

25.1 PURPOSE:

- 25.1.1 Kinship Analysis assesses alternate or competing hypotheses of relatedness. In the forensic context, it is useful for determining familial relationships, the identification of unknown bodies, and the identification of the donor of biological evidence when the donor/body is missing or unavailable.

25.2 RESPONSIBILITY:

DNA Section Personnel trained in Kinship Analysis and CODIS 7.0 Popstats.

25.3 Kinship Evaluations:

- 25.3.1 The DNA profile from the subject/stain in question is compared to the DNA profile of close biological relatives. For parent(s)/child comparisons, the loci are first evaluated to determine whether the individual in question can be excluded as a biological child of the other individual(s). An individual must be excluded at more than two loci (when 13-15 STRs are typed) in order to be eliminated as a potential parent. Regarding apparent mutations using STR systems, the repeat # difference of the putative mutation may be relevant to the final conclusion. In the event of apparent mutations, additional testing may be conducted as appropriate.
- 25.3.2 If the individual cannot be excluded, or for comparisons not involving a parent(s)/child relationship (i.e. siblings), a KI (kinship index) is calculated for each locus using CODIS 7.0 Popstats. Any loci displaying genetic inconsistencies will not be incorporated into the calculation(s).

25.3.3 Popstats then calculates an overall CKI (combined kinship index) by multiplying all of the individual KIs. A probability of relatedness is then calculated using Bayes' theorem and assuming a prior probability of 50% (for non-criminal applications only). In criminal cases with MP/UHR results, the CKI will be reported without the prior probability calculation per *State v. Skipper*, 228 Conn. 610 (1994). A report is printed out from Popstats and is included in the case file as the statistics sheet.

25.3.4 The CT Population Databases (African American, Caucasian, and Hispanic) have been validated and are selected within Popstats for the Kinship calculations.

25.4 Relationship Indexes Evaluated (non-criminal):

25.4.1 Single Parentage- (a) Mother or Father, Alleged Child is the MP/UHR
(b) Child, Alleged Mother or Father is the MP/UHR

25.4.2 Reverse Parentage - Mother and Father, Alleged Child is MP/UHR

25.4.3 Parentage Trio - One Parent and One Child, Other Alleged Parent is MP/UHR

25.4.4 Full sibling - Brother or Sister, Alleged Full Sibling is MP/UHR

25.5 Using Popstats:

25.5.1 For Reverse Parentage or Parentage Trio scenarios:

Launch CODIS 7.0 Analyst Workbench. Click on "Popstats" followed by "Parentage". Click on the "Configuration Summary" tab followed by "Browse" to select the CT population databases. Under the defaulted "FBI" folder, select "STR_Identifier-CT" and click "OK". Once selected, return to the "Parentage" screen. Click on "Reverse" for the Subtype if you have STR profiles from both parents and the alleged child is the MP/UHR sample. Click on "Trio" for the Subtype if you have STR profiles from one parent

and one child and the other alleged parent is the MP/UHR sample. Enter the Specimen ID.

The specimen ID # is the laboratory case # followed by a space then the submission/item # (e.g. 14-xxxx 1G1). For specimens already entered into CODIS, the DNA profile can be retrieved by clicking on the “Retrieve” button, after the specimen ID # has been entered. Enter the STR results for all applicable loci. In the instance of genetic inconsistencies, allelic information will not be entered for that locus for all samples in the comparison. Once the STR profiles have been entered, click “Calculate”. Calculations for each population group will be computed. Print the results by selecting “Print→ Reverse Parentage Statistics” or “Print→ Parentage Trio Calculations” depending on the type of calculation conducted.

Autosomal CKI’s can be combined with mitochondrial DNA and/or Y-STR statistics whenever applicable.

25.5.2 For Single Parentage or Full Sibling scenarios:

Launch CODIS 7.0 Analyst Workbench. Click on “Popstats” followed by “Kinship”. Click on the “Configuration Summary” tab followed by “Browse” to select the CT population databases. Under the defaulted “FBI” folder, select “STR_Identifier-CT” and click “OK”. Once selected, return to the “Kinship” screen. Enter the Specimen ID. The specimen ID # is the laboratory case # followed by a space then the submission/item # (e.g. 14-xxxx 1G1). For specimens already entered into CODIS, the DNA profile can be retrieved by clicking on the “Retrieve” button, after the specimen ID # has been entered. Enter the STR results for all applicable loci. The sample in question (i.e. the DNA profile obtained from the UHR/MP) shall be entered as the “Evidence” and the known sample shall be entered as the “Reference”. Select the relevant Kinship Abbreviation based upon the case scenario. Parent-Offspring is abbreviated PO and Full Siblings is abbreviated FS. De-select all other abbreviations so only one relationship is being evaluated. In the instance of genetic

inconsistencies (PO only), allelic information will not be entered for that locus for both samples in the comparison. Once the STR profiles have been entered and the relationship being compared has been selected, click “Calculate”. Calculations for each population group will be computed. Print the results by selecting “Print→ Popstats Single Parentage Statistics” for PO scenarios or “Print→ Popstats Kinship Locus Report” for FS scenarios.

