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9 SUPERIOR COURT OF CALIFORNIA, COUNTY OF SACRAMENTO

10 PEOPLE OF THE STATE OF
11 CALIFORNIA

12 Plaintiff,

13 vs.

14 PAUL ROBINSON

15 Defendant

Case No.: 00F056236871

Department No. 4/TBA

EXPERT DECLARATION IN SUPPORT
OF DEFENDANT'S MOTION FOR
HEARING

16
17 DECLARATION

18 I, Dan E Krane, being duly sworn, depose and say:

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20 1. I am an expert retained by the defense attorney for the defend-
21 ant in the above-

22 2. I am an Associate Professor in the Department of Biological Sciences at
23 Wright State University in Dayton, Ohio. I have a B.S. degree with a double major in
24 Biology and Chemistry from John Carroll University (Cleveland, OH), and a Ph. D. from
25 the Biochemistry program of the Cell and Molecular Biology Department of the
26 Pennsylvania State University (State College, PA). I have also done postdoctoral
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1 research using the tools of molecular biology to answer questions in the fields of
2 population genetics and molecular evolution in the Genetics Department of the
3 Washington University Medical School (St. Louis, MO) and in the Department of
4 Organismic and Evolutionary Biology of Harvard University (Cambridge, MA). I have
5 published more than 30 scholarly papers in a variety of topics including population
6 genetic studies of the genetic diversity of human populations at DNA typing loci, of
7 organisms exposed to environmental stressors, and the use of DNA typing in forensic
8 science. I have also published a widely-used textbook, “Fundamental Concepts of
9 Bioinformatics.” Since 1991 I have also testified in over 40 criminal cases from at least
10 12 states and in Federal court that have involved forensic DNA typing.

