh. 3, Budowle, Planz, et al.,
8. *Clarification of Statistical Issues Related to the Operation ofCODIS* (Oct. 12, 2006)
9. Proceedings of the 17th Int'l Symposium on Human Identification.)
10. Specifically, while experts acknowledge that "[t]here are suggestions that offender
11. database(s) could be used for empirical studies to provide inferences regarding the validity of the
12. current practices for generating random match probability estimates, "they conclude that" [s]uch
13. suggestions are misleading because current statistical practices do not strictly follow the
14. assumptions of HWE ["Hardy-Weinberg Equilibrium"], and offender databases, such as CODIS,
15. are heterogeneous and would be expected to depart from HWE." In other words,
16. while [s]ome ... have suggested that observing partial matching profiles, such as nine-locus profiles (out of 13 loci) sharing the same genotype, invalidate the manner
17. that forensic laboratories calculate the rarity of a DNA profile ... such logic is flawed. Departures from HWE are expected and any results obtained from such studies would
18. not be relevant and would be misleading. The CODIS DNA database is comprised of

 14

NntirP "nnOhiP.r.tion :m<l Motion to Ouash Subooena Duces Tecum; Objection and Mqtion to Quash; P's & A's

very diverse populations, and the profiles are not apportioned into population categories such as is used for routine casework statistical calculations. Therefore, any

* 1. analyses under the assumption of HWE are not particularly informative because departures are expected in heterogeneous data sets and the results do not assess the
	2. impact of using the population data sets employed for current statistical calculations.
	3. (Exhibit 2, at p. 2.)
	4. In sum, according to the most knowledgeable minds in the field, any defense argument
	5. that "partial matches" in a law enforcement DNA database are statistically significant is
	6. "misleading" and "flawed" logic, and any results of such inquiries "would not be relevant and
	7. would be misleading."
	8. VII.
	9. **DEFENDANT DOES NOT NEED DATA FROM CALIFORNIA'S DNA DATABASE; HE HAS ACCESS TO THOUSANDS OF NON­**
	10. **CONFIDENTIAL DNA PROFILES**
	11. Regardless, defendant has no need for the information sought in the SOT. He already
	12. has access to extensive DNA profile data sets. It is not necessary to violate state and federal
	13. confidentiality protections and place California's entire Data Bank Program in constitutional
	14. jeopardy just so defense experts can conduct mysterious research or engage in data manipulation.
	15. By way of illustration, and to assist defendant in his quest for DNA profiles, the
	16. following are several sources of extensive STR ("Short Tandem Repeat") profile data:
	17. (1) <http://www.fbi.gov/hq/lab/fsc/backissu/julyl>999/budowle.htm [FBI publication containing link to 959 13-locus genotypes for various population groups];

19

(2) Einum and Scarpetta, Genetic Analysis of Large Data Sets of North American

1. Black, Caucasian, and Hispanic Populations at 13 CODIS STR Loci (Nov. 2004) J. Forensic Sci., Vol. 49, No. 6 [indicating the availability of at least 17,000 13-locus
2. genotypes];
3. (3) Weir, et al., Allele Frequency Data for Profiler Plus Loci in Australia (Sept. 2004)

J. Forensic Sci., Vol 49, No. 5 [indicating the availability of more than 12,000 9-locus

1. genotypes].
2. Thus, defendant has ready access to adequate data of the sort contained within
3. California's confidential, privileged, law enforcement database. There is simply no compelling
4. justification for using the State's statutorily protected database as a research tool.

27

28

 15

NntirP ,mri nhiPrtinn Hnri Motion to Ouash Subpoena Duces Tecum; Objection and Motion to Quash; P's & A's

CONCLUSION

* 1. For the reasons set forth above, DOJ respectfully requests that items **1,** 2, 3, and 6 in the
	2. SOT be quashed.
	3. Dated: August 5, 2008 5

6

7

8

9

10

**11**

12

13

14

15

16

17

18

19

20

21

22

23

24

25

26

27

28

Respectfully submitted, EDMUND G. BROWN JR.

Attorney General of the State of California

DANE **R.** GILLETTE

Chief Assistant Attorney General

GERALD A. ENGLER

*Stf*77c1Ilencral

Senior Assistant Attorney General JOYCE BLAIR

MICHAEL CHAMBERLAIN

Deputy Attorney General Attorneys for Real Party In Interest

 16

Notict> and Ohiection and Motion to Quash Subpoena Duces Tecum; Objection and Motion to Quash; P's & A's

EXHIBIT 1

JUL-29-2008 12:56 PUBLIC DEFENDER'S OFFICE 415 553 9646 P. 02,'08

--------------*--.. ,i-'?1./.!i.:.5*

.A)'TORNtY OA PARTY WlT!sOUT A'n'ORNEY */N•mo $1,Vt> i;;Jr* 11,,n,1>t,r *,-r.,/ udar-r,nJ.*

JEFF ADACHI, Public Defender

BICKA BARLOW (SBN 178723)

Deputy Public Defender

*555* s venth St., 2nd Floor, SF, CA 9-1103

TELEPHONE NO.. (415) 575-8830 r,,,. NO *10D/;,J1101/.*

E-MAIL AOOR&SS *(OIJ/ionat)*

ATTORNEY FOR *(NJ/fie)·* LANCE FORD

**SUPERIOR** COURT OF **CALIFORNIA,** COUNTY OF' **San Francisco**

STR£ET AODRess Hall of Justice

MAILING ...ooRess *850* Bryant Sc

cm AND *ZIP* cooe: San Franciscc,. CA 94 I *03*

DAANCHNAME

CASE NAME: PEOPLE OF THF. STI\TE *OF* CALIFORNIA v. FORD

FOR *COURT V3t: ON*,*,.*

ORDER TO ATTEND COURT OR PROVIDE DOCUMENTS:

Subpoena/Subpoena Due Tecum

CASE NUMBER. 2 I *5* I 192

You must attend court or provide to the court the documents listed below. Follow the orders checked in item *2* below If ,11,v

do not, the judge can fine you. send you to pd, or issue a warrant for your arrest.

1. To: *(name or business)* Custodi:m\_ D,\_e ords, California Department or Justi;,:, forensic DNA Laboratory
2. You must follow the court order(sJ checke,d below:
	1. D Attend the hearing.
	2. D Attend the hearing *and* bring all items checked in d. below.
	3. [2[] Provide a copy of these items 10 the court (Do not use this form to obtain Juvenile Court records):
		1. Please see claratio11i!L IJ.QP.01t of Issuance of Subpoena Duces Teeum attached to thjs fonn.

D *If this box* is *checkod. provide all items listed on the attached sheet labeled "Provide These Items.* "

* 1. D If someone else is responsible for maintaining the Items checked inc. above, that person (the Custodian of 1,: 1;..:;;1 ,·/ :; ;-pu:;!

also attend the hearing.

* 1. 00 If this box is checked and you deliver all items listed above to the court within 5 **days** of **service** of thl& ordor 11•1.
* do not have to attend court if you follow the instructions in item 5.
1. Court Hearing Date:

Date: 8/12/08 T.:...:1.:.:.m=e.\_\_9: 011 A.M.

Dept.: *25* ----

The court hearing will **be at** *(name and address of court):*

Hull of Justice, 850 Bryant St., SF, CA 94103

Call the person listed in item 4 br:low 10 make sure the hearing date has not changed. If you cannot go to court on th,•; ,':1(,:

you must get permission from the pcm;on in item 4. You may be entitled to witness fees. mileage. *or* both, In the dis1:1<c1 .J., 1.1i

the court. Ask the person in ite,Tl **4** alter your appearance.

•.·---------------

'-------------·--·

1. The person who has required you to atlend court or provide documents 1s:

Name: BICK!\ BARLOW {SBN J.] 7 ?.3\_,\_

Title: Deputy Puhlic Defendendr ·--·-----------------

Phone No.: U5:·'.i> ,:,: ·.- 1

Address: *555* Seventh Sr., 2 J:.!.Qo.!\_ \_

Number, Street, Apt. No

San F'rancisco

City

Da '.Jr{2.J *{o<t*

##### F ,, ft.1 ro

Cf'I-T2SIJ\1•525 fN- Janua,y, . ?J

Signature

ORDER TO ATTEND COURT OR PROVIDE DOCUMENTS:

Subpoena/Subpoena Duces Tecum (Crlmlnal and Juvenlle)

JUL-29-2008 12:57 PUBL IC DEFEt·lDER 'S OFF I CE 415 553 9646 P.03/08

r------------------------------------,-------\_,.,CR -·1.2.5LJ'.'L: ..i!.tlI

-

CASE NAME. PEOPLE OF THE STATE OF (ALIFORNIA v. LANCE FORD

CASE NUMSER2151 l92 ·

* 1. a. Put all items checked in item *2c* and your completed *Declaration of Custodian of Records* form in an envelope. (Ye,,;,;.,,,, . ,,;.,

the person in item 4 where to gel 111,s forrn.) Attach a copy of page 1 of this order to the envelope.

* + 1. Put the envelope inside another eriv lope Then. allach a copy of page 1 of this form to the outer envelope or writ, 1his information on the outer envelop!?
			1. Case name
			2. Ca6e number
			3. Your name
			4. Hearing date, time. and department
		2. Seal and mail the envelope to the Co, rt Clerk. at the address listed In Item 3. You must mail these documents to thr., .::.:" ·,: within five days of service of this order
		3. If you are the Custodian of Records, you must also mail the person in item **4 a** copy of your completed *Oec/aration ,J*

*Custodian* of *Records.*

*The seNer fills out the section below*

Proof of Service of **CR-125/JV-525**

1. I personally served a copy of this Sl1bpoena on:

Date:

 *~~=+-q~~-(*/ *c) 5(* ·--· Time:

afier *(numqer of attempts1*

a.m, CJ p.m.

attempts because:

Name of the person serve : I

At this address: \_ --'-=f----'-+'l<\..·C. !'"1"'-, *t'* S]O2/4l - '8:f:y *L-{*

After I served this person, I iled or delivered a copy of this Proofof Service to the person in item **4** on *(dat8J:.*

Mailed from *(city): ·- •··•*

1. I **received** this order for service on *(date)* and was not able to serve *(nanw :)i:w1 lJ1·•*

 sftsr *(nl/mberof attempts}* attempts because:

* 1. D The person is not known at this address.

b.D The person moved and the forwarding address is not known.

