

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 9.0 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 13-23 STRs are typed) in order to be eliminated as a potential parent.

25.3.1.1 Regarding apparent mutations using STR systems, the repeat # difference of the putative mutation may be relevant to the final conclusion.

25.3.1.2 In the event of apparent mutations, additional testing may be conducted as appropriate.

25.3.1.3 If one or two loci have an apparent mutation, they are included in the kinship index since a mutation rate is incorporated in the calculation.

- 25.3.1.4 If an alleged parent and child are both homozygous at a locus (but for different alleles), a null allele could be a possibility. On a case by case basis and with TL approval, this locus will not be used in the statistical calculation.
- 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 9.0 Popstats.
- 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 FBI 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 9.0 Analyst Workbench. Click on “Popstats” followed by “Parentage”. 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 9.0 Analyst Workbench. Click on “Popstats” followed by “Kinship”. 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 (see section 25.7.7 for further guidance). 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 four decimal places), 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 individuals in the X population. 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 (assuming a 50% prior probability) in the Caucasian population group, and XX times more likely (assuming a 50% prior probability) 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:

Note: This statement will be used only if an alleged parent and child are both homozygous at a locus (but for different alleles), and a null allele could be a possibility. It will be used on a case by case basis, with TL approval.

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 Mutation Rates

The below equation is used for the Kinship Index at any locus where an apparent mutation has occurred. Popstats automatically incorporates the mutation rate into the calculation.

$$KI = \frac{\mu}{\bar{A}}$$

Where: μ = mutation rate at the locus

\bar{A} = Average Probability of Exclusion for the locus

Mutation Rates per Locus

Locus	Mutation Rate (%)
CSF1PO	0.16
FGA	0.28
TH01	0.01
TPOX	0.01
vWA	0.17
D3S1358	0.12
D5S818	0.11
D7S820	0.10
D8S1179	0.14
D13S317	0.14
D16S539	0.11
D18S51	0.22
D21S11	0.19
Penta D	0.14
Penta E	0.16
D2S1338	0.12
D19S433	0.11
SE33	0.64
D1S1656	0.002
D2S441	0.002
D10S1248	0.002
D12S391	0.002
D22S1045	0.002

25.10 References

Approved by Director: Dr. Guy Vallaro

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

Scientific Working Group on DNA Analysis Methods: Guidelines for Missing Persons Casework. Approved 01/09/14.

STRBase: <http://strbase.nist.gov/mutation.htm>

25.11 Appendix

Single Parentage Equations

Paternity calculations in cases where only the child’s and alleged father’s (or alleged mother’s) genotypes are known.

Prob (E|U, C, F) is the probability that the evidence would be observed given that the alleged father was a biological parent of the child.

Prob (E|U, C, U) is the probability that the evidence would be observed given that the alleged father was not the biological father of the child.

LR is the ratio of the two possibilities (likelihood ratio) =

$$\frac{\text{Prob (E|U, C, F)}}{\text{Prob (E|U, C, U)}}$$

P_A , etc., is the estimated frequency of the “A” allele in the population

	Child	Alleged Father	Prob (E U, C, F)	Prob (E U, C, U)	LR
1	AA	AA	$P_A * (P_A)^2$	$(P_A)^2 * (P_A)^2$	$1/ P_A$
2	AA	AB	$P_A * 2P_A P_B * 1/2$	$(P_A)^2 * 2P_A P_B$	$1/(2P_A)$

3	AB	AA	$P_B * (P_A)^2$	$2P_A P_B * (P_A)^2$	$1/(2P_A)$
4	AB	AB	$(P_A + P_B) * 2P_A P_B * 1/2$	$2P_A P_B * 2P_A P_B$	$(P_A + P_B)/(4P_A P_B)$
5	AB	AC	$P_B * 2P_A P_C * 1/2$	$2P_A P_B * 2P_A P_C$	$1/(4P_A)$

Reverse Parentage Equations

Paternity calculations in cases where the mother’s and father’s genotypes are known.

Prob ((E|M, F, Q) is the probability that the evidence would be observed given that the mother and the father were the parents of the evidence sample (Q)

Prob (E|M, F, U) is the probability that the evidence would be observed given that a random member of the population was the was the questioned sample

LR is the ratio of the two possibilities (likelihood ratio) =

$$\frac{\text{Prob} ((E|M, F, Q)}{\text{Prob} (E|M, F, U)}$$

P_A , etc., is the estimated frequency of the “A” allele in the population

	Mother	Q	Father	Prob ((E M, F, Q)	Prob (E M, F, U)	LR
1	AA	AA	AA	$(P_A)^2 * (P_A)^2$	$(P_A)^2 * (P_A)^2 * (P_A)^2$	$1/(P_A)^2$
2	AA	AA	AB	$(P_A)^2 * 2P_A P_B * 1/2$	$(P_A)^2 * 2P_A P_B * (P_A)^2$	$1/(2(P_A)^2)$
3	AA	AB	BB	$(P_A)^2 * (P_B)^2$	$(P_A)^2 * (P_B)^2 * 2P_A P_B$	$1/(2P_A P_B)$
4	AA	AB	AB	$(P_A)^2 * 2P_A P_B * 1/2$	$(P_A)^2 * 2P_A P_B * 2P_A P_B$	$1/(4P_A P_B)$
5	AA	AB	BC	$(P_A)^2 * 2P_B P_C * 1/2$	$(P_A)^2 * 2P_B P_C * 2P_A P_B$	$1/(4P_A P_B)$
6	AB	AB	BB	$2P_A P_B * (P_B)^2 * 1/2$	$2P_A P_B * (P_B)^2 * 2P_A P_B$	$1/(4P_A P_B)$