14 **3.** A “match” between the DNA profiles of two different samples means little
15 without accompanying data on both the chance of coincidental matches and the
16 possibility of false positives. Until recently, the DNA profiles that have been generated
17 for forensic purposes have been almost exclusively those that could be characterized as
18 “probable cause matches,” in which DNA testing has been performed upon a reference
19 sample taken from a suspect that has already been linked to a crime by direct or
20 circumstantial evidence. A new category of DNA profile “matches” are becoming
21 increasingly common however – those that are generated as a result of “cold hits” that
22 result from the trawling of a large number of DNA profiles maintained in databases
23 (usually those of previously convicted offenders). Since the primary difference between
24 these kinds of matches is the manner in which a suspect is first identified, it is generally
25 accepted that it is not possible to convert one type of case into the other (for instance, by
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1 simply retesting a reference sample once a “cold hit” has been identified). By the same
2 token, subsequent matches with evidence in other cases need to also be considered “cold
3 hits” because of the way in which a suspect was first identified. It is also generally
4 accepted in the scientific community that the statistical significance of “cold hit” and
5 “probable cause” DNA profiles matches should be determined differently. However,
6 there are at least three different commonly held opinions on how the statistics associated
7 with “cold hits” should be generated and presented.
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10 4. The first group to address this issue was a body of experts appointed to the
11 Committee on DNA Science by the National Research Council in 1992. The position of
12 this group is that database searches should be used to identify potential suspects but not
13 to calculate frequency estimates. When successful, suspects identified by these searches
14 would then be tested at a completely different group of independent genetic markers that
15 would also be compared to the evidence. If these additional genetic loci also match
16 between the suspect and evidence sample, they alone would be used to compute
17 probabilities that reflect the significance of a match. With this methodology the genetic
18 markers used in the original database search are specifically and deliberately excluded
19 from any statistical calculation.
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23 5. A second committee of prominent experts advocated a significantly different
24 approach in 1996. They specifically recommended that, “When the suspect is found by a
25 search of DNA databases, the random-match probability should be multiplied by N , the
26 number of persons in the database.” (*The Evaluation of Forensic DNA Evidence*, 1996,
27 National Research Council Press, p. 40, 161). Proponents of this approach feel that the
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1 first method is too conservative. Their alternative method differs in three ways: 1) no
2 testing is performed at additional loci; 2) genetic markers used in the original database
3 search are included in the statistical calculations; and 3) the size of the database being
4 searched (N) is taken into consideration.
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6 6. A third group is comprised of individual scientists who have published peer-
7 reviewed manuscripts in which they argue that a “cold hit” should actually be given more
8 weight than a match found in a “probable cause” case. Their position is based on the
9 thinking that not only has the defendant been found to match the evidence, but many
10 more individuals have been found to not match. In “probable cause” cases where only a
11 single match is found during the course of DNA testing, there is at least still a formal
12 possibility that one or more untested people may also match the evidence –that possibility
13 becomes increasingly less likely as the database used for a cold hit becomes larger.
14 Proponents of this approach also feel that the first method is too conservative. Their
15 method differs from it in three ways: 1) no testing is performed at additional loci; 2)
16 genetic markers used in the original database search are included in the statistical
17 calculations; and 3) the size of the database being searched (N) is taken into
18 consideration. It also differs from the second in one very important way: the effect of the
19 database size on the significance of a match is precisely opposite – large databases
20 generate the most damning statistics for a defendant while, in the second approach, the
21 larger the database the less damning the statistics become to a defendant. The second and
22 third approaches are diametrically opposed with respect to implications of the size of the
23 database that is searched.
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1 7. The proponents of each of these three approaches include many eminent
2 scholars in the field of genetics and statistics. For instance, the blue ribbon panel of
3 experts that generated the first National Research Council on DNA typing report (which
4 supports the first approach as described in paragraph 4 above) includes Drs. Mary-Claire
5 King, Richard Lempert, Eric Lander, Ruth Macklin, Thomass Marr, Victor McKusick,
6 and Philip Reilly. Members of the second National Research Council on DNA Typing
7 (which recommends the second approach as described in paragraph 5 above) include
8 prominent population geneticists and statisticians such as Drs. James Crow, Arno
9 Motulsky, Thomas Nagylaki, Mashotoshi Nei, David Siegmund and Stephen Stigler. The
10 third approach (described in paragraph 6 above) is one that has been principally
11 advocated by very influential and often cited geneticists and statisticians such as Drs.
12 David Balding, Peter Donnelly and Bruce Weir (as in publications such as: *Errors and*
13 *Misunderstandings in the Second NRC Report*, D. J. Balding, *Jurimetrics*, Summer 1997,
14 37:469-476; *Evaluating DNA Profile Evidence When the Suspect s Identified through a*
15 *Database Search*, D. J. Balding and P. Donnelly, *Journal of Forensic Science*, 1996,
16 41:603-607; and *Interpreting DNA Evidence*, I. W. Evett and B. S. Weir, Sinauer Press,
17 1998, pp. 219-222). This represents a genuine split between three fundamentally
18 different approaches by experts who are significant both in number and in eminence
19 within their fields.
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26 8. While I acknowledge that rigorous and compelling arguments have been
27 presented by all three groups, I am personally in agreement with the position of the first
28 group. In my opinion, this is the only approach that can consistently generate

1 conservative statistics that still reflect the power of DNA typing methodologies. My own
2 analyses of the population databases generated by state laboratories suggests that it may
3 not actually be possible to resolve the conflict between the other two groups due to subtle
4 and pervasive complications arising from extensive population substructuring within the
5 general population (let alone within the subpopulation of those that are included in
6 databases of convicted offenders). An abundant number of genetic markers available at
7 the present time allow the creation of a useful database consisting of one set of genetic
8 markers *and* the subsequent generation of probative forensic evidence relying upon
9 information from a different set of loci. In short, this approach allows a conservative
10 estimate of the significance of a “cold hit” match to be generated that still reflects the
11 resolving power of DNA typing techniques. In those rare instances where greater
12 resolving power might be needed an easily implemented solution would be to simply
13 examine additional, previously untested loci.
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