1. D There is no such address.
2. D The address is in a different county,

e0. I was not able to serve by the hearing date.

f. c::lther *(exp/sin):*

------------------------------------··-- -

3. Server's name:  *t* c},.\_J.?...-.-....w.;.....·.!.....c:\_w ·---------

1. The server *{check one)*

Plione no.

* 1. D is a registered process sEwer

**b.j81 is** not a registered proces:, server

1. D is a sheriff, marshal, or cc,nstable.
2. D works for **a** registered process server.
3. D is exempt from registration under Business and Profess,onai *<;c* ;,\_

section 22350(b).

1. Server's address: If server is a registered process server:

County of registration: -- Registration no.:

I declare under penalty of perjury under the) laws of the State of California that I am at least 18 years old and not involv, ,:; .,, :t,,.\_,

case and the information above is true and correct.

Date: *r/i,'l{OK:*

► --

*TYPE OR PRINT NAME OF SERVeR*

CR-125/JV·525 IN- J::an l)I 1. 100 ) ORDER TO ATTEND COURT OR PROVIDE DOCUMENTS;

Subpoena/Subpoena Duces Tecum (Criminal and Juvenile

JUL-29-2008 12:57 PUBLIC DEFEtlDER'S OFFICE 415 553 9646 P.04/08

I

JEFF ADACHI

Public Defender

1. City and County of San Francisco TERESA CAFFESE
2. Chief Attorney

STEVEN GAYLE, SBN: 200911

1. BICKA BARLOW, SBN: 178723 Deputy Public Defender
2. 555 Seventh Street

San Francisco, CA 941OJ

6 (415) 575-8836; 553-167 !

7 Attorneys for Lance Ford

8

9 SUPERIOR COURT OF CALIFORNIA

10 COUNTY OF SAN FRANCISCO

11

PEOPLE OF THE STATE OF CALIFORNIA,

Plaintiff,

**vs.**

LANCE FORD,

f.)efendant.

MCN: 2151192

12 SCN: 196780

1. DAfE:

TIME:

1. DEPT:

15

16

17

1. **DECLARATION OF BICKA BARLOW IN SUPPORT OF ISSUANCE**
2. **SUBPOENA DUCES TECUM**
3. I am an attorney duly licensed to practice law in the State of California and a deputy
4. public defender in the Office of the Public Defender, San Francisco California. Steven Gayh:.
5. also a deputy public dcfc11dcr, is lead counsel and attorney of record for the defendant, Lance
6. Ford, in the above entitled matter.
7. Based on discussi,10s with Mr. Gayle and review of discovery relating to DNA e\·iderK-.
8. in this case, I am informi.-!d and believe the following:
9. Mr. Ford is charged wi\h one cow1t of Penal Code § 187, with a special circumstai1ci:s
10. alleged of rape under Pen.ii Code§ l 90.2(c)(3)(iii).

**28**

JUL-29-2008 12:57 PUBL IC DEFEtlDER' S OFF I CE 415 553 9646 P.05/08

I

I

### I

The alleged crime occurred in 1982 in the City and County of San Francisco. On

2 November 12, 2003, the San Francisco Crime Lab issued a report indicating that a"foreign *I)/\* i.

1. profile was generated for the sperm donor" found on the vaginal and rectal swabs taken fron. *!·•*
2. victim, **Annie** Barcelon. The profile was to be submitted to the California state ..Combined !),•.; *:.*
3. Index System (CODIS) Jal.:ibase.'· On January 2, 2004, a suppll!me::ntal report issued stating 1L.u
4. the lab had electronicall) ubmitted the unknown male profile lo CODIS. and on January *2.*
5. 2004, the Oregon State P..:.1lice Forensic Laboratory confirmed that a senrch of the National nr,
6. Index System (NDlS) showed a match to or 'cold hit' between the evidence swabs and a folon
7. identified as Lance Ford, (OR 4116547), at 13 AmpFLSTR Profiler Plus and Cofiler DNA
8. markers.
9. On February 12, 2004, another report was issued describing results of testing of oral
10. swabs taken from Lance Ford i.lnc.l a comparison of the swab results to the previously tested
11. evidence. The report incl udcd the calculation of the random match probability for the unkIHw·, 1
12. male profile in Items 4A SP·· vaginal swab. sperm, and 4E-2 - rectal swab, spenn, as: l in 4r,-
13. quadrillion for US Caucasians. l in 460 trillion for African Americans, l in 65 quintillion for
14. California Hispanics. and J. in 3 quintillion for the general Asian population.
15. The requested info1111ation is material, necessary and essential for the defense in the
16. above-captioned case.
17. The defendant is informed and believes that the California Department ofJustice,
18. Forensic DNA Laboratory, Richmond, California, is in possession of the following material
19. information which is unavailable Lo the defendant through other means:
20. I. Records and documentation of any nine (9) locus or more matches between
21. individuals in the convicted offender database whose DNA profiles were typcJ
22. using either or both Profiler Plus and Cofiler, or Identifiler, which resulted fron1
23. searches or unknown evidence samples against the convicted offender databank
24. known by CODIS. or any other name;
25. *Ill*
26. *Ill*

JIJL-29-2008 12:57 PUBL I c DEFHmER• s OFF I CE 415 553 9646 P.06/08

2.

2

3

4

5

6 3.

7

**8**

9

10 4.

11

12

13

14

15 5.

16

17

**18**

19 6.

20

21

22

23

#### 24

25 7.

Record ..md documentation of any nine (9) or more locus matches between individuals whose DNA profiles were lyped using either or both Profiler Plu:- :-,:,,: Cofiler, or 1dL·nti1i1er, which resulted from searches of convicted offender s.im1 ,; . · for quality control/quality assurance or re.search purposes in the convicted offender datahank;

AII records and documents of matches between individuals of nine (9) or mmc loci that were detcrmint:d to be different individuals, regardless of the source including reports from local and county crime labs or agencies, federal labs 111 agencies, or ,my other DOJ laboratory or facility;

All record:; and documcms ofmatches made between evidence and a convicted

offender profile, where, atier investigation, Cal-DOJ or a local, county, or fcdr.:r ,\_,I law enforcemcnt agency determined that it was impossible or unlikely for the convicted offrmfor to be the perpetrator of the crime which resulted in the data.bank. hit:

All standard operating procedures, policy manuals and quality control/quality assurance manuals for convicted offender database sampling including but no1 limited to the reporting of multiple hits to one profile and documentation of multiple hilc; to one profiJe; or

In the alternative, please provide a copy of all convicted offender samples, ah!:ic:1;I identifying infonuation in a searchable formal. This databa-,e should be providt as an electronic tile consisting of the complete genetic profiles (multiloclli. genotypes) of eve1y individual in the convicted offender database. Explanatory material such a.s the order of loci on the file and the characters used for missinµ data should also be indicated; and

Any studies cunducted by the Cnl DOJ or their agents, including oulside

1. independc11L experts and contractors, or kinship analysis of the Cal SDIS datab 1·.,:
2. and
3. *Ill*

JUL-29-200a 12:59 PUBL IC DEFEt,lDER 'S OFF I CE 415 553 '3646 P.07/08

8. Any requests by outside experts to obtain and study the profiles contained in tn,

* 1. Cal SDIS database. including but not limited Lo the written proposals for stuJic
	2. and any rt:'spnnse by Cal DOJ to the requests.
	3. I declare under p nalty of perjury, that the foregoing is true, and that those matters sL:11,,:J
	4. upon information and belief, ar true and correct to the best of my knowledge.
	5. Executed this *.2/1 Y* of July. 2008, at San Francisco, CA.

7

8

9

10

11

12

13

14

15

16

17

' I 8

19

20

21

22

23

24

25

26

27

28

-

BICKA BARLOW

JUL-29-200s 12:59 PIJBL IC DEFEtsJDER ' S OFFI CE 415 553 9646 P.08/08

 



FILE NO." 150

START=JUL-29 12:45 ENIPJUL-2S 12:47

STN NO.

001

COM

OK

ABEi< NO. STATI ON ' i=r1E/Tfa,. NO.

91Sl02 1874a

-PUBLl C DE ENDER ' S O FI CE -

415 553 SE4E- "'"'\*"''".,-1<., ·•

**,Al"l'OllfllV O P...-r,'** wrn,cnJT **ATTO/U<fY** ,- ...., ., .....,bor ***...i -.r,***

**JffP ADACHI,** PUbtic t>eCend:r

**BICKA BARLOW(SBN** 178723)

**Depuiy Public Dd'Ct1der**

*SSS* Sf'Venth St., 2,.. floor, SF, C.-'. IO.'

TQ.iPHONE NO· (415) 575,&BJ CJ ,,..NO *,:\_,..,,*

-'CDAE,U q

ATT011H(YF0'1-J LA'N'Ct f(llU)

**5UIIERIOR COURT OF' CALIFORNIA,** COUMTY OF **San Fninclseo**

**nMrT A00tll!U** Hall of hmic:i:

i&/IILl"G **AOOllt'8: *850* Bryant** $1.

err,**""o ZIP coo . San** Francisco. *CA* 94103

**llt,INCH NAM6;**

CASE NAME: PEOPLE OF rtiE TATE OF CALIFORNIA v, FORD

1-------------· -----------------i----------

CASEN'-"IIEA 2) 1192

ORDER TO ATTEND COURT OR PROVIDE DOCUMENTS:

Subpoen.a/Subpoena Ouc:n Tecum

You must **:altend** cour1 or provide *tD* Ille cou"1he dooumen **liBted** below. Follow 1he ordt:rs c:haclced in item 2 btlow Ii .,,.,, do not. the judgt can fine yo1J. se:na y011 10 jail, or i1m1ti a warrant for your arresl.

