REPORT CHANGES, STRMIX, & THE LIKELIHOOD RATIO

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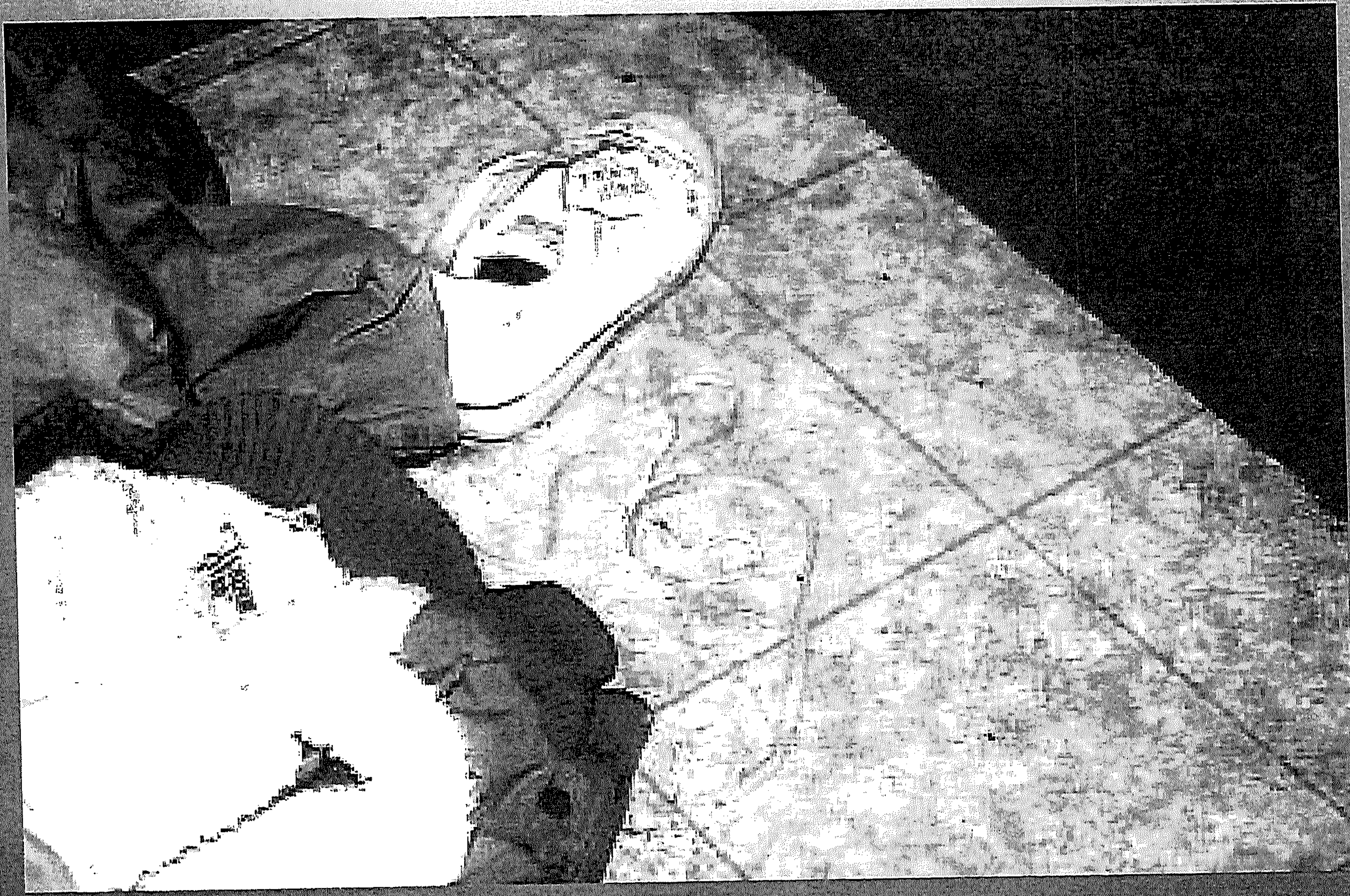
OUTLINE

