DNA: Profile Interpretation

Interpretation of profiles

The interpretation of DNA profiles is a matter of professional judgment and expertise. At times, the analyst may choose to deviate from the following steps as long as an explanation is documented and the deviation occurs prior to the comparison of reference samples.

Interpretation-Identifiler® Plus

The following table outlines the steps involved in the interpretation of Identifiler® Plus profiles.

Step	Action
1	Identify the profile as being from a single contributor or multiple contributors. For single-contributor profiles, identify DNA typing results at all loci, if possible. Proceed to Step 6.
2	Estimate the minimum number of contributors.
3	Identify alleles from an assumed known contributor, if applicable. Determine the approximate ratio of the contributors to the mixture, if possible.
4	Identify the mixture type.
5	Depending on the mixture type, identify the genotypes that must be present in the profile of a true contributor.
6	Compare to reference profiles.

For a comprehensive explanation of these steps, refer to *DNA: Steps for Profile Interpretation.*

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DNA: Profile Interpretation, Continued

Interpretation-Yfiler®

The following table outlines the steps involved in the interpretation of Yfiler® profiles.

Step	Action
1	Identify the profile as being from a single contributor or multiple contributors. For single-contributor profiles, identify DNA typing results at all loci, if possible. Proceed to Step 6.
2	Determine the assumed number of contributors.
3	Subtract alleles from an assumed known contributor, if applicable.
4	Evaluate the signal intensity to determine whether a major/minor contributor relationship exists.
5	Identify all loci in irresolvable mixtures that are suitable for comparison.
6	Compare to reference profiles.

Composite profiles

A *composite profile* is a DNA profile generated by combining typing results from multiple injections of the same amplified sample and/or multiple amplifications of the same DNA extract. An analyst may report a composite profile.

If a composite profile is not reported, then the other amplifications/injections will be compared for concordance.

Conclusions

The four types of conclusions are inclusion, exclusion, inconclusive, and no results.

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DNA: Profile Interpretation, Continued

Inclusion

An individual is **included** when:

- Alleles in the reference profile are detected in an evidence profile.
- Alleles in the reference profile are included as being a reasonable genotype/haplotype identified from the true contributor.
  - An individual may still be included even if some of the loci were determined to be inconclusive.
  - For partial profiles with a considerable amount of allele dropout, analysts should take caution when making an inclusion.
- No more than two obligate paternal allele mismatches are identified after comparing the reference profile of the child to the reference profile of the alleged father. The maximum of two mismatches for an inclusion applies exclusively to the interpretation of paternity samples.

NOTE: Patrilineal male relatives will have the same haplotype (barring genetic mutations). The possibility that a close relative of the suspect is a potential contributor to an evidence haplotype should be considered.

Statistics will be reported for all inclusions except for associations made between the profile derived from an intimate sample and the individual from whom the sample was collected. Depending on the case scenario, statistics may not be provided for associations made between an individual and items that can reasonably be expected to have his or her DNA present.

Inclusion statistics

Reports for Identifiler® Plus inclusions should indicate whether the statistics were arrived at using *Random Match Probability* or *Combined Probability of Inclusion.*

Reports for Yfiler® inclusions should indicate that the statistics were arrived at using the online US Y-STR database calculations.

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DNA: Profile Interpretation, Continued

Exclusion

An individual is **excluded** when:

- Alleles in the reference profile are not detected in an evidence profile and there is no scientific explanation for the non-match.
- Alleles in the reference profile are not included as being a reasonable genotype/haplotype identified from the true contributor and there is no scientific explanation for the non-match.
- Three or more obligate paternal allele mismatches are identified after comparing the reference profile of the child to the reference profile of the alleged father. The requirement of three or more mismatches for an exclusion applies exclusively to the interpretation of paternity profiles.
- The statistical result obtained for an evidence profile is 1 in 1 and the alleles in the reference profile are not detected in the evidence profile.

Inconclusive

A profile is **inconclusive** when:

- None of the loci are suitable for comparison to reference profiles.

No results

A finding of **no results** is reported when:

- No non-artifactual fluorescent signal greater than or equal to the detection threshold is observed. See *DNA: Sample Evaluation* for values.

Y-STR paternity

Due to the inheritance of a male haplotype from father to son, it is possible to perform paternity analysis in criminal paternity cases. This may be particularly useful in analyzing products of conception where it may not be possible to separate maternal DNA from the DNA of a male fetus.

In the instance that the alleged father's haplotype is very similar to the male child's haplotype, mutation rates for the locus or loci should be taken into consideration. For current Y-STR mutation rates, see the *Y Chromosome Haplotype Reference Database* website at www.yhrd.org.

Second analyst review

A second analyst will review the DNA data and initial and date the data sheet.

Refer to *DNA: Data Review by Second Analyst* for additional information.