,. To: (name arbusinoss) :..!.'l3.":nnJs, •lirarnl;1 O.:p1rtlT1C'll! oI.T lioc, Fon:nsic D'NA ubon10rv

1. You mucl follow lhe court oraer(si ct11 ci<ed b low
	1. D Anand the hearing,
	2. D A!ICnd lhe !'\earing and bring al/ items cnecxed in d. below.
2. [!J Provide **a** c:opy of tl'lese Items to the court (Do n01 use lhia form to obtain Juvenile Court records):
	1. f,km: ieO Ilt i(J°W. IJ.11\ S!!r lS§UjlQC:J'. a(SU pOCQI OUC:I!§ Tecum auachcd lp µIIJ fonn

(21

(3)

D *If /hi& bo1t* is *ch cl<ed.* fJl'tl"•da *1111 I/ems listed on lhe att,ched .sliest labeled ··Proo,,,111, These /t,mt.."*

d, D If tomeone else.: respon ible 1or mllinl.aining the items checked in c. above, that per&on (the CuJt.odi:in of ;.'.,1;:,·,.• .. Js • ,. •

also attend lhe h■aring.

e, 00 If tnis box i, checitccl a11d you del,ver all ,1oms Iisled above lo the court within S da.yc *of* aervic:u or tnl& orcl11r. , .

do not have to 3llcnd eow1 if you follow the ,nstrudianJ In item 5.

1. Court **11uring D.1te:**

Dale: 8112101 -··-Tim '.'·ll'l A.M.

The oourt hearing •ill be at *(nom9 nd aaa,u.: of co1,1rt)*

 H•11 p[Justics, sso Bryant St., Sf. CA 94103

Oepl.: 25 -----

 --8.m..,

Call the **person** Lsled in 11cm 4 btlow to **m11<e** ,ure tt,e heiring da111 ha.snot chlngod. II you cannot go 10 court 01'1111, dai,: you mu gel perrnis.s,011 lrom *IN.:* pe on In •l m **4.** Vou may be tn'lllled lo wilnes.s roes. mileage, or both. Ir, lht! d, ct'-i,11·,,1 *vi* 1he c:ourt -'s.k the per,on 1ri '""' 4 alltr your eppearanca.

1. The peBon ""'10 has reciulrna yotJ 10 attend coun or pr011ide doeumen1& ,s

N<ame BJCKA 96[U.OW 1SBN n"'2j

TIiie: Deputy Publjc o rso

..2

**Addrna:** ,U.S SgysmJb Sc Fl,1..,;\_r\_.

HU"'INf. St,.el. AO! *No* ---------------

**$NJ** Enneju:o

S1gn11urt

Subpo•"elSubp- Du ce ■ Tec:um

C'1)'

 0•1m *1 .1(o*



(Crltnlnal •"d Juvenilel

TIJTAL P.08

# EXHIBIT 2

Int J Legal Med

DOI I 0.1007/s00414-008-0239-1

.

. - - . . - . '. . .

- -

irfrJc l:;;u?!11n:·:,:•),iL i l'o1ITTE.

**Partial matches in heterogeneous offender databases do not call into question the validity of random match probability calculations**

**Bruce Budowle , F. Samuel Baechte**,**l Ranajit Chakraborty**

Received: *5* November 2007 / Accepted: 25 March 2008

(C Springer-Verlag 2008

**Abstract** Offender DNA databases have been highly successful tools for generating investigative leads. Due to their success, the database sizes have increased such that some have suggested using the DNA profiles in offender databases for empirical paitwise studies to provide inferences regarding the validity of the current practices for generating random match probability estimates. These critics use observations under the assumption of independence to suggest that the current forensic DNA statistical calculations are invalid. However, some of these databases, such as CODIS, are not appropriate for such studies because they contain duplicate profiles and profiles of close relatives and are highly heterogeneous (i.e., comprised of individuals from many different population groups with unknown proportions). Observed departures from expectations will occur using these databases, but would have no relevance for questioning the reliability of statistical practices because the very heteroge­ neous data sets would be expected to violate the basic assumptions of independence. In addition, 9-, I 0-, 11-, and 12-locus (out of 13 loci) matching profiles have been observed, arc expected, and do not call into question the

8. Budowlc (kJ) · F S. Bacchtcl FBI Laboratory,

250 I Investigation Parkway,

Quantico, VA 22 I 35, USA

e-mail: brucc.budowle@ic.tbi.gov

R. Chakraborty

Center for Genome lnfonnation,

Department of Environmental Health, College of Medicine, University of Cincinnati,

3223 Eden Avenue, C111cinnat1, OH 45276. USA

reliability of statistical practices. The phenomenon of match­ ing profiles is similar to the concept of the birthday scenario. Regardless, simple computations under the assumption of independence for guideline purposes only show that partial matches observed in offender databases are not inconsistent with expectations. Indeed, computed random match probabil­ ities that explain the observed matching profiles from paiiwise comparisons are smaller than those observed based on routine casework calculations. Data analyses from offender databases based on assumptions of independence do not provide any basis for questioning the legitimacy of computations of random match probability values of any specific target profile based on the modified product rule that are currently followed in the DNA forensic community. Defined population data, which are sufficiently abundant, have already demonstrated the validity of the basic assumptions of DNA forensic statistical assumptions.

**Keywords** Matching profiles• Statistics· Random match probabilities• Pairwise comparisons • Population heterogeneity• STR loci • Offender databases

**Introduction**

Because of the success of offender DNA databases [I, 2), their size has increased substantially. For example, CODIS for the US Combined DNA Index System and NDNAD for the UK National DNA Database each contain more than four mi II ion profiles. There are suggestions that offender database(s) could be used for empirical studies to provide inferences regarding the validity of the current practices for generating random match probability estimates (as de-

i} Springer

##### •

Int J Legal Med

scribed in [3]). In some US legal proceedings [4), some have suggested that the demonstration of matching pairs of 9 ( I 0, 11, I 2, or 13) loci out 13 loci profiles in these large data sets violate the Hardy-Weinberg expectations (HWE). Because the HWE arc violated, these critics argue that the currently used statistical approaches arc invalid and that **DNA** evidence should not be admitted in court proceedings. Such suggestions are misleading because current statistical practices do not strictly follow the assumptions of HWE [3], and offender databases, such as CODIS, are heteroge­ neous and would be expected to depart from HWE.

This technical note is *not* about developing a conserva­ tive statistical approach by using 0 adjustment fonnulas for ameliorating the effects of population heterogeneity (substructure) and when using average allele frequencies for statistical calculations. The NRC II Report [3] assumed that departures from HWE would occur and already offers

0 adjustment formulas, which are routinely used by the forensic community, for such phenomena. Indeed, Weir [5) demonstrated that 0 adjustment using the pragmatic values recommended by the NRC II Report [3] are more than adequate for overcoming effects found in heterogeneous databases similar (but not exactly) to the construct of the CODIS database. In contrast, this paper identifies the flaws in arguments raised by those in recent legal proceedings [4] who do not use 0 adjustment formulas but instead strictly assume HWE and misapply average allele frequencies to assess departures from expectations in heterogeneous database.

Use of large offender databases to question strict rule of independence

Pairwise profile analysis can be a meaningful test of the reliability of the basic statistical assumptions used for generating DNA profile frequencies [6]. Therefore, some­ one might perceive the available profile data in these large offender databases as an opportunity to carry out pairwise profile comparisons studies (and compare the observations with expectations under the assumption of HWE). Some [4] have suggested that observing partial matching profiles, such as nine-locus profiles (out of 13 loci) sharing the same genotype, invalidate the manner that forensic laboratories calculate the rarity of a DNA profile. However, such logic is flawed. Departures from HWE are expected and any results obtained from such studies would not be relevant and would be misleading. The CODIS DNA database is comprised of very diverse populations, and the profiles are not apportioned into population categories such as is used for routine casework statistical calculations. Therefore, any analyses under the assumption of HWE arc not particularly informative because departures are expected in heteroge­ neous data sets and the results do not assess the impact of

using the population data sets employed for current statistical calculations.

Another obstacle to usmg the CODIS database for evaluating (under assumptions of HWE) the statistical legitimacy of using allele frequency estimates under current forensic practices is that the databases contain duplicate profiles and profiles of close relatives. Before any such inferences could be drawn from a pairwise database analysis, it would be imperative to remove matching or partially matching profiles contributed by relatives. The 0 adjustment approach does not address directly the presence of relatives. Moreover, the removal of such profiles would be a monumental task that would have to be coordinated by all 50 states.

The impact of the presence of relatives in the database may be illustrated by Fig. I where the distribution of matching loci in pairwise comparisons of DNA profiles in four hypothetical databases is plotted. The distributions clearly show that the number of matched loci becomes highly distorted toward the direction of a larger number of matched loci in the presence of relatives in the database, and the deviation depends on the extent of the number of relatives as well. Note that while the distribution of matched loci is affected by the presence of relatives in the database, as long as the loci do not have any viability or fertility consequences, the presence of relatives in a database does not influence allele frequency estimates of the loci (data not shown). Thus, a few relatives in a database will increase the number of matching loci observed by pairwise comparisons.

An advocate of using an offender database for evaluating the validity of the statistical practices would now have to ignore concerns about using a very heterogeneous database [7]. The CODIS database qualifies as one of the most heterogeneous DNA profile databases available. It is comprised of individuals from many different population groups (African American, Asian, Caucasian, Hispanic, Native American, and Oceanian), the proportions are unknown, and it is likely that the propo11ions of these groups in the database are not the same as they are in the greater US population.