Autosomal CKI’s can be combined with mitochondrial DNA and/or Y-STR statistics whenever applicable.

25.6 Reporting Results

25.6.1 All comparisons will be reported. The DNA report should state the results for one race, preferably the race of the individual in question. If the race is unknown, then all three major population groups (African American, Caucasian, and Hispanic) will be reported. Instances where the race provided is not one of the three major population groups will be handled on a case-by-case basis, with approval by the TL.

25.6.2 The DNA report must list the race(s) used for the calculation(s), the CKI, the assumed prior probability, the probability of relatedness expressed as a percentage (rounded to the millionth), and a statement that calculations compare the tested individual to either an unrelated or related individual. Any loci not used in the calculation(s) will also be listed in the report.

25.6.3 The following sibling CKI’s are used as a guide for report wording:

Full Sibling CKI

<1- does not support sib-ship

1-9- limited support of sib-ship

10-99- moderate support of sib-ship

100-999- strong support of sib-ship

1000+- very strong support of sib-ship

If the race is unknown, the lowest CKI will be used for qualitative purposes.

25.7 Report Examples

25.7.1 The following examples are intended to provide a general guideline for the preparation of DNA reports as it pertains to Kinship Analysis. However, it is not an exhaustive list of all possible casework scenarios. Other reporting strategies may be used with approval of the TL.

25.7.2 Single Parentage:

The DNA results are consistent with Karen Smith being a parental contributor to item #1. It is XX times more likely (assuming a 50% prior probability) that Karen Smith is the biological mother of the source of item #1 as opposed to a random, untested individual in the X population who is unrelated to Karen Smith. The relative probability of maternity is XX.

25.7.3 Reverse Parentage:

The DNA results are consistent with Karen Smith and Mark Smith being parental contributors to item #1. It is XX times more likely (assuming a 50% prior probability) that Karen Smith and Mark Smith are the biological parents of the source of item #1 as opposed to random, untested individuals in the X population who are unrelated to Karen Smith and Mark Smith. The relative probability of parentage is XX.

25.7.4 Parentage Trio:

The DNA results are consistent with Karen Smith and the source of item #1 being parental contributors to the DNA profile obtained from Jason Smith. It is XX times more likely (assuming a 50% prior probability) that Karen Smith and an individual with a DNA profile matching item #1 are the parents of Jason Smith rather than if the DNA profile from item #1 is from a random, untested individual in the X population who is unrelated to Karen Smith and Jason Smith. The relative probability of paternity is XX.

25.7.5 Full Siblings:

It is XX times more likely (assuming a 50% prior probability) that Karen Smith and the source of item #1 are related as full siblings rather than being unrelated. This is xx support of sib-ship. The relative probability of full sib-ship is XX.

25.7.6 Unknown Race:

The DNA results are consistent with Karen Smith being a parental contributor to item #1. It is XX times more likely (assuming a 50% prior probability) in the African American population group, XX times more likely in the Caucasian population group, and XX times more likely in the Hispanic population group that Karen Smith is the biological mother of the source of item #1 as opposed to a random, untested individual in the African American, Caucasian, and Hispanic populations who is unrelated to Karen Smith. The relative probability of maternity is XX in the African American population group, XX in the Caucasian population group, and XX in the Hispanic population group.

25.7.7 Mutation Event:

The DNA results are consistent with Mark Smith being a parental contributor to item #1. It is XX times more likely (assuming a 50% prior probability) that Mark Smith is the biological father of the source of item #1 as opposed to a random, untested individual in the X population who is unrelated to Mark Smith. The relative probability of paternity is XX.

A genetic inconsistency between Mark Smith and item #1 was observed at (locus name). This inconsistency could be due to a mutation event; therefore, this locus was not included in the above calculations.

25.8 Probability of Kinship Worksheet

25.8.1 To calculate the relative probabilities of kinship for the appropriate population group(s), the Probability of Kinship Worksheet QR-46 is utilized. The worksheet uses the combined kinship index number calculated by Popstats and the below statistical formula to calculate the overall relative probability:

Prior Probability: 50%

$$\text{Probability of Kinship} = \frac{CKI}{CKI+1} \times 100$$

Note: This calculation is already listed on the Popstats printout for Parentage Trio Calculations, therefore, it does not need to be repeated.

25.9 References

Evetts, I.W. and Weir, B.S. (1998) *Interpreting DNA Evidence: Statistical Genetics for Forensic Scientists*. Sunderland, MA: Sinauer Associates.

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Page **8** of **8**

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