- Case example
- What is STRmix?
- How STRmix works
- What are Likelihood Ratios?
- Changes to our DNA reports

CASE BACKGROUND

- 84 year-old victim
- Murdered in her home
- Lunch was brought to her around noon, she was fine
- Relative arrived at 4:25 pm to bring her dinner and found her dead, sexually assaulted with her cane, and house ransacked
- She lived alone at the time of the crime, but her elderly brother had lived with her until he recently moved out

THE KEY EVIDENCE

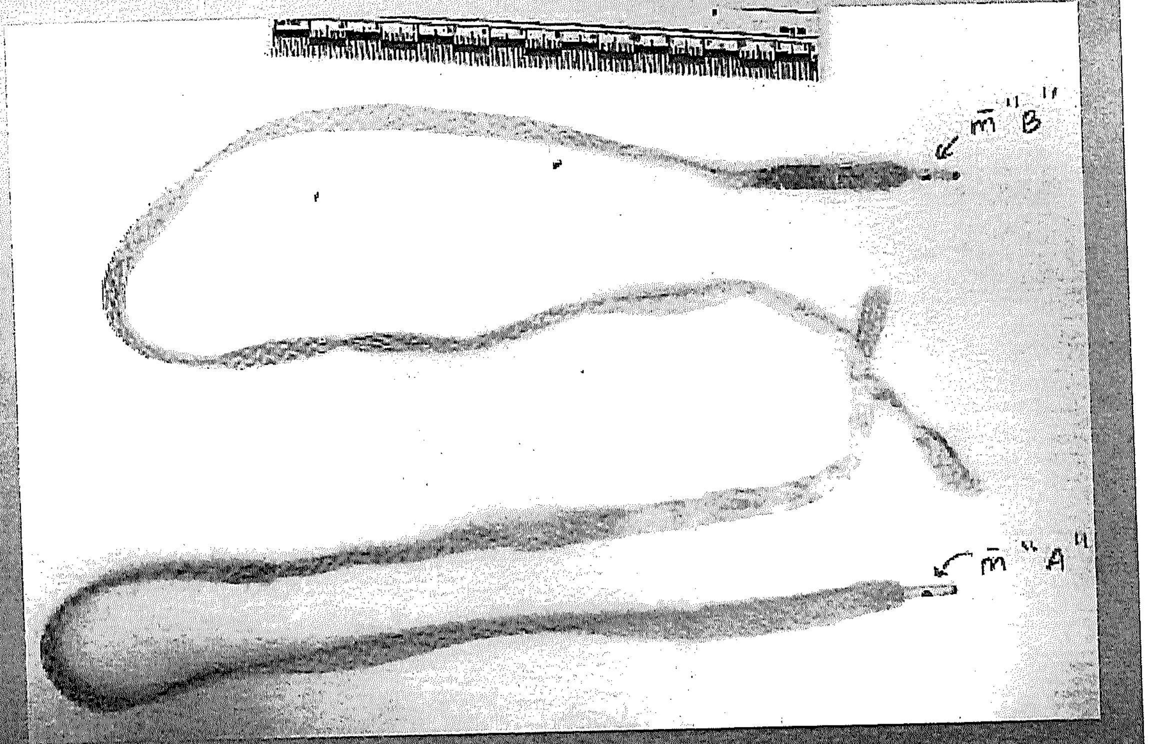


THE KEY EVIDENCE

- *Trace swabs were taken, avoiding blood*
- *These shoes were identified as belonging to victim*