Frequency of pairwise comparison matches within offender databases as a surrogate for legitimate profile frequency estimates

When conducting pai1wise DNA profile comparisons using offender database data, it is important to recognize that the number of profile matches that might be found at nine or more loci (out of 13 loci) is predictable. Troyer et al. [8] reported a nine-locus (i.e., partial out of 13 loci) match between an African American and a Caucasian profile in the Arizona offender database. The random match proba-

Springer

Int J Legal Med

**Fig.** I Effect of the presence of relat1ves on the number of matching loci. The four hypo­ thetical databases illustrated consist of 13 CODIS STR loci profiles (based on Caucasian allele frequencies, as reported in *[* I OJ) on 1,000 individuals in which all 1,000 individuals were unrelated *(filled diamonds),* 998 were unrelated and I pair of full siblings was included *(filled squares),* 980 were unrelated

**1000000**

**100000**

**10000**

**1000**

**100**

**10**

·;

-

**a. 0.1**

Effect of Presence of Relatives

(Caucasian data on CODIS loci, *0=0,* **N** = 1000)

|  |
| --- |
| - |
|  |
| ---------- |
| "- |
|  |
| "-----,.  |
| ---.,.  |
| --------- "--- |
| "'----.. |
|  |
| "'- **"-a** |
| '\\_ "-. |
| '\. |
| '\ |
| '\ . |
|  |

and IO pairs of full siblings were

included *(Ji/led triangles},* and

**0**... **CII**

**0.01**

~~"'~~ ""

800 were unrelated and I 00 pairs of full siblings were in­ cluded (x). Note that the Y-axis is in logarithmic scale, visually decreasing the degree of deviation

**.c 0.001**

**E**

**z::i 0.0001**

**0.00001**

**0.000001**

**1E-07**

**1E-08**

**1E-09**

**1E-10**

**0 2 3 4 5 6 7 8 9 10 11 12 13**

**Number of Loci**

-+- **Unrelated** ....., **1 Full slb -+--10** Full **slbs** --><-- 100 Full slbs

bility (RMP) frequency under the assumption of HWE for the nine loci was approximately 1/500,000,000. Yet, the database size contained only 8-10,000 profiles. The "coincidental match" did seem surprising to Troyer et al.

1. as the observation appeared to associate two unlikely individuals at a frequency more likely than seemed plausible. However, such a finding is entirely expected and predictable based on probability theory.

The matching pair at nine out of 13 loci that was observed is analogous to the well-known phenomenon the "birthday scenario" [9]. Similarly, matches will occur in offender databases, although at first glance it may seem counterintuitive with profile frequencies estimated to be less than 10- 12. The total number of pairwise comparisons for an II individual size database is *n(n-* 1)/2. So for a database with approximately 3,000,000 profiles, there are more than four trillion pairwise comparisons. Although the birthday scenario and the observation of matching profiles at 9, I 0, 11, or 12 (out of 13 loci) in large-sized offender databases would seem obvious to the infonned, such statistics from pairwise comparisons of profiles (again under the assumptions of HWE) are cited as a rationale, although erroneous, to question current statistical practices for estimating the rarity of a **DNA** evidence profile. Although average allele frequencies are used, a threshold may be determined as a guide to detennine whether such observations can be expected. The computations below illustrate that such statistics of partial matches in offender databases do not dispute the legitimacy of the reported

RMP values in casework analyses that use the modified product rule. We do not advocate the following calculations as accurate, they are merely used to show that the expectations even when assuming HWE and average allele frequencies (as some critics might use) of observing partial matches are well within the plausible range.

RMP and partial match computations

The computations are based on partial matches in the Arizona State offenders' database. The Arizona offender database contained 65,493 offender 13-locus DNA profiles. In a pairwise comparison of these profiles, there were observed 122 pairs of profiles that matched at 9 loci, 20 pairs matched at IO loci, and 1 pair each matched at 11 and 12 loci (K. Troyer and D. Duplissa, Arizona Department of Public Safety, Phoenix, Arizona, personal communication). To exemplify what range of values of RMP (under HWE) would support such observations, the steps of the computations are: (I) compute the \_number of pairwise comparisons for the databases; (2) compute the number of possible combinations of loci (out of 13 loci) with reference to which the autosearch statistics were reported; (3) compute the range of possible number of distinct genotypes for the combination of loci; and (4) finally, compute a value of RMP that would be consistent with the observed number

of partial matches.

The results are: (I) With 11=65,493 profiles there are 2,144,633,778 pairwise comparisons of profiles in the AZ

Springer

Int J Legal Med

**Table** I Number of alleles with frequencies :::0.0 I and genotypes for the STR loci

Loci Number of segregating Possible number of alleles *(k)°* genotype, ***k(k+*** I )/2

|  |  |  |
| --- | --- | --- |
| CSFI PO | 8 | 36 |
| FGA | 21 | 231 |
| TII0I | 6 | 21 |
| TPOX | 7 | 28 |
| vWA | 9 | 45 |
| D3S1358 | 8 | 36 |
| D5S818 | 8 | 36 |
| D7S820 | 8 | 36 |
| D8S1179 | 10 | *55* |
| D13S317 | 7 | 28 |
| D16S539 | 7 | 28 |
| D18S51 | 15 | 120 |
| D21S11 | 17 | 153 |

Data from [ I OJ.

* Number of segregating alleles is based on total observed at each locus.

database; (2) There are 715 combinations of 9 loci out of the 13 CODIS STR loci used for DNA profiling in the database; (3) Using the statistics of the number of segregating alleles observed in the DNA forensic databases (e.g., [10]) and noting that with *k* segregating alleles at a locus, one can observe *k(k+* 1)/2 possible distinct genotypes at that locus, the range of possible multi locus genotypes can

be computed from Table I; and (4) The **RMP** *(p)* values for 122 matching 9 locus pairs are between 1.523 *x* 10- 12 and 6.769x 10- 14 (the same logic can be used for computing 10 or more locus matches [data not shown]).

These **RMP** values are typically smaller (i.e., rarer) than those reported for target profiles in casework using the modified product rnle (as per recommendations in [3]). The above computations clearly indicate that the number of partial matches in pai1wise comparisons of DNA profiles in the A1izona offender database, even when they are looked at without the inherent complicacies of the databases, does not, in general, provide any basis for questioning the legitimacy of computations of **RMP** values of any specific target profile based on the modified product rule that are currently followed in the DNA forensic community.

Given the three levels (minimum allele frequency, 8 adjustment, and tenfold rule) of conservatism built into the current calculations used by the forensic community [3, 11], the predicted number of partial matches based on forensic calculations would be larger that that observed. Even with the large size of the offender database, many of the rare DNA profiles (out of all possible DNA profiles) would not be observed in the database. This makes observing pairs of partial matches appear smaller than expected (based on an average allele frequency).

Using 8 adjusted calculations with reasonable 8 values more than compensate for the degree of substructuring such as

**Fig. 2** Specific genotype and average match probability

using Caucasian population data [8)

-.,.+.,.;.>

**..0**·-

**t'tl**

Specific Genotype and Average Match Probability (Caucasian Data)

***0=0***

**o.a**

+

♦

**..0 0.2**

**0c..**

**Q..**

**..c**

(.) +

+ +

+

•

•+ +

+

,+,;>

+ +

+

**0.1** + +

* + ***t***

.'

+ +

**:E** \*

**f**

.. +

•+ **t** + + •

+ ***i*** +

I

*:* + t ! **t**

+ *t* +

+

+ + ; t • **t**

**t**

**:t** + \* \*

t +

Springer

Int J Legal Med

that encountered in heterogeneous offender databases (note that reference databases for population inferences are not so heterogeneous) [5]. It is important to reemphasize that the criticisms that have arisen in US legal proceedings are not based on analyses such as those carried out by Weir [5]. The 0 adjustment approach is ignored and instead tests demon­ strating a violation of independence are sought.

Another point to consider is that computations of RMP in the context of specific forensic casework refer to a specific target profile. In contrast, pairwise comparisons of profiles in a database yield statistics of matches and partial matches with regard to any of the possible profiles, a concept that can be related to what may be termed as average match probability. For each of the loci used in current platforms of DNA forensic work, genotype-specific match probability can differ drastically from such average match probability. When summary statistics are used from allele/genotype sharing from pairwise comparisons of 11 profiles in the database, the summary statistic derived from *n(n-1* )/2 comparisons may approximate the estimate of true averages, if *n* is sufficiently large. However, if a small number of these pairs of subjects are related (for each of which one needs to invoke kinship adjustment over and beyond 0 adjustment), observations on allele-genotype sharing for these pairs would be sensitive to their specific profiles differing substantially from the average which would produce discordances that are irreconcilable without knowing their exact DNA profiles. This is illustrated by Fig. 2 where using the Caucasian allele frequencies (extracted from [JO]), the genotype-specific match proba­ bilities were computed for all possible genotypes at each of the 13 loci (represented by the plus sign, and the average locus-specific match probability represented by dots). These show that a target-specific match probability can be drastically different from the average match probability. Although the computations of this figure were done using the HWE of genotype frequencies, the results are qualita­ tively the same even after adjustments for population substructure effect (i.e., with 0 adjustment).

**Conclusions**

The CODIS database is an excellent database for investi­ gative leads; it is an extremely poor database to analyze for inferences regarding the assumptions of independence. The profiles in CODIS do not lend themselves to good quality population studies; they are not properly annotated and duplicates and relatives reside in the database. If one takes a very simplistic view about the complexity of the heteroge­ neous offender database and then observes pa11ial matches inconsistent with the assumption of independence, he/she

provides no basis to invalidate current forensic practices. Such departures are expected and do not reflect the population statistics databases used by the forensic com­ munity for routine statistical calculations.

Extremely important arc that concerns exist and will arise about the privacy and confidentiality of data retrieved from matches found during a pairwise comparison of offender DNA profiles. The names of individuals with matching and partial matching profiles would have to be disclosed to scientists and police when there is no criminal investigation underway. The names would be obtained because of a "research experiment." To further annotate such data may not be possible. However, not having annotated data for population studies does not compromise CODIS for its primary purpose that is developing investigative leads.

**Acknowledgment** This is publication number 07-03 of the Labora­ tory Division of the Federal Bureau of Investigation. The names of commercial manufacturers are provided for identification only and inclusion does not imply endorsement by the Federal Bureau of Investigation.

