	Intermountain Forensics	SOP #	IAC-204
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YSTR Interpretation

1. Purpose

To describe the procedure for YSTR data analysis and interpretation

2. Summary

Determine the Number of Contributors, Assess Locus Suitability, Perform Comparisons, and Report Conclusions. ArmedXpert™ software is used to assist in statistical calculations and mixture interpretation.

3. Procedure

Number of Contributors:
1. Determination of the number of contributors is made by assessing the total number of alleles at each locus.
   a. An analyst may adjust the number of contributors reported based on additional factors (duplication, etc.) at their discretion.

Single Source Haplotype:
2. All called alleles are determined to be from the same contributor.

3. If there are indications of an additional contributor (1+), use the Interpret with Extra Caution Threshold for assistance.

4. Refer to the **Minimum Suitability Requirement** section for profile suitability minimums.

Mixtures:
Major Haplotype:
5. The Major/Minor disparity is calculated by dividing the allele height of the minor allele by the peak height of the major allele.

6. Suitability is determined on a locus-by-locus basis, but the entire mixture should have the general visible appearance of a major haplotype.

   a. Disparity percentages must be below the values in the table.

   b. High level samples
      i. ForenSeq Signature total sample YSTR reads >80,000

Number of Contributors	Number of called Peaks	Minimum Disparity
1+, 2	1	Suitable
	2	50%
2+, 3	1	Suitable
	2	40%
	3	50%
3+,4	1	Suitable
	2	30%
	3	40%
	4	50%

   Note: A sample with >80,000 reads is assumed to have each major allele well above the IWEC values.

   c. Lower level samples
      i. ForenSeq Signature total sample YSTR reads <80,000

Number of Contributors	Number of called Peaks	Minimum Disparity
1+, 2	1	---

	2	40%
2+, 3	1	---
	2	30%
	3	40%
3+,4	1	---
	2	20%
	3	30%
	4	40%

Note: Use the IWEC values along with analyst discretion for evaluation of single allele loci.

7. Refer to the **Minimum Suitability Requirement** section for profile suitability minimums.

Minor Haplotype:
8. A minor haplotype may only be called in a two-person only mixture.

9. Any alleles not belonging to the major haplotype are obligated to belong to the minor.
    a. If dropout or stutter interference of the minor is not a concern a single peak would indicate overlap and the locus can be deemed suitable for comparison.

10. Refer to the **Minimum Suitability Requirement** section for profile suitability minimums.

Deductions:
11. When it is reasonable to assume that a sample has a known contributor, entering the reference in ArmedXpert™ may provide additional interpretational assistance.

12. For two person mixtures:
    a. Any alleles not belonging to the assumed donor are obligated to belong to the deduced profile.
    b. If dropout or stutter interference of the deduced profile is not a concern, a single allele would indicate overlap and the locus can be deduced and deemed suitable for comparison.

13. Use analyst discretion for deductions on any mixtures with more than two contributors.

14. Refer to the **Minimum Suitability Requirement** section for profile suitability minimums.

Non-Discernable Mixtures:
15. If no major profile is present and a deduction cannot be performed, the entire mixture can be evaluated for dropout.

16. An assessment for the possibility of potential dropout is performed for each locus using the Interpret with Extra Caution values.
    a. Use caution with any mixture where dropout is occurring in portions.
    b. If a specific number of contributors is assumed (2-only, 3-only), a locus may be suitable for comparison if the maximum number of alleles are present at a locus, even if there are alleles below the stochastic threshold.

17. If there is a visible distinction between two major donors and the minor portion, a Co-Major may be present.

Co-Majors:
18. The Co-Major/Minor disparity is calculated by dividing the peak height of the tallest minor allele by the peak height of the lowest Co-Major allele at each locus.

19. Use the disparity requirements in 6a and 6b, treating the co-major as a single contributor.

Statistics:
20. Haplotypes are compared to YHRD YSTR databases to determine the estimated frequency of occurrence.
    a. Single Source
        i. Enter haplotype alleles and search
            1. Manually
            2. Upload
        ii. Select the Dataset

  iii. Click the "Add feature to this Report drop-down and select "National Database (with Subpopulations, 2014 SWGDAM-compliant"
  iv. Use the drop-down arrows in the results boxes to display the 95% Upper Confidence Interval (UCI)
  v. Select the kit
  vi. Print resulting page to include in the case file.
   Note: If manually entered, add Sample Identification information to the PDF printout.

  vii. Use the Observed 95% UCI value for reporting.
 b. Non-Discernable Mixtures
  i. YHRD Mixture Tool requires a suspect reference haplotype
   1. Enter haplotype alleles
    a. Manually
    b. Upload
   2. Select the Global database and search
   3. Print results page
   4. Use the likelihood ratio for reporting

Minimum Suitability for Comparison:
21. A minimum rarity for statistical calculation of 1 in 100 is required for profile comparison suitability.
 a. Any haplotype that is more common than 1 in 100 at the reported statistical calculation does not meet the minimum suitability requirement.
 b. Any haplotype that is more rare than 1 in 100 statistical calculation is assigned an individual number (Individual 01, Individual 02, etc.) and is noted on the report.

22. Any test result that does not meet **Minimum Suitability for Comparison** is deemed not suitable for comparison.

23. Mixtures that contain at least five contributors are considered uninterpretable due to the complexity of the mixture.

Comparisons:
24. All samples with results that are determined to be suitable for comparison are compared to all known reference samples that are provided for that case.

25. All matches and inclusions not considered to be intimate require statistical calculations to be performed and reported.
 a. Intimacy to an item is reported as an assumed contributor.

26. A **Match** is considered to be when all alleles of a comparable haplotype are consistent with a known haplotype.
 a. The Minimum Suitability for Comparison requirement must be met to be reported.
 b. If this requirement cannot be met, no meaningful comparison can be made.

27. An **Inclusion** is considered to be when a haplotype can be included in a non-discernable mixture.

28. Any indication that haplotypes do not match, or a haplotype could not be a possible contributor of a mixture, results in an **Exclusion**.

Thresholds:
29. Interpret with Extra Caution (IWEC)
 a. ForenSeq Signature

Locus	Locus Reads
DYS505	1178
DYS570	972
DYS576	2646
DYS522	308
DYS481	245
DYS19	671
DYS391	813
DYS635	601
DYS437	700
DYS439	731
DYS389I	1458
DYS389II	217

DYS438	3992
DYS612	818
DYS390	963
DYS643	961
DYS533	631
Y-GATA-H4	222
DYS385a-b	973
DYS460	321
DYS549	1004
DYS392	2754
DYS448	1096
DYF387S1	557

b. Yfiler Plus

Locus	RFU
DYS385a-b	160
DYF387S1	180

4.   References

SWGDAM Interpretation Guidelines for Y-Chromosome STR Typing by Forensic DNA Laboratories

5.   Definitions

Inclusion: When the donor of a known haplotype can be included as a possible contributor in a mixture.
Duplication: Multiple alleles attributable to the same individual where traditionally only one allele is present in the general population
Exclusion: When there is evidence that donor of a known haplotype cannot be the source of the DNA result or cannot be included as a possible contributor in a mixture.
Match: When two haplotypes have no unexplainable differences when compared.
Mixture: Indications that more than one contributor is responsible for the data obtained.
Non-Discernable Mixture: A DNA mixture in which relative allele ratios are insufficient to attribute alleles to individual contributor(s).