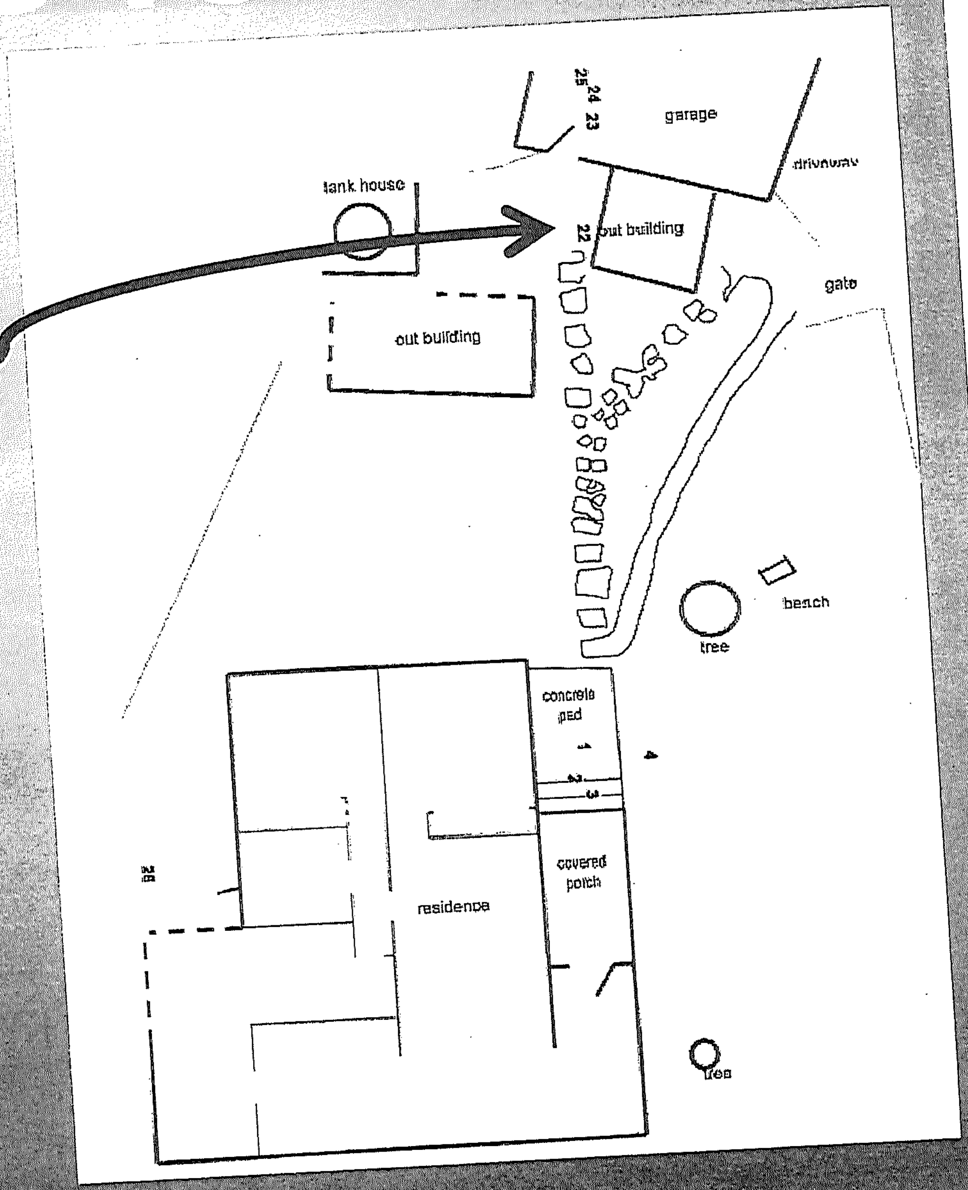
- *Investigators believed assailant tried to bind her hands with the laces first, but they broke*

- *Then hands were bound with pantyhose*



SUSPECT TIED TO SCENE

- A hat found outside, near an outbuilding
  - Sweatband of hat swabbed
  - Profile consistent with one of the suspects



- However, he had been outside of house previously
- Victim's relative worked on his car outside of house
- Suspect stated he was never inside the house

SUSPECT TIED TO SCENE

- A mask was found behind the house
- Mixture of 3 detected for mask swab
- A major male profile consistent with the same suspect from the hat
- But again, it was found outside the house

SHOELACE RESULTS

- The DOJ report issued in 2014 included results from swab of the shoelace
  - At least 3 contributors (at least one male)
  - Reported as "indistinguishable" and not "suitable for comparison to references."
- Twenty months later, our laboratory evaluated the mixture to see if it is suitable for re-analysis with STRmix.

WHAT IS STRmix?