**References**

I. Budowle B, Moretti TR, Niezgoda SJ, Brown BL (1998) CODIS and PCR-based short tandem repeat loci: law enforcement tools In: Second European Symposium on Human Identification 1998, Promega Corporation, Madison, Wisconsin, pp 73-88

1. Martin PD (2004) National DNA databases: practice and practica­ bility. A forum for discussion. Prog Forensic Genet I 0:1-8
2. National Research Council II Report (1996) The evaluation of forensic evidence. National Academy Press, Washington, DC
3. The People of the State of Illinois v Juan Luna, In The Circuit Court Of Cook County, Illinois, Criminal Division, No. 02 CR 15430, 2006
4. Weir BS (2004) Matching and partially-matching DNA profiles. J

Forensic Sci 49:1009-1014

1. Chakraborty R, Stivers ON, Su B, Zhong Y, Budowle B {1999) The utility of STR loci beyond human identification: Implications for the development of new DNA typing systems. Electrophoresis 20:1682-1696
2. Shields **WM** (1992) Problems and solutions associated with

matching and generating inclusion probabilities. In: Proceedings of The Third International Symposium on Human Identification, Promega Corporation, Madison, Wisconsin, pp 1-50

1. Troyer **K,** Kilboy T, Koeneman B (200 I) A nine STR locus match between two apparently unrelated individuals using AmptlstJ"'I'. Profiler PlusTM and Cofilerrn. In: Proceedings of the Twelfth International Symposium on Human Identification, Promega Corporation. Available at <http://www.promega.com/genet1cidproc/> ussymp I 2prociabstracts.htm
2. Feller W (1968) An introduction to probability theory and its applications, vol. I. 3rd edn. Wiley, New York, p 33

I 0. Budowle B, Shea B, Niezgoda S, Chakraborty R (200 I) CODIS STR loci data from 41 sample populations. J Forensic Sci 46:453 *489*

1. Chakraborty R, Lee HS, Budowle B (2004) Response to Krane et al. J Forensic Sci 49:1390-1393

Springer

# EXHIBIT 3

**Clarification of Statistical Issues Related to the Operation of CODIS\*** Bruce Budowle1, John V. Planz2, Ranajit Chakraborty3, Thomas F. Callaghan1, and Arthm J. Eisenberg2

* 1. Laboratory Division, FBI, Quantico, VA
	2. Center for Human Identification, UNfHSC, Ft. Worth, TX
	3. Center for Genome Information, Department of Environmental Health, University of

Cincinnati, College of Medicine, Cincinnati, OH

,

* ***From the Proceeedings of the 17'1' International Symposium on Human ldentJfication, October 12, 2006\****

"

Clarification of Statistical Issues Related to the Operation of CODIS

Bruce Budowle1

,

John V. Planz2

Ranajit Chakraborty\ Thomas F. Callaghan1

and Arthur J.

Eisenberg2

,

,

1. Laboratory Division, FBI, Quantico, VA
2. Center for Human Identification, UNTHSC, Ft. Worth, TX
3. Center for Genome Information, Department of Environmental Health, University of Cincinnati, College of Medicine, Cincinnati, OH

Introduction

DNA databases, such as CODIS (Combined DNA Index System), have proven to be

extremely useful for developing investigative leads for a variety of crimes where there is no known suspect, for linking multiple cases committed by the same individual, and for identifying human remains attributed to a missing person (1-6). Such databases routinely assist law enforcement in solving crimes by more quickly identifying true perpetrators and preventing future crimes by these.individuals. In addition, searching a 10-13 short tandem repeat (STR) profile derived from an evidence sample against a large repository of Offender DNA profiles in effect excludes an extremely large number of individuals as being the source of an evidence sample. The multi-tiered structure of CODIS database, as well as its diverse use, make the construction *as* well as maintenance of this database a complex operation.

*)*

As in any complex operation, issues arise that may need clarification. There are three areas where information contained within CODIS and/or the interpretation of candidate matches obtained through CODIS searches may be misinterpreted or inappropriately applied. These are 1)

1

using the large number of reference offender DNA profiles to improperly validate or refute the current assumptions for assessing the statistical significance of an evidence profile that cannot be excluded as originating from a particular individual(s); 2) using the (relative) frequency of observing a DNA profile in the offender database in lieu of the more appropriate random match probability (or likelihood ratio) for assessing the rarity of a DNA evidence profile in a particular case; and 3) using the current searching algorithms in an attempt to identify perceived highly probable kinship relationships between an evidence sample and a offender DNA profile.

Should the CODIS Database be used to Invalidate Current Statistical Practices of Assessing Significance of a DNA Match in Casework Analysis? .

In the U.S., the number of Offender DNA profiles in National DNA Index System

(NDIS) has increased to 3,528,903 as of August 2006 (3). Recently, there have been legal attempts to obtain the computerized records of DNA profiles contained within e Offender database to perform empirical studies with the stated goal of assessing the validity of the current practices for generating random match probability estimates (as described in the NRC II Report

(7) and generally followed throughout the United States by DNA forensic science practitioners).

•

Toe premise is that pairwise profile comparisons (with more than 3 million profiles in CODIS

there will be greater than 4 trillion comparisons) can generate data to empirically verify or invalidate current statistical practices (8).

These efforts are misguided because the nature and design of CODIS make it an

inappropriate and meaningless source of DNA data for assessing the rarity of any specific DNA profile. No valid analyses using such a repository can be carried out regarding the reliability of current statistical practices because there are duplicate profiles and profiles from relatives (of

2

varied and unknown kinship category) contained within the database, and the population data are heterogeneous. The structure of the CODIS database in actuality is even more complex. For example, the number of relative pairs and the relative composition of different population groups embedded in the database are not readily available, nor can they be precisely estimated. This is so because of anonymity features of the offender profiles to ensure privacy of subjects in the database prescribed by the legal mandates of creation and maintenance of the CODIS system.

Therefore, any results obtained from studies assessing the number of observed and expected genotypes at a number of lo9i from the offender database would be virtually irrelevant and would be misleading for either supporting or refuting current forensic DNA statistical practices. Among the criteria that define the evaluation of the statistical legitimacy of using allele frequency estimates under the assumption of independence (which is not the actual current forensic practice) are that the databases contain little or no duplicate profiles or profiles of close relatives. Therefore, before any legitimate inferences could be drawn from such databases, it would be imperative to remove as many as possible of the duplicates or profiles contributed by close family members. It is widely known that the current offender DNA databases unavoidably contain duplicate profiles and profiles of relatives. Maintaining such profiles in an offender database does not compromise its use for developing investigative leads. However, identifying and resolving (and then removing) these profiles would be a monumental task and would not be readily possible to accomplish. Regardless, such expenditure of resources would gain little insight into the intricacies of forensic statistics.

In the early 1990s there were debates on the statistical practices used to assess the rarity of a DNA profile. One of the most notable criticisms was that the use of allele frequency data from heterogeneous databases is improper; because it would violate the basic assumptions of

3

, allelic independence (i.e., Hardy-Weinberg expectations) (9-12). The argument was that major population groups, such as Caucasian and African American, are composed of subgroups, and the allele frequencies (and thus the predicted genotype frequencies) may be quite different among the subgroups within a major population group. This would then cause the assumption that the alleles at a genetic marker are independent to be erroneous within the particular sample population data set. Thus, multiplying allele and genotype frequencies to derive an estimate of the rarity of a DNA profile would be inappropriate. These criticisms have been shown to be of minimal concern when following current forensic practices of compiling broad population group data sets, such as African American and Caucasian, and following the recommendations of the National Research Council (7, 13-20; note: only a few references are provided because they are too numerous to list). However, these concerns about population substructure apply even more critically to the use of an offender DNA database to verify the assumptions of allelic independence (for reasons stated above). Obviously, the compiled profiles in the data set are not

from any single major population group; instead the DNA profiles derive from individuals from

'

the various major population groups of unknown proportions. Indeed, CODIS qualifies as one of the most heterogeneous DNA profile databases available. It is comprised of individuals from many different population groups: African American, Asian, Caucasian, Hispanic, Native American, and Oceanian. Such population heterogeneity is an irresolvable issue because population affinity is not maintained with the DNA profile data. This lack of information prevents the data being parsed into more homogeneous major population groups (i.e., the population partitions used by forensic scientists). Observed departures from expectations would have no relevance for questioning the reliability of statistical practices because 1) the very heterogeneous data set would be expected to violate the basic assumptions of independence; and

4

2) the data are not separated into populations as used by the DNA forensic community. The issue of having relatives (of unknown kinship types and their unknown proportions) also is a serious consideration; it is well known that inclusion of relatives in databases can cause discernable departure from expectations of multilocus matches based on standard population genetic assumptions, even after adjustments for embedded population substructure (21,22).

Better defined population data, those partitioned into major population categories, which are sufficiently abundant, would provide a more meaningful assessment of the validity of allelic independence and the current statistical practices used in forensic DNA analyses. Many studies on better defined population data sets already have addressed the validity of the basic assumptions of DNA forensic statistics and overwhelmingly support that the current statistical practices are reliable (7, 13-20; note: only a few references are provided because they are too numerous to list). \_

Even if the above complicated matters are ignored, analyzing the more than 3 million profiles in CODIS to test the assumption that the alleles among the various loci are statistically independent will shed little insight, because the use of the product rule is not strictly applied by United States forensic practitioners. The current practices for estimating the rarity of a DNA

profile assume there are violations of the as,sumption of independence and use the coancestry coefficient described as "8" in the calculations (7,23). Basically, undetected substructure in a

population is assumed and the value 8 is used to adjust the product rule accordingly. Thus, tests demonstrating a violation of independence add little to refute the current practices since the assumption of independence is not made.

