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SUPERIOR COURT OF CALIFORNIA, COUNTY OF SACRAMENTO

PEOPLE OF THE STATE OF CALIFORNIA Plaintiff, vs. GREGORY MONTGOMERY Defendant	Case No.: 00F05623 Department No. 62 EXPERT DECLARATION IN SUPPORT OF DEFENDANT'S MOTION FOR HEARING

DECLARATION

I, Laurence D. Mueller, being duly sworn, depose and say:

1. I am an expert retained by the defense attorney for the defendant in the above entitled action.

2. I am a Professor in the Department of Ecology & Evolutionary Biology at the University of California, Irvine. I have a B.S. degree in Chemistry and an A.M. in Biology from Stanford University, a Ph. D. from the University of California, at Davis in Ecology, and I have done postdoctoral research in population genetics in the Department of Biological Sciences at Stanford University. I have published nearly 70 scholarly

papers in a variety of topics including theoretical and experimental population genetics and the use of DNA typing in forensic science. Since 1989 I have also consulted in over 100 criminal cases that have involved forensic DNA typing.

3. There are three groups of experts who have different views on the statistical interpretation of DNA in a "cold hit" or database search case.

4. The first group believes that database searches should be used to identify potential suspects but not to calculate frequency estimates. When successful, suspects identified by these searches would then be tested for another group of independent genetic markers that would be compared to the evidence. When these additional genetic loci confirm the match, they alone would be used to compute frequencies for this evidence. Under this methodology the genetic markers used in the original database search would never be part of any statistical calculation.

5. This group is comprised of eminent scholars in the field of genetics and statistics. They include Newton Morton, and members of the first National Research Council on DNA typing, like Mary-Claire King, Richard Lempert, Eric Lander, Ruth Macklin, Thomass Marr, Victor McKusick, and Philip Reilly.

6. The second group believes that a database search provides greater certainty of the true identity of a DNA evidence sample. The logic here is that in addition to the match found between the evidence DNA and a member of a database there also will be many people excluded, thus narrowing down the field of possible contributors. The clearest illustration of this is when all possible suspects can be typed and compared to evidence DNA. Suppose that one match is found and all others are excluded. This means

the match must have identified the true culprit, since all possible suspects were typed. Evidence like this is viewed as much stronger evi dence than just finding a match between one person and the evidence. With only a single match and no exclusions the possibility still exists that one of the untested people may also match the evidence, no matter how rare the frequency of the genetic profile.

7. The second group is comprised of eminent scholars in the field of genetics and statistics such as Peter Donnelly and David Balding. Donnelly and Balding are both well respected and widely published scholars in genetics and statistical applications to genetics.

8. The third group is believes that a database match is less probative than a single DNA match since the chance of finding a match to a particular evidence DNA profile increases as it is compared to more people. Thus, finding that a single person chosen at random is left handed is somewhat unusual but finding at least one left handed person in a sample of 1000 is not at all surprising. Those sharing this belief suggest that any frequency that accompanies a match found from a database of *N* people must have the individual profile frequency multiplied by *N*, making it a more common number.

9. This third group is comprised of eminent scholars in the field of genetics and statistics including the members of second NRC committee on DNA typing such as James Crow, Arno Motulsky, Thomas Nagylaki, Mashatoshi Nei, David Siegmond, and Stephen Stigler. It is worthwhile noting that the second and third group not only disagree on the exact quantitative methods for assessing a database match but also the qualitative effect, e.g. is the match more or less probative. The uncertainty in this regard is even

evident in the second NRC report (pg. 40) "If the database searched includes a large portion of the population, the analysis must take that into account. In the extreme case, a search of the whole population should, of course, provide a definitive answer." Here, the second NRC committee is implicitly admitting that, at some point, a database search will become more probative than their recommendation suggests.

10. I agree with the first group. This approach can both take advantage of a genetic database as an investigative tool and yield probative evidence that can be evaluated by the same statistical techniques used in standard cases. There exist today a sufficient number of genetic markers to allow the creation of a useful database and the production of probative forensic evidence. The differences that exist between groups two and three revolve around fairly sophisticated statistical issues that are not likely to be easily explained to lay people. For instance, the conclusions of the third group rely on the database representing a sample of the potential suspect population. To the extent that many members of a convicted felon database might have been in jail at the time a particular crime was committed erodes a crucial premise of this technique. Trying to verbally or quantitatively discount for this would be problematic at best.

11. These three groups are clearly in disagreement with each other regarding the statistics to be used in a "cold hit" or database search case.

I declare under penalty of perjury that the foregoing is true and correct.

Executed at Irvine, California.

DATED: 26 June 2002

Respectfully submitted,

Professor of Ecology & Evolutionary Biology