- Probabilistic Genotyping (PG) software
- Mixture interpretation the "Old Way"
  - Take all possibilities for profiles of contributors
  - See if you can exclude any of them based on our lab-validated technical procedures
  - All not excluded get equal share of the probability (if 3 profiles remain, all are 100% possible)
  - Report Random Match Probability (RMP) that answers this question: "What is the chance of picking one person, at random, from the population and they would have this profile?"

HOW DOES STRmix WORK?

- Analyst inputs the mixture results and tells STRmix how many contributors are in the mixture
- STRmix then builds an "expected" mixture:
  - Randomly picks a profile for each contributor
  - Randomly picks a DNA amount for each contributor
  - Randomly picks a PCR efficiency for each area of DNA tested
  - Randomly picks a degradation amount for each contributor
  - Compares the expected profiles (based on the randomly chosen parameters) to the actual observed results

HOW DOES STRmix WORK?

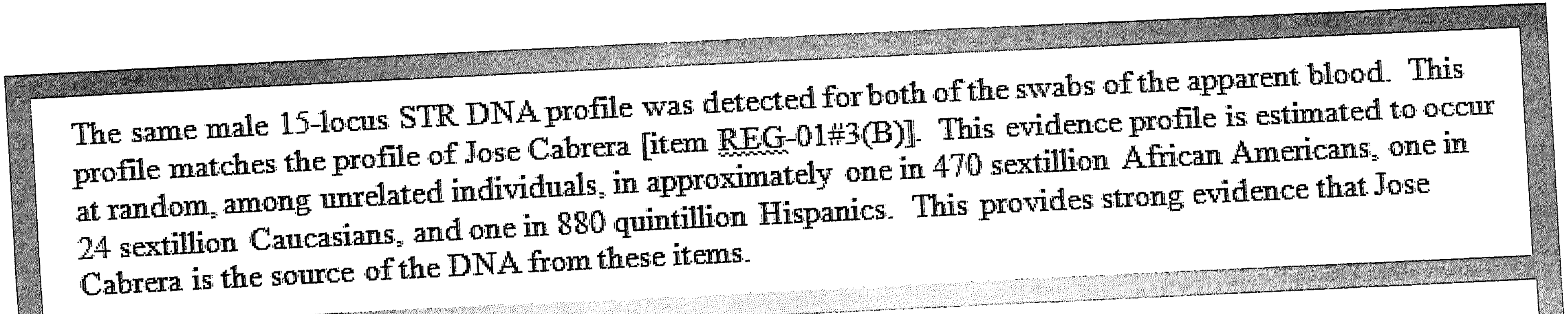
- When the expected profile is close to the observed, that set of parameters gets a higher score. When expected profile is far from observed, that set of parameters gets a lower score.
- This process occurs hundreds-of-thousands to billions of times
- The profiles that the process spent the most time on get more of the weight/probability assigned to them than the others
- These weights are the ultimate, end-goal of STRmix

HOW DOES STRmix WORK?

- *Last step:*
- *Calculate a Likelihood Ratio (LR) that answers this question:* "How much more likely is it to have detected this DNA result under one set of conditions compared to a different set of conditions?"
  - "Conditions" → "Propositions" → "Hypotheses"
- The weights produced by STRmix are reflected in the size of the LR
- A combination of persons who fit the observed data better will get a higher LR than a combo of people who fit less well