When conducting pairwise DNA profile comparisons using offender DNA profiles even

if the population data set were relatively homogeneous, it is important to recognize that

1

5

observing a number of profiles matching at, for example, 9 or more loci is predicted, is directly related to the basic principles used to generate a random match probability estimate, and is grounded in well-established probability theory (note: these profiles are not high stringency matches as defined for direct matching for CODIS purposes; they are exclusions. The discussion here is solely for addressing the current forensic practices for estimating a DNA profile frequency). The principle is the same as that for the well-known "birthday scenario." If asked "asswning the probability of having a birthday is independent and all birthdays are equally distributed, how many people WC?uld have to be gathered in a room for odds to be better than even that two people share the same birthday?" most people answer this question with numbers of 180 or more. In fact, only 23 people need to be gathered for odds to be better than even that two will share the same birthday, which could be any of the 365 possible birthdays (24). This· result may seem counterintuitive; however, one must appreciate the question being asked. The question is not "what is the chance of a match between a specific person(s) and a specific birthday?" Instead, the question is "what is the chance that any two people might share any birthday, with the birthday not being specified?" The latter is based on the number of pairwise comparisons. When seeking a match of a specific birthday in a group of 23 people, there are only

23 comparisons made. For any two to share a birthday out of23 people, there are 253 total

pairwise comparisons. The same principle applies to "matches" and "partial matches" in the offender database. In fact, this similarity becomes fairly obvious when one reviews the actual profiles of the ..matches" or ''partial matches!, that had been reported from pairwise comparisons databases. These profiles are arbitrary ones, and not specified or previously targeted. The total number of pairwise comparisons, for example, for the CODIS database with approximately 3,000,000 profiles would be more than 4 trillion. Databases with only 100,000 samples would

6

enable more than a few billion pairwise comparisons. Thus, with so many pairwise comparisons, matches at 9 or more of the 13 loci are expected (25). Observing such partial matches would not call into question the current forensic practices. Indeed, it would support the current statistical practices.

Offender databases are excellent tools for providing investigative leads (1-6). However,

they are extremely poor for inferences regarding the assumptions of current forensic statistical practices. The current statistical practices are well established and grounded on numerous population studies readily available in the scientific literature (13-20; note: only a few references are provided because they are too nwnerous to list). The DNA profiles in offender databases are

not well-suited for quality population statistics studies, because they are not properly annotated for population affinity, are not parsed out into major population categories, and duplicates and

relatives reside in the database. Any results obtained from population genetic and forensic statistics validity studies using the data in its current form would be meaningless. Lastly, to attempt to resolve any matching or partially matching profiles would require obtaining names of individuals within the database and investigating the relationships of these people when no criminal investigation is underway; such disclosure of names is beyond the intent of the use of the offender database and is a violation of Federal law.

.0

Statistical Assessment of a Matching Profile Derived from a Database Search

The significance of observing a matching profile found by searching a offender database of "N" individuals versus the estimate of the rarity of a DNA profile for assessing the weight of the evidence in a case was described by the NRC II Report (7) and clarified by the DNA Advisory Board (26). Two different questions distinguish these scenarios: (1) What is the rarity

7

of the DNA profile? and (2) What is the probability of finding such a DNA profile in the database searched? The different questions will produce different answers for the same profile because they address different issues. The first question, which addresses the random match probability, is always of interest to the fact finder and forms the foundation for addressing the second question.

Consider a comparison is made of DNA profiles derived from evidence and a reference sample from a suspect and there is a failure to exclude the individual as the source of the sample. In this case, the weight of the evidence is determined using a statistical assessment, such as the

random match probability with modifications (7) to convey bow common or rare is the observed DNA profile. In other words, the statistics used are designed to answer the first question, stated above. In contrast, when a DNA profile from a crime scene sample matches a single profile in a felon DNA database, the NRC II Report (7) recommended a formula multiplying N times p, where N is the size of the database and p is the random match probability (RJ\.fl>). This formula conveys the probability of finding the DNA profile in the database searched and may have investigative value. This formulation answers the second question stated above and was not intended to be used to estimate the frequency of observing an evidentiary DNA profile in an unrelated randomly selected individual.

Using the database search calculation as a true RMP would give a false impression that more people share the profile than is reasonably possible. Suppose a RMP was estimated as 1 in 1 million and the size of the database searched is N *=* 1 million; using the NRC II formula Np,

the value would be 1. If the value of 1 is then used to convey rarity of the evidence DNAprofile

to the fact finder, it would erroneously imply that 100% of the population carries the profile. Conveying such is not particularly useful to a jury that is being asked to consider a body of

8

evidence and to decide whether or not a defendant has been proven guilty beyond a reasonable doubt. It grossly understates the value of the evidence when it is being considered in the context of the case.

The Np calculation was not recommended to replace the true RMP, and any assertion of such erroneously cites the language ofNRC II Report (7). On page 40 of the NRC II Report the following is stated: "If one wishes to describe the impact of the DNA evidence under the hypothesis that the source of the evidence sample is someone in the database, then the likelihood ratio should be divided by N,, (7,27). Thus, the formula was not intended to supersede the random match probability estimate; it addresses a different issue.

Familial Searches and Partial Matches are not Equivalent

The identification of matching DNA profiles between a forensic sample and a felon sample in CODIS is referred to as a "high stringency match.,, The software currently in use in CODIS for high stringency matching requires that the genotypes in the files be identical at all loci between the two samples. Because of the potential for allele dropout (28,29) and limitations in identifying some obligate alleles in mixtures (for entry into CODIS), a "moderate stringency match" search also is employed using CODIS software. For a moderate stringency candidate match, the following profile associations per locus, where AiAj represents a heterozygote and AiAi represents a homozygote, are recognized:



2· A·I AI·=A·AI ·J

9

For example, a 15,16 type can be associated with a 15,15 or a 16,16; and a 16,16 type can be associated with any heterozygote that contains allele 16 (such as 16,17; 16,18; 16,19...). As few as one locus up to all loci in the two profiles can be moderate for the profiles to be designated as a moderate stringency candidate match. The following are a few examples of two profiles that would be designated as moderate stringency matches:

Scenario I - although an extreme example, all loci in one profile are heterozygous and in the corresponding profile all loci are homozygous (or pseudohomozygous).

|  |  |  |  |
| --- | --- | --- | --- |
| Locus | Offender | Forensic | Forensic8 |
| D3S1358 | 15,16 | 15,15 | 15 |
| vWA | 17,18 | 17,17 | 17 |
| FGA | 21,22 | 22,22 | 22 |
| D8S1179 | 13,14 | 13,13 | 13 |
| D21S11 | 29,30 | 30,30 | 30 |
| D18S51 | 14,17 | 14,14 | 14 |
| D5S818 | 11,12 | 11,11 | 11 |
| D13S317 | 11,12 | 11,11 | 11 |
| D7S820 | 10,11 | 10,10 | 10 |
| CSFIPO | 11,12 | 11,11 | 11 |
| TPOX | 8,11 | 8,8 | 8 |
| TH0l | 6,9.3 | 9.3,9.3 | 9.3 |
| D16S539 | 11;12 | 12,12 | 12 |

a) In the database, a locus that is either a homozygote or a pseudohomozygote is displayed with

only one allele

Scenario 2 - approximately half the loci in one profile are heterozygous and these correspond to homozygous (or pseudohomozygous) loci in the other profile.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Locus | Offender | Forensic | Offender8 | Forensic8 |
| D3S1358 | 15,16 | 15,15 | 15,16 | 15 |
| vWA | 17,18 | 17,17 | 17,18 | 17 |
| FGA | 21,22 | 22,22 | 21,22 | 22 |
| D8Sl 179 | 13,14 | 13,13 | 13,14 | 13 |
| D21Sll | 29,30 | 30,30 | 29,30 | 30 |
|  |  |  | 10 |  |

**l**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| DI 8S51 | 14,17 | 14,14 | 14,17 | 14 |  | "" |
| D5S818 | 11,12 | 11,11 | 11,12 | 11 | *r* |  |
| D13S317 | 11,11 | 11,12 | 11 | 11,12 |  |  |
| D7S820 | 10,10 | 10,11 | 10 | 10,11 |  |  |
| CSFlPO | 11,11 | 11,12 | 11 | 11,12 |  |  |
| TPOX | 8,8 | 8,11 | 8 | 8,11 |  |  |
| THOl | 9.3,9.3 | 6,9.3 | 9.3 | 6,9.3 |  |  |
| D16S539 | 12,12 | 11,12 | 12 | 11,12 |  |  |

a) In the database, a locus that is either a homozygote or a pseudohomozygote is displayed with

only one allele

In both Scenarios 1 and 2 all loci between the two profiles meet the moderate stringency criterion; i.e.,.one locus in one profile is heterozygous and the same locus in the other profile is homozygous and the two profiles at that locus share a common allele.

Scenario 3 - also is considered a moderate stringency candidate match. Some loci (the first four

listed) are high stringency matches and the rest meet a moderate stringency match criterion. In J

this scenario 9 loci are a moderate stringency match.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Locus | Offender | Forensic | 0 :ffender8 | Forensic8 |
| D3S1358 | 15,16 | 15,16 | 15,16 | 15,16 |
| vWA | 17,18 | 17,18 | 17,18 | 17,18 |
| FGA | 21,22 | 21,22 | 21,22 | 21,22 |
| D8S1179 | 13,14 | 13,14 | 13,14 | 13,14 |
| D21S11 | 29,30 | 30,30 | 29,30 | 30 |
| D18851 | 14,17 | 14,14 | 14,17 | 14 |
| D5S818 | 11,12 | 11,11 | 11,12 | 11 |
| D13S317 | 11,12 | 11,11 | - 11,12 | 11 |
| D7S820 | 10,11 | 10,10 | 10,11 | 10 |
| CSFlPO | 11,11 | 11,12 | 11 | 11,12 |
| TPOX | 8,8 | 8,11 | 8 | 8,11 |
| THOI | 9.3,9.3 | 6,9.3 | 9.3 | 6,9.3 |
| D16S539 | 12,12 | 11,12 | 12 | 11,12 |

a) In the database, a locus that is either a hornozygote or a pseudohomozygote is displayed with only one allele

11

If only one locus showed a moderate stringency and all other loci were at a high stringency match, the two profiles would still be classified as a moderate stringency candidate match. However, such a scenario would likely be considered a high stringency match with one locus demonstrating allele drop out.

