
Procedure for Statistical Interpretations

1.0 Purpose - This document provides the procedure for calculating statistical data on single source, predominant profiles and mixed DNA samples.

2.0 Scope - Qualified DNA Analysts in the Forensic Biology Section shall use this procedure when performing statistical analysis on DNA profiles and mixtures.

3.0 Definitions

- **Combined Probability of Exclusion (CPE):** The probability that a random person would be excluded as a contributor to the observed DNA mixture.
- **Combined Probability of Inclusion (CPI):** The probability that a random person would be included as a contributor to the observed DNA mixture.
- **Minimum allele frequency:** A frequency which shall be used for any allele which is observed 5 or less times in the population frequency database (to include variant and off-ladder alleles). The formula for this frequency is $5/2N$ ($2N = \#$ alleles in the population database at that locus).
- **Heterozygote:** Two different alleles at a particular gene locus on homologous chromosomes.
- **Homozygote:** Same alleles at a particular gene locus on homologous chromosomes
- **Product Rule:** A calculation that can be used if a locus is inherited independently of the other loci. The calculation can be made by multiplying each individual genotype frequency together.
- **Random Match Probability (RMP):** The formulas used in the calculation of the frequency of a DNA profile. These formulas are in accordance with those published in the NRC II guidelines and in PopStats.

4.0 Equipment, Materials and Reagents

- Computer with Microsoft Excel
- CPE 1.0.xls program (or most current) found on Forensic Biology Section shared drive
- PopStats software program located on the CODIS computer with Print to PDF software.

5.0 Procedure

5.1 Random Match Probability

5.1.1 For guidance on when to perform PopStats calculations see the Autosomal DNA STR Interpretation Procedure.

5.1.2 The formulas used in the calculation of the frequency of a DNA profile shall be in accordance with those published in the NRC II guidelines and in PopStats.

5.1.2.1 Heterozygote frequencies: $2pq$ (p and q are the frequencies of the alleles observed).

5.1.2.2 Homozygote frequencies: $p^2 + p(1-p)\theta$, where $\theta = 0.01$. Where p is the frequency of the allele observed and θ is an empirical determination of subpopulations.

5.1.2.3 Multi-locus frequencies: the product rule shall be used.

5.1.3 Procedure for performing PopStats

5.1.3.1 Log onto a CODIS computer.

5.1.3.2 Open CODIS programs.

5.1.3.3 Open PopStats.

5.1.3.4 The case number and the item number(s) descriptors (e.g., R201001234#1) shall be noted in the “Specimen ID” and/or “comments” box.

5.1.3.5 In the STR/PCR block type in the alleles.

5.1.3.6 Click calculate statistics (3rd button from the left).

5.1.3.7 Print the Forensic/Broward report using the Print to PDF and add it to the FA case record object repository.

5.1.4 See the Forensic Biology Section Autosomal DNA STR Interpretation Procedures for reporting guidelines.

5.2 Combined Probability of Exclusion/Inclusion for DNA mixtures (CPI Calculations)

5.2.1 For guidance on when to perform CPI calculations, see the conclusion area in the Autosomal DNA STR Interpretation Guidelines.

5.2.2 **Formulas for CPE:** If an evidence sample includes three alleles at a locus (A_1, A_2, A_3) then:

$$5.2.2.1 P = A_1 + A_2 + A_3 \text{ and}$$

$$5.2.2.2 Q = 1 - p$$

$$5.2.2.3 PE = Q^2 + Q\theta(1-Q) + [2Q(1-Q)\theta] \quad \theta = 0.01$$

5.2.2.4 The probability of exclusion (PE) is calculated at each locus. Then the PEs from the multiple loci are combined through the following equation:

$$CPE = 1 - [(1 - PE_1) \times (1 - PE_2) \times \dots (1 - PE_n)]$$

$$CPI = 1 - CPE$$

5.2.3 Calculating CPI using CPE Excel Program

5.2.3.1 Using the CPE Program, choose the “Mixtures-CPE” tab.

5.2.3.2 Click on the “Clear” tab at the top left section of the spreadsheet to ensure all previous entries are clear.

5.2.3.3 Enter Item number(s) (e.g., R20100000#1) in “Case Information” box. Enter the State Crime Laboratory Case number in either the header or in the “Case Information” box.

5.2.3.4 Perform a QC Check

Enter Expected Results for 9947A/MJB into the spread sheet. This shall be completed prior to any other calculations and the program cannot be shut down/closed between

calculations and shall be performed the same day. The bottom of the notes shall be date and time stamped.

- 5.2.3.5** Determine if CPI values are correct. If values are correct, then the program may be used for CPI Calculations. The correct values are listed in the table below.

Expected values for 9947A/MJB Mixture:

Race	CPI Results
NC Caucasian	1 in 50.15 Million
NC Black	1 in 9.65 Billion
NC Hispanic	1 in 187.33 Million
NC Lumbee Indian	1 in 69.87 Million

- 5.2.3.6** Click on the “Clear” tab at the top left section of the spreadsheet to ensure all previous entries are clear.
- 5.2.3.7** When performing statistics to determine the probability of a person being included in a mixture, only the genetic markers where that individual CANNOT be excluded shall be used in the CPI calculations.
- 5.2.3.8** Once it is determined that the person’s profile cannot be excluded from the mixture, then all the alleles contained in the mixture that include the person’s profile shall be entered into the spread sheet. (Example: If a person is a 12, 14 at D8 and the mixed profile is 12, 13, 14, 16, then 12, 13, 14, 16 would be entered into the spreadsheet).
- 5.2.3.9** Enter the allele calls for each locus used in the CPI calculations as determined above into the spreadsheet. Note: Population frequency data for D2S1338 and D19S433 have not been determined for the NC Populations and shall not be used for calculations. Amelogenin frequencies also are not used for this calculation.
- 5.2.3.10** Print to PDF both the QC check and the calculations with the case profiles. Save the PDF file and save it in the FA case record object repository.

6.0 Limitations – N/A

7.0 Safety – N/A

8.0 References

Forensic Biology Section Procedure for Autosomal DNA STR Interpretation

National Research Council Committee on DNA Forensic Science (1996) An Update: The Evaluation of Forensic DNA Evidence. Washington, D.C., National Academy Press.

9.0 Records - N/A

10.0 Attachments – N/A

Revision History		
Effective Date	Version Number	Reason
09/17/2012	1	Original Document
10/26/2012	2	Corrected the CPI numerical results in the table to update the statistics due to a CODIS upgrade. 5.1.3.4 - corrected name of areas to enter information. 5.2.3.3 - adjusted where case and item numbers can be entered in CPI document.