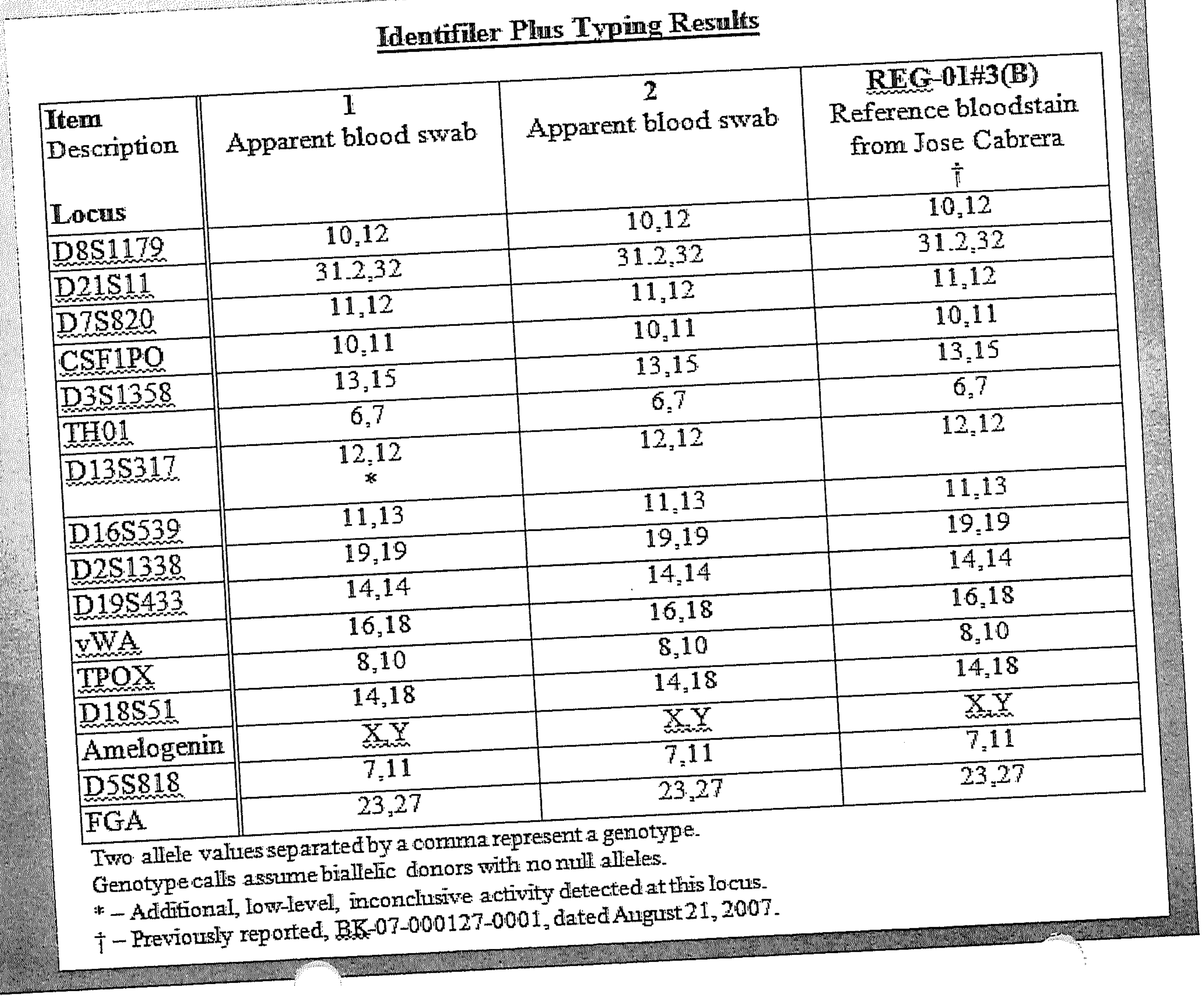
WHAT DOES AN LR MEAN?

- It is a comparison of 2 conditional probabilities
- Takes the form of: $LR = \frac{Hp}{Hd} = \frac{Prosecution\ Proposition}{Defense\ Proposition}$
- In this case, the LRs were:
- $LR = \frac{P(E|Victim+Her\ Brother+Unknown)}{P(E|Victim+Unknown+Unknown)} = 490x109$
- $LR = \frac{P(E|Victim+Suspect+Unknown)}{P(E|Victim+Unknown+Unknown)} = 1.2x10^{18}$
- $LR = \frac{P(E|Victim+Her\ Brother+Suspect)}{P(E|Victim+Her\ Brother+Unknown)} = 1.8x10^{18}$



The same male 15-locus STR DNA profile was detected for both of the swabs of the apparent blood. This profile matches the profile of Jose Cabrera [item REG-01#3(B)]. This evidence profile is estimated to occur at random, among unrelated individuals, in approximately one in 470 sextillion African Americans, one in 24 sextillion Caucasians, and one in 880 quintillion Hispanics. This provides strong evidence that Jose Cabrera is the source of the DNA from these items.