"Partial matches," as shown in the scenarios above, are a very small subset of moderate

stringency candidate matches. Because CODIS is designed to facilitate obtaining direct matches, partial matches constitute exclusions. However, some may seek to use moderate stringency search algorithms with hopes of finding investigative leads to identify the somces of evidentiary material through kinship or familial inferences. The premise is that close relatives, i.e., parent­ offspring and sib-sib, would share more alleles in common than unrelated individuals. Therefore, when there is no high stringency match obtained via a CODIS search, a moderate stringency candidate match may associate an evidence profile to a relative of the true source of the evidence profile. Indeed, a moderate stringency match does meet the general criterion for a potential relative (often favoring a parent-offspring relationship) being the source, because there is one allele in common at all loci. However, caution should be taken before proceeding with such a proposition.

One may believe that a moderate stringency match is strong evidence for there being a

kinship relationship. To support this contention, a kinship index (KI) might be calculated for the two profiles. In Scenarios I and 2, the Kl favoring parentage or full sibship versus unrelated are 1135 and 4.23, respectively, based on Caucasian population data. For Scenario 3, the KI favoring parentage or full sibship versus unrelated are 1792 and 358, respectively, based on Caucasian population data. Using African American population data, however, the results are markedly different. In Scenarios 1 and 2, the KI favoring parentage or full sibship versus unrelated are

12

. *..,,,(.iii,:* ,, '

. . ·-\_,-...

**r,**

,...-...\; '. :/ /:·,: ,,. ' ;·

**sibshjp,,;;!pL....**

135,500 and 212, respectively. For Scenario 3, the Kl favoring parentage or full

unrelated are 180,500 and 2,155, respectively. The reason for the larger Kls in AfriCBJl*.:*. . ;cl!)' .". ....

('.' < \*- - - *:* .. ' ,./ r: \'

. ' :-'·--:; .\_. · - - \\··: 1- ·: .

is that the alleles in the scenarios are the most common alleles in the Caucasian popul :; rir-,•

- ', ", ,• AJ/•·

*;: tr,/*

These KI results seem compelling. However, they are taken out of context.

#### . -11- irtnf -. .

◄-i\

consideration of the number of samples searched (i.e., greater than 3 million people).}. : :• Uf•t ;>

··,· .'\,.-,•. .f,;I ,•Jt-• •i'i!t 1 *•J,.*

--- !,'f:.,\_ --".·.

many profiles, there is a high probability that twp unrelated people could have m 1 .t;3:;'.C'·

.-'-\_;•, '.i\ f;?:·;\t>.\"..

stringency matching profiles. Recent studies show that in some cases a number of

. . . . *'•:• ---* .. '

cannot be excluded as a potential biological father of a child and at times the **Paternit,JfNP:I .**

. ,, .: ,..'( ..'·. .. .' .

is greater than that for the true biological father. A test familial database was creat l, ,i "'iT:

' ·"<·:t--· . f; : '

3, ;." \f;::;'. ,: -

.

paternity cases (from the Center for Human Identification, UNTIISC) containing

. . ... ,.....

individuals (12,836 biological fathers, 11,113 bjological mothers, and 14,295 children'-tt,>:s 61· · ·

. . .*::.* : *':;.'(\_.-,.;* ·-- - .... :-:,''.:•. -\-!'{(,:\_,.-.,

unidentified person samples). Searches were performed to detect associations betweeii:·:: *·::"}::.) : .* · \_.-\_·\_. ·

0

. ··--:;..W•i;:,;f>J;: ,'.t::1-ti

individuals that could not be excluded as a possible parent-offspring relationship. Th 'fii/.·• 'ii< .;:'.:,:"'.\ :-

. *\_r·\.•\_;•.::(,. - \>.•,i,-·-1·' -\*

\i• .

-- - , 1 ,::1 · *,:(* ;":;:.'/';\_;

required a single allele match at each of the 13 STR loci, i.e., the equivalent to a low.:: f f'::.,

. . ,. ,· *'- :;•*

o t*{;*

search. The search returned 174,807 matches meeting the requirement of sharing atleast allele at all loci which is consistent with a possible parent-offspring relationship. Of these matches, 21,805 represent the true parent-offspring matches and 152,908 (note: that these numbers do not sum to exactly 174, 807 because a few individuals are entered more than once

under different paternity cases) are fortuitous parent-offspring matches in which a false father or mother was associated with an individual classified as a child. Over 400 of these fortuitous matches had paternity indexes (Pls) in excess of 1 million, with the greatest false parentage association yielding a PI of 914 million. A sibship search would be less stringent, as the

13 .

requirement of a shared allele at each locus would not be required. On average approximately 25% of the loci between full sibs would be expected not to share any alleles.

Poetsch et al (30) performed a similar study with a smaller data set (based on 13-15 STR loci) and found similar results. They compared 336 children with 348 unrelated men and observed 26 pairs in which there were no non-excluding STR loci. This empirical value was close to the predicted nwnber of fortuitous matches (23.4 or approximately 0.02% of comparisons). Of the 26 pairs, 19 of them had identified the biological father (the other 7 pairs

were fro cases where the alleged father was excluded). In these 19 pairs, three. unrelated men

had Pls higher·than the true biological father. Using this empirical observation, the number of fortuitous non-excluded profiles in the CODIS database would be approximately 600 and 95 pairs would have greater Pls than true fathers (note that this is an extrapolation assuming a homogeneous database, a criterion that CODIS does not meet; therefore the values are meant only to provide context). With fewer than 13 loci, the number of non.,;,excluded unrelated profiles would increase substanµally. If a sibling relationship also is considered, the nwnber of potential profiles would be immense. Currently, the participants of CODIS cannot address so many candidate matches and remain functional.

In addition to the fact that the K.Is may be misleading, reliance on a moderate stringency

match as providing strong evidence for a kinship relationship (again favoring the parent­ offspring scenario with one allele in common at each locus) ignores the many candidate profiles that would meet the criterion of a potential kinship relationship are not identified by current CODIS searches. Consider the D13S317 locus type 12,13. This type could only moderately match types 12,12 and 13,13. Thus, types 8,12; 9,12; 10,12; 11,12; 12,14; 12,15; 8,13; 9,13;

10,13; 11,13; 13,14; and 13,15 would not be included as candidate moderate stringency matches.

14

Because on average the majority of loci in a profile are heterozygous, the overwhelming majority of profiles that meet the criterion of sharing an allele in common at each locus is not identified.

r

Another exacerbating factor in missing potential relatives is that the moderate stringency search algorithms do not allow for the phenomenon of mutation. If a mutation occurs for the allele transmitted from a true biological parent and its offspring, it is possible they will show no alleles in common at that locus. Even though 12 of the 13 core CODIS loci would meet the moderate stringency criterion, the 13th locus would eliminate the profile as a candidate and it would never be registered. If a mutation did occur and a one or two locus mismatch was allowed, there will be an extreme number of fortuitous matches with Pis greater than the true biological father.

Lastly, a one allele per locus matching criterion (of which a moderate stringency search

finds a very limited subset) favors a parent-offspring scenario over a sib-sib relationship. Again, many potential kinship relationships that may be plausible would not be identified under the current CODIS searching algorithms.

0

Conclusion

A number of issues have arisen due to the application of CODIS for developing

,

.

investigative leads or because of legal proceedings. This paper addresses several topics that required some elucidation. First, CODIS is an excellent investigative tool, but not a good source for validati.Il;g statistical practices for estimating DNA profile frequencies, because of the heterogeneous nature of the database and the existence of an unknown number of duplicates and relatives in the database. Voluminous already published population studies demonstrate the validity of current forensic practices for estimating the rarity of a DNA profile. Second, the RMP

15

·:;. ,::· ·1

'\_:'• t :;t ; '

. .*•-::.* - ·; t..

(or LR) is always meaningful in describing the rarity of a DNA profile and forms the ,Y :. "·

*.. •.i,.".·: ;'., -*

estimating the probability of observing a specified DNA profile in a database of ''N'' indf d;mk· ;, ·

...

' .......... ;·.. -"'

... ··•J••

The RMP and the database search probability address different questions. Therefore, t .·. :.:

. *\_:: :-:* ; :. ;

values are expected. Such.differences do not infer that there is any discord. Third, -":•. ·

.·· ·'.\_;,\_...,\_ *.i*

moderate stringency candidate match as an investigative lead for identifying a close **relaa.vc·in**

. ··: ., ---.,. .

most cases is not likely to be successful. CODIS currently is not designed for the **pu.rpo1$**

' .. ; .:\_,. : .-'

identifying suspects through kinship analysis. However, the attempts to apply current p,ptial .

. , ,.....-:;•,::,-,. .. *:*

matches to familial searches suggest that discussion is needed on proper requirements amt(or·

. . .·.t; ; "':!'-" *i ""* ·:

practices for familial searching. It is important to frame criteria to enable successfql Jcfflitjent

, •• :,\_,·.,.. I,:

familial searching of forensic DNA databases. Topics in this regard include evaluating exi ,

.; ., . ,... ');.;,\_'

•·

. . ... ·.• .. ;:.· ......

or developing effective familial searching software; use of additional autosomal loci **aruf··lineage·.**·. •

• . *; ·-,"1:·* - ;;"',' ·.-·... .'4f- . \•.

based genetic markers, such as Y STRs, for more efficient searching and resolving fo .:. ,? -'.:.:f;...

:·. •.!-,'!: \ *;,·?;i ;. -·:* ,.·.

candidates; and establishing thresholds for selecting candidate matches from famjljaJ *· -:*·*·* ,-"'•1> :., :,. ·

. *:* -- :1 ,..,: . ...

candidate lists.

Acknowledgments

We would like to thank Frederick Bieber and Rock Harmon for their thoughtful comments.

\_ This is publication number 07"01 of the Laboratory Division of the Federal Bureau f Investigation. Names of commercial manufacturers are provided for identification only, and inclusion does not imply endorsement by the Federal Bureau of Investigation.

