

STATEMENT OF DR. JAMES CROW, PH.D

1. I am Dr. James Crow, Professor Emeritus of Genetics at the University of Wisconsin.
2. For over sixty years, I have studied, researched and taught genetics, with an emphasis on experimental, human, and population genetics. I have authored approximately 250 articles on those subjects.
3. Among my professional memberships, I am a member of the National Academy of Sciences, National Academy of Medicine, the Genetics Society of America (President, 1960), and the American Society of Human Genetics (President, 1962).
4. I have served at the national level as a member of the General Advisory Committee to the Director of the National Institute of Health; I have also chaired the National Institute of Health Genetics Study Section and the Mammalian Genetics Study Section.
5. Since 1955, I have served on or chaired more than half-a-dozen special committees of the National Academy of Sciences (NAS). Most recently, from 1994 to 1996, I was Chair of the NAS/National Research Council Committee on DNA Technology in Forensic Science, which published the report: The Evaluation of Forensic DNA Evidence (NRC II). Following that appointment, I was asked to serve on The National Commission on the Future of DNA Evidence, where, from 1998 to 2000, I chaired the Research and Development Working Group.
6. I am aware that there have been theoretical discussions among statisticians regarding how to evaluate the fact that a criminal defendant is first identified as a suspect through a search of DNA profiles in a criminal offender database system. This scenario is commonly referred to as a cold hit case.
7. As discussed below, there are a number of practical issues, financial factors, scientific limitations, and other considerations that have caused statisticians and others

to debate the best way in which to evaluate the fact of a cold hit from an offender database. However, it is important to understand that the mathematics and science underlying the various statistical approaches being discussed are all scientifically sound. The proper statistical calculation will depend upon the question being asked. Obviously, different questions result in different answers, *i.e.*, different statistical probability calculations. Thus, the debate has not centered on scientific acceptance, but rather on other policy considerations that do not implicate the scientific integrity of the various approaches.

8. The most common question that is asked in DNA cases, regardless of how a suspect is initially identified, is how rare is the DNA profile found in the biological evidence that is believed to come from the perpetrator of the crime. The overall rarity of a DNA profile can be expressed by estimating the frequency that one might expect to find a particular DNA profile in a given population. The frequency of a profile is calculated first by estimating the frequency that a particular pattern of paired alleles or genotypes appear at various locations, among the chromosomes in a cell. Once the frequency of the genotype is calculated for each of the identified loci, those frequencies are multiplied together to produce a number that represents the estimated frequency with which one would expect to find that particular DNA profile at random in a particular population. Multiplication of frequencies across loci represents application of a well established mathematical principle known as the product rule. Application of the product rule to estimate the rarity of a DNA evidence profile is generally accepted among scientists. The resulting number is known as the Random Match Probability (RMP).

9. In my view, the rarity of a profile is always a relevant question for the trier of fact, regardless of how a suspect is first identified. This question is answered by the RMP calculation.

10. In NRC II, the committee recommended, in Recommendation 5.1, that an additional number should be calculated in a cold hit case by multiplying the RMP by the number of profiles in the searched database. This calculation is different than the RMP because it answers a different question, i.e., what are the chances of finding a profile that matches the DNA evidence profile in a database of a known size?

11. As the Chair of NRC II, I do not believe that Recommendation 5.1 was intended to eliminate the use of the RMP as one number in the context of cold hit cases. Both the RMP and the number derived from Recommendation 5.1 are based upon scientifically valid methodologies and each provides information that could be useful for the trier of fact in a cold hit case. The RMP is a constant and it informs the jury of the overall rareness of the DNA profile. The RMP is unaffected by the fact that a database search has been conducted. The number that results from Recommendation 5.1, on the other hand, is a sliding scale. As the number of profiles searched increases, the chance of finding a match increases. In other words, this calculation depends upon the size of the database(s) searched. Of course, if the size of the database were to include the population of the entire world, the reasoning of NRC II would lead to the absurd conclusion that chance that this result was purely coincidental would be 100%. Obviously, if a search includes the world population and reveals only one match, the logical conclusion would be just the opposite, i.e., that the single match was the source of the DNA of interest.

12. Thus, to counterbalance this illogical effect, where Recommendation 5.1 is used, it is also important to point out that all of the other profiles in the database searched were eliminated, thus eliminating a significant number of people as potential contributors. Depending on the size of the database searched, this can be extremely relevant and inculpatory evidence against the defendant.

13. It is important to note that current PCR/STR analysis enables scientists to amplify DNA at highly discriminating sites at a high number of different markers

(typically 13 separate loci). This, in turn, results in RMP calculations that are so rare, e.g. 1 in trillions or less, that scientists are able to state with a reasonable degree of scientific certainty that a particular suspect is the source of an evidence sample. In fact, I am not aware of a single instance in which two individuals have ever been identified as sharing the same DNA profile at 13 loci amplified under PCR/STR methods (excluding identical twins who share identical DNA).

14. In 1996, when NRC II was issued, a number of members on the committee were concerned with coincidental matches which might implicate the wrong person. As noted above, however, this concern has been negated by the advancements in DNA technology resulting in smaller random match probabilities.

15. In NRC II, we noted that the approach discussed in a prior NAS/NRC committee report, NRC I --in which they recommended discarding markers utilized in database search -- was not a mathematically invalid approach, but unnecessarily wasted information, and depended on the assumption that DNA could be retested which is not always true. The NRC I recommendation pertaining to cold hit cases was the result of technological limitations regarding forensic DNA science as it existed in the early 1990s. The NRC I committee adjusted for these limitations by significantly overstating the probability calculations. These concerns, however, no longer exist in light of the advancements in forensic DNA methodologies. Thus, while the underlying mathematics set forth in NRC I are valid, no laboratories utilize this approach because it is outdated and impracticable.

16. The reliability and discriminatory power of a DNA match has changed dramatically since the 1996 when the last NRC report on the forensic use of DNA evidence was published. With 13 STR loci, random match probabilities are much less than they were using the DNA analytical techniques that were available in the first half of the 1990s. Currently, random match probabilities are usually considerably less than the reciprocal of the world population. With such small probabilities, it is likely that a

particular DNA sample is unique (except possibly for close relatives), and the manner in which it was developed becomes irrelevant.

17. I am familiar with the procedure used by the FBI to determine whether an analyst will be allowed to opine that a particular DNA profile is unique. I believe that the FBI procedure is appropriately conservative, especially in light of the superior power of discrimination that current methods provide. The procedure also properly takes various uncertainties into account.

T James F. Crow
Dr. James Crow, PhD.

State of Wisconsin

County of Dane

Before me the undersigned, a Notary Public for Madison County, State of Wisconsin, personally appeared James Crow, and he being first duly sworn by me upon his oath, says that the statements contained in the above declaration are true.

Signed and sealed this 3rd day of September 2004.

Kathleen Mary Kaul

My commission expires May 25, 2008.