Won't have these statistics anymore



Identifiler Plus Typing Results

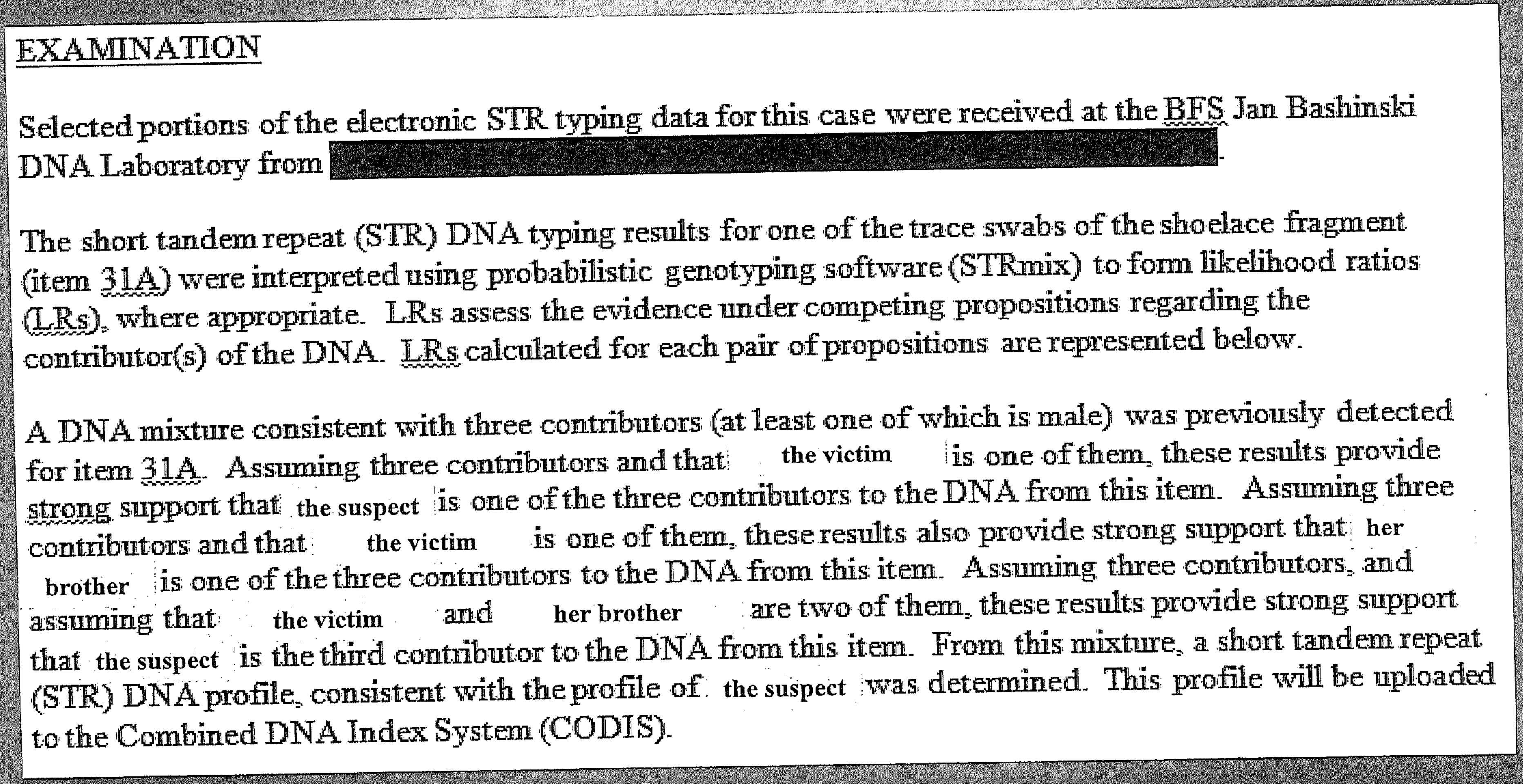
Item Description	1 Apparent blood swab	2 Apparent blood swab	REG-01#3(B) Reference bloodstain from Jose Cabrera †
Locus			
D8S1179	10,12	10,12	10,12
D21S11	31.2,32	31.2,32	31.2,32
D7S820	11,12	11,12	11,12
CSF1PO	10,11	10,11	10,11
D3S1358	13,15	13,15	13,15
TH01	6,7	6,7	6,7
D13S317	12,12 *	12,12	12,12
D16S539	11,13	11,13	11,13
D2S1338	19,19	19,19	19,19
D19S433	14,14	14,14	14,14
vWA	16,18	16,18	16,18
TPOX	8,10	8,10	8,10
D18S51	14,18	14,18	14,18
Amelogenin	X,Y	X,Y	X,Y
D5S818	7,11	7,11	7,11
FGA	23,27	23,27	23,27