References

16

1. Budowle, B., Moretti, T.R., Niezgoda, S.J., and Brown, B.L. (1998) CODIS and PCR-based short tandem repeat loci: Law enforcement tools. In: Second European Symposium on Human Identification 1998, Promega Corporation, Madison, Wisconsin pp 73-88.
2. Budowle, B. and Brown, B.L. (2001) The use of DNA typing for forensic identification. Forensics 1(1):9-37.
3. CODIS. Available at <http://www.fbi.gov/hq/lab/codis/indexl>.httn.
4. Martin P.D. (2004) National DNA databases: practice and practicability. A forum for discussion. Prog. Forensic Genet. 10:1-8. ·
5. Werrett D.J. (1997) The national DNA database. Forensic Sci. Int. 88:33--42.
6. Werrett, D.J. and Sparkes, R. (1998) 300 matches per week -- the effectiveness and future development of DNA intelligence databases. In: Ninth International Symposium on Hwnan Identification. Genetic Identity Conference Proceedings, available at [http://www.promega.com/geneticidproc/ussymp9proc/.](http://www.promega.com/geneticidproc/ussymp9proc/)
7. National Research Council Report (1996) The Evahµition of Forensic DNAEvidence, Washington, D.C., National Academy Press.
8. People of the State oflliinoisv Juan Luna, In The Circuit Court Of Cook County, County Department- Criminal Division, No. 02 CR 15430, 2006.

**j**

1. Lander, E.S. (1989)Population genetic considerations in the forensic use of DNA typing. In Banbury Report 32: DNA Technology and Forensic Science. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, pp. 143-156.
2. Lander, E.S. (1991) Invited editorial: Research on DNA catching up with courtroom application. Amer. J. Hum. Genet. 48:819-823.
3. Lewontin, R.C. and Hartl, D.L. (1991) Population genetics in forensic DNA typing. Science 254:1745-1750.
4. Shields, **W.M.** (1992) Problems and solutions associated with matching and generating inclusion probabilities. In: Proceedings of The Third Inte tional Symposium on Human Identification, Scottsdale, AZ, Promega Corporation, pp 1-50.
5. Alshamali, F., Alkhayat, A., Budowle, B., and Watson, N.D. (2005) STR population diversity in nine ethnic populations living in Dubai. Forens. Sci. Int. 152:267-279.

17

1. Ang, H.C., Somarajah,R., Lim, S.E.S., Syn, C.K.C., Tan-Siew, W.F., Chow, S.T., and . ···- ·

Budowle, B. (2005) STR data for the 13 CODIS loci in Singapore Malays. Forensic Sci. I11tt .·,

148(2-3):243-245. .,,.'". / I

1. Budowle, B., Chidambaram, A., Strickland, L., Beheim, C.W., Taft, G.M., and. Chakraborty, R. (2002) Population data at 13 STR loci for three Native Alaska population groups. Forens. Sci. Int. 129(1):51-57. .\_:...
2. Budowle, B., Nhari, L.T., Moretti, T.R., Kanoyangwa, S.B., Masuka, E., Defenbaugh,:D.A., and Smerick, J.B. (1997) Zimbabwe black population data on the six short tandem repeaUoci-· CSFlPO, TPOX, THOI, D3S1358, VWA, and FGA. Forens. Sci. Int. 90:215-221.
3. Budowle, B., Shea, B., Niezgoda, S., and Chakraborty, R. (2001) CODIS STRlocidatafrom 41 sample populations. J. Forens. Sci. 46(3):453-489.
4. Henke, L., Aaspollu, A., Biondo, R., Budowle, B., Drobnic, K.,·van Eede, P.H., Eelske,;.Zech, H., Fernandez de Simon, L., Garafano, L., Gehrig, C., Luckenbach, C., Malik, N., **M,1.d; ;:··**

Parson, W., Primorac, D., Schneider, P.M., Thomson, J., and Vanek, D. (2003) Eval.1U¢1oll o.fithe STR typing kit PowerPlex™ 16 with respect to technical perfonnance and populatioh g et16s:,'8 multicenter study. In: Progress in Forensic Genetics 9,(Brinkmann, B., and Carraced(>, A1·:eas1, ,\_ Elsevier, Amsterdam, pp. 789-794. ;,:

, • , 1:f',' , , ' '

.. *-;!*

1. Lim, S.E.S., Tan-Siew, W.F., Syn, C.K.C., Ang, H.C., Chow, S.T., and Budowle,B;:(200S ;

Genetic data for the 13 CODIS STR loci in Singapore Indians. Forensic Sci. Int. **148(1):6 ;**· )

... *'":'* . ,, ..

. .

1. Syn, C.K.C., Chuah, S.Y., Ang, H.C., Lim, S.E.S., Tan-Siew, W.F., Chow, S.T.,:and., Budowle, B. (2005) Genetic data for the 13 CODIS STR loci in Singapore Chinese. Forensic Sci. . Int. 152:285-288.
2. Teshmia, **K.M.,** Lee, H.S., and Chakraborty, R. (2002) Population substructure effects on the extent of genotype sharing: A tool for detecting the presence of relatives in databases. Amer. J.

· Hum. Genet. 71:A570. ·

1. Lee, H., Hwang, J.J., and Chakraborty, R. (2003) Inclusion of relatives in a sample produces intra-and inter-locus association of alleles without biasing allele frequency estimates. Amer. J. Hum Genet. 73(5):619.
2. **Weir,** B.S. and Cockerham, C.C. (1984) Estimating F-statistics for the analysis of population structure. Evolution 38: 1358-1370.
3. Birthday scenario. <http://en.wikipedia.org/wiki/Birthday_paradox>
4. Weir, B.S. (2004) Matching and partially-matching DNA profiles. J. Forensic Sci.

49(5):1009-1014.

18

* ., ....,. ·,, .

·•·'.

\i. .t: ;.:..·::.

' :\_·: C:.:•

1. DNA Advisory Board (2000) Statistical and population genetics issues affecting the < • . "'.\:/l' · evaluation of the frequency of occurrence of DNA profiles calculated from pertinent·pgpuliiti• :.< database(s). Forensic Sci. Comm. 2(3) JULY 2000, available at ' · *:\_-: ·* ,; --

[.http://lab.tbinet.tbi/library/fsc/backissu/july2000/index.htm.](http://lab.tbinet.tbi/library/fsc/backissu/july2000/index.htm) ··'i .. ; ,>"; . ·"''•·

,· ,..

'"

. ,' 1 ., *,;:·* .... . '' !'-

1. Crow, J.F. (1998) The 1996 NRC Report: Another look. In: Ninth International Sym. •·.::., on Human Identification. Genetic Identity Conference Proceedings, available at · *·:,* [http://www.promega.com/geneticidproc/ussymp9proc/.](http://www.promega.com/geneticidproc/ussymp9proc/) ·;. *-ff* -- ;; .,,.
2. Budowle, B., Masibay, A., Anderson, S.J., Barna, C., Biega, L., Brenneke, S., Brown;$[,., . Cramer, J., DeGroot, G.A., Douglas, D., Duceman, B., Eastman, A., Giles, R., Hamill,J.,·Haase,

D.J., Janssen, D.W., Kupferschmid, T.D., Lawton, T., Lemire, C., Llewellyn, B., Mo ;[., ---­ Neves, J., Palaski, C., Schueler, S., Sgueglia, J., Sprecher, C., Tomsey, C., Yet, D. (2001YSTI: primer concordance study. Forens. Sci. Int 124:47-54. , ,·t0,'./...'

. . .. :1,·'•/•1-;

29\_. Budowle, B. and h<:1', C.J: (2001) Concordance studfMon pcpulation database :\_:·· usmg the PowerPlex 16 Kit and AmpFlSTRe Profiler Plus Kit and **AmpFlSTR.e** ;C-G)AletJ?!,fy•- Kit. J. Forens. Sci. 46(3):637-641. · ···

.,, ..illf ,,.:·;:··•'.,,.,,1,,·····.....

:t·:::·:·- -,

30. Poetsch, M., Ludeke, C., Repenning, A., Lutz, F., Malyusz, V., Simeoni, E., Lignitz,·E -\ Oehm.ichen, N., and von Wurmb-Schwark, N. (2006) The problem of single parent/child .. ·?.;: ;: *:,* ' '."'...

,

paternity analysis -practical results involving 336 children and 348 unrelated men. Fo l!it-i'-·'··-- ··".·1-:,:.

·;·

'Int. 159:98-103. · '.··-"'7

.-··fr·" · ::; .. ·

..\_,; i,.:/···•·'.c· :.\_..'

19

•

##### •

**DECLARATION OF SERVICE BY U.S. MAIL**

Case Name: ***People v. Lance Ford***

I declare:

Nos.: MCN: 2151192 and SCN: 196780

I am employed in the Office of the Attorney General, which is the office of a member of the California State Bar at which member's direction this service is made. I am 18 years of age or older and not a party to this matter. I am familiar with the business practice at the Office of the Attorney General for collection and processing of correspondence for mailing with the United States Postal Service. fu accordance with that practice, correspondence placed in the internal mail collection system at the Office of the Attorney General is deposited with the United States Postal Service that same day in the ordinary course of business.

On August 6. 2008, I served the. attached

NOTICE OF OBJECTION AND MOTION TO QUASH SUBPOENA DUCES TECUM; OBJECTION AND MOTION TO QUASH; POINTS AND AUTHORITIES

by placing a true copy thereof enclosed in a sealed envelope with postage thereon fully prepaid, in the internal mail collection system at the Office of the Attorney General at 455 Golden Gate Avenue, Suite 11000, San Francisco, California 94102-7004, addressed as follows:

Bicka Barlow

**Deputy Public Defender**

**San Francisco Public Defender's Office 555 Seventh St, 2nd Floor**

**San Francisco, CA 94103**

**Claudia Phillips**

**Assistant District Attorney**

**San Francisco District Attorney's Office 850 Bryant Street, Room 322**

**San Francisco, CA 94103**

**Michon Martin**

**Assistant District Attorney**

**San Francisco District Attorney's Office 850 Bryant Street, Room 322**

**San Francisco, CA 94103**

I declare under penalty of perjury under the laws of the State of California the foregoing is true and correct and that this declaration was executed on August 6, 2008, at San Francisco, California.

 S. CHIANG

' .,.-

Declarant Signature