7	AB	AB	AB	$2P_A P_B * 2P_A P_B * (1/4 + 1/4)$	$2P_A P_B * 2P_A P_B * 2P_A P_B$	$1/(4P_A P_B)$
8	AB	AB	AC	$2P_A P_B * 2P_A P_C * 1/2 * 1/2$	$2P_A P_B * 2P_A P_C * 2P_A P_B$	$1/(8P_A P_B)$
9	AB	AA	AA	$2P_A P_B * (P_A)^2 * 1/2$	$2P_A P_B * (P_A)^2 * (P_A)^2$	$1/(2(P_A)^2)$
10	AB	AA	AB	$2P_A P_B * 2P_A P_B * 1/2 * 1/2$	$2P_A P_B * 2P_A P_B * (P_A)^2$	$1/(4(P_A)^2)$
11	AB	AA	AC	$2P_A P_B * 2P_A P_C * 1/2 * 1/2$	$2P_A P_B * 2P_A P_C * (P_A)^2$	$1/(4(P_A)^2)$
12	AB	AC	CC	$2P_A P_B * (P_C)^2 * 1/2$	$2P_A P_B * (P_C)^2 * 2P_A P_C$	$1/(4P_A P_C)$
13	AB	AC	BC	$2P_A P_B * 2P_B P_C * 1/2 * 1/2$	$2P_A P_B * 2P_B P_C * 2P_A P_C$	$1/(8P_A P_C)$
14	AB	AC	AC	$2P_A P_B * 2P_A P_C * 1/2 * 1/2$	$2P_A P_B * 2P_A P_C * 2P_A P_C$	$1/(8P_A P_C)$
15	AB	AC	CD	$2P_A P_B * 2P_C P_D * 1/2 * 1/2$	$2P_A P_B * 2P_C P_D * 2P_A P_C$	$1/(8P_A P_C)$

Parentage Trio Equation

Paternity calculation in cases where mother’s, child’s and alleged father’s genotypes are known.

Prob (E|M, C, F) is the probability that the evidence would be observed given the mother and alleged father were the biological parents of the child.

Prob (E|M, C) is the probability that the evidence would be observed given that a random member of the population was the biological father.

LR is the ratio of the two possibilities (likelihood ratio) =

$$\frac{\text{Prob} ((E|M, C, F))}{\text{Prob} (E|M, C)}$$

P_A , etc., is the estimated frequency of the “A” allele in the population

	Mother	Child	Alleged Father	Prob (E M, C, F)	Prob (E M, C)	LR
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1	AA	AA	AA	$(P_A)^2 * (P_A)^2$	$(P_A)^2 * (P_A)^2 * P_A$	$1/P_A$
2	AA	AA	AB	$(P_A)^2 * 2P_AP_B * 1/2$	$(P_A)^2 * 2P_AP_B * P_A$	$1/(2P_A)$
3	AA	AB	BB	$(P_A)^2 * (P_B)^2$	$(P_A)^2 * (P_B)^2 * P_B$	$1/P_B$
4	AA	AB	AB	$(P_A)^2 * 2P_AP_B * 1/2$	$(P_A)^2 * 2P_AP_B * P_B$	$1/(2P_B)$
5	AA	AB	BC	$(P_A)^2 * 2P_BP_C * 1/2$	$(P_A)^2 * 2P_BP_C * P_B$	$1/(2P_B)$
6	AB	AB	BB	$2P_AP_B * (P_B)^2 * 1/2$	$2P_AP_B * (P_B)^2 * 1/2 * (P_A + P_B)$	$1/(P_A + P_B)$
7	AB	AB	AB	$2P_AP_B * 2P_AP_B * (1/4 + 1/4)$	$2P_AP_B * 2P_AP_B * 1/2 * (P_A + P_B)$	$1/(P_A + P_B)$
8	AB	AB	AC	$2P_AP_B * 2P_AP_C * 1/2 * 1/2$	$2P_AP_B * 2P_AP_C * 1/2 * (P_A + P_B)$	$1/(2P_A + 2P_B)$
9	AB	AA	AA	$2P_AP_B * (P_A)^2 * 1/2$	$2P_AP_B * (P_A)^2 * 1/2 * P_A$	$1/P_A$
10	AB	AA	AB	$2P_AP_B * 2P_AP_B * 1/2 * 1/2$	$2P_AP_B * 2P_AP_B * 1/2 * P_A$	$1/(2P_A)$
11	AB	AA	AC	$2P_AP_B * 2P_AP_C * 1/2 * 1/2$	$2P_AP_B * 2P_AP_C * 1/2 * P_A$	$1/(2P_A)$
12	AB	AC	CC	$2P_AP_B * (P_C)^2 * 1/2$	$2P_AP_B * (P_C)^2 * 1/2 * P_C$	$1/P_C$
13	AB	AC	BC	$2P_AP_B * 2P_BP_C * 1/2 * 1/2$	$2P_AP_B * 2P_BP_C * 1/2 * P_C$	$1/(2P_C)$
14	AB	AC	AC	$2P_AP_B * 2P_AP_C * 1/2 * 1/2$	$2P_AP_B * 2P_AP_C * 1/2 * P_C$	$1/(2P_C)$
15	AB	AC	CD	$2P_AP_B * 2P_CP_D * 1/2 * 1/2$	$2P_AP_B * 2P_CP_D * 1/2 * P_C$	$1/(2P_C)$

Full-Sibling Equations

Note: p and q are the frequencies of the alleles shared between genotypes #1 and #2

	#1	#2	Full-Sib	Unrelated
1	AB	AB	$1 + p + q + 2pq$	$8pq$
2	AA	AA	$(1 + p)^2$	$4p^2$
3	AA	AB	$1 + p$	$4p$
4	AB	AC	$1 + 2p$	$8p$
5	AB	CD	1	4
6	AA	BB	1	4