Two allele values separated by a comma represent a genotype.
Genotype calls assume biallelic donors with no null alleles.
* – Additional, low-level, inconclusive activity detected at this locus.
† – Previously reported, BK-07-000127-0001, dated August 21, 2007.

Won't see these tables anymore

OUR REPORTS

- *An example of the language you might see:*



EXAMINATION

Selected portions of the electronic STR typing data for this case were received at the BFS Jan Bashinski DNA Laboratory from [redacted].

The short tandem repeat (STR) DNA typing results for one of the trace swabs of the shoelace fragment (item 31A) were interpreted using probabilistic genotyping software (STRmix) to form likelihood ratios (LRs), where appropriate. LRs assess the evidence under competing propositions regarding the contributor(s) of the DNA. LRs calculated for each pair of propositions are represented below.

A DNA mixture consistent with three contributors (at least one of which is male) was previously detected for item 31A. Assuming three contributors and that the victim is one of them, these results provide strong support that the suspect is one of the three contributors to the DNA from this item. Assuming three contributors and that the victim is one of them, these results also provide strong support that her brother is one of the three contributors to the DNA from this item. Assuming three contributors, and assuming that the victim and her brother are two of them, these results provide strong support that the suspect is the third contributor to the DNA from this item. From this mixture, a short tandem repeat (STR) DNA profile, consistent with the profile of the suspect was determined. This profile will be uploaded to the Combined DNA Index System (CODIS).

OUR REPORTS

- No typing results tables

Propositions regarding the contributors to the trace swab of the shoelace fragment (Item 31A):	Likelihood Ratio:	Verbal equivalent:
1. The victim, her brother, and one unknown contributor vs. 2. The victim, and two unknown contributors	AA: 490 billion	The likelihood ratio provides strong support for proposition 1.
	Cauc: 36 billion	
	Hisp: 190 billion	
3. The victim, the suspect, and one unknown contributor vs. 2. The victim, and two unknown contributors	AA: 1.2 quintillion	The likelihood ratio provides strong support for proposition 3.
	Cauc: 280 quintillion	
	Hisp: 29 quintillion	
4. The victim, her brother, and the suspect, vs. 5. The victim, her brother, and one unknown contributor	AA: 1.8 quintillion	The likelihood ratio provides strong support for proposition 4.
	Cauc: 360 quintillion	
	Hisp: 40 quintillion	

10,000,000 +	Provides strong support for
1,000 +	Provides moderate support for
10 +	Provides weak support for
Between 0.1 and 10	Uninformative

0.1 –	Provides weak support against
0.001 –	Provides moderate support against
0.000,001 –	Provides strong support against
0	Exclusion

REPORT DIFFERENCES

- When there is a probative comparison between evidence profile and a suspect or victim reference profile:
  - LR instead of the old RMP statistic
- When there is no probative comparison between evidence and a reference profile:
  - Profile being uploaded to CODIS is based on STRmix
- No table of DNA profile results (in the past, attorneys have liked presenting these to the jury)
- So far, these differences have presented more of a challenge for attorneys in the courtroom than for law enforcement agencies

QUESTIONS???

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