DNA: Steps for Profile Interpretation- Step 3

Step three   *Identify alleles from an assumed known contributor, if applicable, and determine the approximate ratio of the contributors to the mixture, if possible.*

Mixtures with known contributors

In some cases, mixture profiles contain DNA from an individual who is reasonably expected to be a part contributor to the mixture. Whenever possible, the genetic profile of the assumed known contributor can be used to infer the genetic profile of the remaining contributor(s) in the case. Examples of assumed known contributors include:

- Intimate samples are collected from an identified anatomical location (ex: body orifice, skin surface, fingernail scrapings) and/or a piece of apparel (ex: panties, bra, shirt), where documentation exists that the clothing was removed from the individual during evidence collection and/or worn at the time of the offense. That individual is reasonably expected to be a known contributor to any profile obtained from those items.
- A profile (evidence or reference) from an individual who may reasonably be expected to contribute to a mixture may be assumed to be a known contributor.
- A profile obtained from an individual's personal belongings may also reasonably be expected to contain the DNA of an assumed known contributor.
- Identifying a known contributor also applies to evidentiary items from which DNA is isolated by a differential extraction. In such situations, the single-source or major contributor typing results from one fraction (sperm or non-sperm) can be used to deduce information from its complementary fraction.

Any assumptions that account for the subtraction of the profile of a known contributor should be documented in the notes and stated in the report. Statistical associations will not be provided for the profile of an individual whose DNA is reasonably expected to be on an item.

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DNA: Steps for Profile Interpretation- Step 3, Continued

Donor ratio   A donor ratio is the ratio of DNA proportions of multiple individuals to a mixed DNA typing result. The donor ratio is calculated using the following formula:

$$\begin{pmatrix} RFU\ contribution \\ of\ apparent\ Major \\ component \end{pmatrix} : \begin{pmatrix} RFU\ contribution \\ of\ apparent\ Minor \\ component \end{pmatrix}$$

To calculate the donor ratio for a 2-person mixture, identify the loci which do not appear to have allele sharing between contributors:

- For loci with four alleles, sum the RFUs of the two larger alleles divided by the sum of the two smaller alleles.

    - Example: Alleles with RFUs of 1000, 800, 250 and 200.
        (1000 + 800) : (250 + 200)
        4 : 1 ratio

- For loci containing three alleles in which the major contributor appears to be homozygous and the minor contributor appears to be heterozygous, divide the RFU of the largest allele by the sum of the RFUs of the two smaller alleles.

    - Example: Alleles with RFUs of 1500, 160 and 140.
        1500 : (160 + 140)
        5 : 1 ratio

If there is an assumed known contributor to the mixture, additional loci with unshared alleles may be identified and used for donor ratio calculations.

Occasionally, there are not any loci where unshared alleles can clearly be identified. In this case, the analyst may still attempt to estimate a donor ratio approximation using likely allele pairings of the contributors. Donor ratios calculated using potentially shared alleles may not be as reliable as those calculated using unshared alleles. The analyst should proceed with caution when using these donor ratios to further interpret the mixture.

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Donor ratio
(continued)

- Example: In a two-person mixture, assuming a male and a female contributor, at Amelogenin the following alleles were detected:
  - X allele: 2000 RFU
  - Y allele: 200 RFU

  Assuming a 100% peak height ratio between the X and the Y,
    (2000 - 200) : (200 + 200)
    1800 : 400
    4.5 : 1

Determining the donor ratio in a 3+ person mixture can be very difficult unless there are clear differences in donor contribution or if a known contributor is assumed to be present.

In a 3+ person mixture, a donor ratio approximation may be calculated between the major component alleles and the minor component alleles.

Profiles showing signs of degradation (especially differential degradation) may lead to unreliable donor ratio calculations.

The donor ratio can and does vary from one locus to another within one amplification. To estimate the donor ratio across the entire profile, average the individual donor ratios obtained from all applicable loci.

DNA: Steps for Profile Interpretation- Step 3, Continued

Donor ratio range

A donor ratio range can be calculated to aid in the interpretation of 2-person mixture components. Examples include major/minor, known/unknown, or mixtures with two components. A donor ratio range is calculated from the average donor ratio in the following manner:

- A donor ratio range of a factor of 2 (2x) each way is acceptable for data when all alleles at the locus are greater than the stochastic threshold.
  - Example: The observed donor ratios for a 4:1 mixture could range from 2:1 up to 8:1.
- A donor ratio range of a factor of 3 (3x) each way is acceptable for data if any alleles at the locus are less than the stochastic threshold.
  - Example: The observed donor ratios for a 4:1 mixture could range from 1.3:1 up to 12:1.

NOTE: In a 4:1 or greater mixture, the "major" donor is expected to be the "major" at all loci.