# **DNA Analysis Report**

STRmix Re-Interpretation Request

Investigating Officer: Detective Jones Report Date: April 30, 2017

Persons of Interest:

Victim: Maria Murphy Suspect: Sebastian Bruno

#### List of Evidence:

**04-05-AA:** right hand fingernail swabs

**03-01:** cuttings of three stains having the appearance of semen

Requested Analysis: Reinterpret previously developed profiles utilizing probabilistic genotyping.

### Evidence Description, Results of Analysis and Interpretation:

## 03-01: cuttings of three stains having the appearance of semen

The previously developed DNA profile from this item was re-assessed utilizing probabilistic genotyping.

The DNA profile from this item is interpreted as a mixture of three individuals.

The probability of obtaining this profile if the DNA came from Maria Murphy and two unrelated, unknown individuals is 500,000 times greater than the probability of obtaining this profile if the DNA came from three unrelated, unknown individuals. This likelihood ratio indicates strong support for the proposition that Maria Murphy is a possible contributor to the profile (refer to Appendix).

The probability of obtaining this profile if the DNA came from Sebastian Bruno and two unrelated, unknown individuals is 5,000,000 times greater than the probability of obtaining this profile if the DNA came from three unrelated, unknown individuals. This likelihood ratio indicates very strong support for the proposition that Sebastian Bruno is a possible contributor to the profile (refer to Appendix).

The probability of obtaining this profile if the DNA came from Maria Murphy, Sebastian Bruno, and one unrelated, unknown individual is 5,000,000,000,000 (5.0 trillion) times greater than the probability of obtaining this profile if the DNA came from three unrelated, unknown individuals. This likelihood ratio indicates very strong support for the proposition that Maria Murphy and Sebastian Bruno are possible contributors to the profile at the same time (refer to Appendix).

### 04-05-AA: right hand fingernail swabs

The previously developed DNA profile from this item was re-assessed utilizing probabilistic genotyping.

The DNA profile from this item is interpreted as a mixture of two individuals with Maria Murphy as an assumed contributor. Based on the likelihood ratio result, Sebastian Bruno is excluded as a contributor to the profile (refer to Appendix).

## Investigative Leads and Requirements for Further Analysis:

Please submit a reference sample from any other potential contributors if further comparisons are needed.

The DNA profile foreign to Maria Murphy from the right-hand fingernail swabs will be entered into the Combined DNA Index System (CODIS) and will be searched against the local, state, and/or national databases.

## **Disposition:**

The DNA extracts were retained. The remainder of the evidence has been returned to your agency.

## **DNA Report Appendix**

#### **Likelihood Ratios:**

If the report contains likelihood ratios, they are calculated based on allele frequency data from the U.S. Caucasian, African American, Asian (Investigator 24plex kit only) and Hispanic population groups. Any likelihood ratio information in the report represents the lowest likelihood ratio calculated from these groups, and other likelihood ratios are present in the case record which may be discoverable under Article 39.14 of the Texas Code of Criminal Procedure.

Likelihood ratios occur on a continuum from zero to infinity and are calculated by dividing the probability of the evidence given proposition 1 by the probability of the evidence given proposition 2. Typically, proposition 1 is an explanation of the DNA profile if it originated from a person of interest while proposition 2 is an explanation of the DNA profile if it originated from an unknown, unrelated individual.

A likelihood ratio of greater than 0.5 but less than 2 is termed uninformative and indicates both propositions are nearly equally supported.

A likelihood ratio of below 0.01 indicates an exclusion.

Likelihood ratios of greater than or equal to 0.01 and less than or equal to 0.5 are converted prior to reporting by using the formula Z = 1/likelihood ratio. For example, if a likelihood ratio of 0.2 was obtained, this number would be converted by dividing 1 by 0.2 to get a reported likelihood ratio of 5. As the reported likelihood ratio (Z) increases in value from 2, it indicates a stronger degree of support for the second proposition that the DNA profile is explained if it originated from an unknown, unrelated individual.

Likelihood ratios of 2 or greater are not converted prior to reporting. As these likelihood ratios increase in value from 2, they indicate a stronger degree of support for the first proposition that the DNA profile is explained if it originated from the person of interest.

DPS validations have shown that, when using the Identifiler Plus or Investigator 24plex amplification kits, a likelihood ratio between 0.01 and 1000 may indicate adventitious support for an incorrect proposition. For the Minifiler amplification kit, a likelihood ratio between 0.01 and 10,000 may indicate adventitious support for an incorrect proposition.

Table 1. Scale of verbal qualifiers for reporting likelihood ratios

$LR$ for $H_{ m p}$ Support and $1/LR$ for $H_{ m d}$ Support	Verbal Qualifier
1	Uninformative
2 – 99	Limited Support
100 – 9,999	Moderate Support
10,000 – 999,999	Strong Support
≥1,000,000	Very Strong Support

#### **PCR Amplification Kits:**

The Texas Department of Public Safety reports information from several PCR (polymerase chain reaction) amplification kits. These kits use PCR to amplify STR (short tandem repeat) loci. The Profiler Plus kit amplifies the following loci: D3S1358, vWA, FGA, Amelogenin, D8S1179, D21S11, D18S51, D5S818, D13S317, and D7S820. The Cofiler kit amplifies the following loci: D3S1358, D16S539, Amelogenin, TH01, TPOX, CSF1PO, and D7S820. The Minifiler kit amplifies the following loci: D13S317, D7S820, Amelogenin, D2S1338, D21S 11, D16S539, D18S51, CSF1PO, and FGA. The Identifiler and Identifiler Plus kits amplify the following loci: D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, Amelogenin, D5S818, and FGA. The Investigator 24plex kit amplifies the following loci: Amelogenin, TH01, D3S1358, vWA, D21S11, TPOX, DYS391, D1S1656, D12S391, SE33, D10S1248, D22S1045, D19S433, D8S1179, D2S1338, D2S441, D18S51, FGA, D16S539, CSF1PO, D13S317, D5S818, and D7S820.

DNA profiles from evidentiary items were evaluated prior to any comparisons to reference samples.