Crime Laboratory Directive No. 98-05
Effective Date: March 15, 2003

TO: Laboratory SAC's and Supervisors

FROM: Assistant Director Jerry Richardson

SUBJECT: **New DNA Reporting and Testimony Guidelines - Updated**

On April 27, 1998, the Molecular Genetics Section attended a seminar offered by Dr. Bruce Weir of the Department of Statistics at North Carolina State University. Dr. Weir addressed some of the current issues in the use of population frequency analysis in the interpretation of forensic DNA casework. Dr. Weir was asked to provide this seminar and some recommendations regarding interpretational guidelines. After an open discussion on these issues and careful consideration, the following changes in interpretational guidelines were made.

1. OPEN TESTIMONY ON THE ISSUE OF UNIQUENESS

Analysts in the Molecular Genetics Section will now be allowed to provide opinion testimony as to the uniqueness of a DNA profile in cases which meet the criteria established below. As expert witnesses, these analysts have always had the legal authority to provide such testimony, but the North Carolina State Bureau has opted not to exercise this authority; choosing instead to be more conservative.

Other analysts in Latent Evidence, Questioned Documents, and Firearms have been offering this type of testimony for years. Now that the main issues dealing with the population genetics of DNA have been laid to rest with the National Research Council's 1996 publication entitled "The Evaluation of Forensic DNA Evidence", and a firm legal foundation for DNA testing is now in place, not only in this state and nation, but worldwide, the time to move forward has arrived.

<u>Analysts are to advise the District Attorney of this change in Section policy in advance of their testimony, and provide the District Attorney with the following question to ask:</u>

Special Agent _______, based on your professional knowledge, careful reading of the pertinent scientific literature, and years of experience with forensic DNA testing, have you developed an opinion, satisfactory to yourself as to whether or not the stain on State's Exhibit # ___ (description of the State's exhibit item) could have originated from (the defendant or victim) <u>__(Name)</u>?

Analysts are to use great care with the wording of their opinion on the uniqueness of the DNA profile and are to paraphrase the following statement as close as possible (to fit the case scenario):

It is my opinion that it is scientifically unreasonable to expect that the DNA profile derived from the (semen, blood, saliva) stain detected on State's Exhibit # ____ (description of the State's exhibit item) could have originated from anyone other than ___(Name)__, unless this individual has an identical twin.

The Molecular Genetics Section will not use a probability calculation to determine uniqueness, nor will this agency make statements of uniqueness in the laboratory report. Rather, the criteria used will be:

a. A five locus RFLP match of at least 9 bands, or
b. Population frequency calculations which exceed the current estimated population of the world (*6 billion - new estimate just received from the U. S. Census*)

Please note that until all of the thirteen (13) CODIS required STR loci have been validated, analysts reporting STR results will not make opinion statements in court of uniqueness, excepting when the population frequency calculations exceed 6 billion.

2. REPORTING POPULATION FREQUENCY DATA IN LABORATORY REPORTS

Whether or not to report of population frequency results in a laboratory report is a controversy that dates back to conventional serology days. Since the Molecular Genetics Section offers both RFLP and STR DNA typing, since the power of discrimination between an 8 locus RFLP match and a 3 locus (soon to be 8-13 locus) STR match is different, and since it is not always possible for forensic samples to yield a complete DNA profile, the Molecular Genetics Section will continue to report population frequency calculations. It is important to be able to offer information of how strong a match is to all parties in the criminal justice system so that they can make informed decisions on whether the DNA match is significant enough to issue an arrest warrant based solely on the DNA evidence, to take a plea in a case, etc.

Effective this date, we will provide population frequency data in terms of a likelihood statement.

To illustrate this important change, we will look at a recent case.

CURRENT REPORTING -
CONCLUSIONS (CALCULATION OF POPULATION FREQUENCY DATA):

In this case, the DNA banding pattern obtained from the male fraction of the cutting of the panties (Item 1d) and from the male fraction of the fabric from the victim's bed (Item 6) MATCHED the DNA banding pattern from _(Name of the suspect) (Item 3a). This match was made for the loci D1S7, D2S44, D4S139, D5S110, D7S467, D10S28, and D17S79, which is an extremely rare event.

A set of combined population frequencies has been generated for this match using the North Carolina white, black and Lumbee Indian databases available at this time. The probability of selecting another individual having the same DNA profile is approximately:

1 in more than 5.5 billion for the North Carolina white population*

1 in more than 5.5 billion for the North Carolina black population*

1 in more than 5.5 billion for the North Carolina Lumbee Indian population*

*NOTE: Laboratory policy states that frequency data in excess of the world's population will be reported as "more than 5.5 billion", the estimated population of the earth.

NEW REPORTING -
CONCLUSIONS (CALCULATION OF LIKELIHOOD DATA):

In this case, the DNA banding pattern obtained from the male fraction of the cutting of the panties (Item 1D) and from the male fraction of the fabric from the victim's bed (Item 6) MATCHED the DNA banding pattern from (Name of the suspect) (Item 3a). This match was made for the loci D1S7, D2S44, D4S139, D5S110, D7S467, D10S28, and D17S79, which is an extremely rare event.

This laboratory maintains population databases for the North Carolina white, black, and Lumbee Indians and also has access to other population databases which can be used as appropriate.

Using these databases:

for the North Carolina Caucasian population it is 3.0 trillion times more likely
for the North Carolina Black population it is 1,900 trillion times more likely
for the North Carolina Lumbee Indian population it is 12 trillion times more likely

that the DNA profile derived from the male fraction of the cutting of the panties (Item 1d) and the male fraction of the fabric from the victim's bed (Item 6) originated from the suspect (Name) than another unrelated individual in the population.

> *Additional Notes:*
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> *Analysts will report numbers in excess of a trillion only in terms of trillions (like the example above - 1,920 trillion). Most people cannot conceive of values above a billion, but at least they have heard the term trillion before, especially if they read about the U. S. National debt).*
>
> *If the victim or suspect is Hispanic or Oriental, the appropriate databases will be reported as well.*

This change in reporting format will allow us to remove the artificial cap on the numbers provided (currently set at 5.5 billion) to give a more realistic picture of how rare the profile really is. Analysts are to ensure that the courts understand that the likelihood data provided is NOT the probability of guilt.

cc: Director Robin P. Pendergraft