

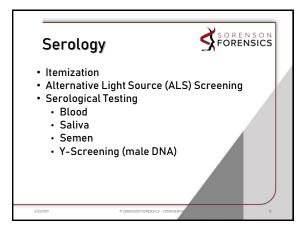
Nuclear DNA DNA is like a large encyclopedia with lots of books that make up the whole. Each book is called a chromosome. Humans have 23 pairs of chromosomes Just like a book, each chromosome contains articles or genes.

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Genes There are two basic types of genes, coding & non-coding. Coding: Instructions on how to make EVERYTHING made "in-house" Non-Coding: Used to be called "junk DNA" These are the genes of interest in forensic DNA







Extraction



- Apply the use of detergents to break open cells, then isolate DNA
- Two types of extraction methods
 - Non-differential (References & Question samples with no sperm suspected)
 - Differential (sperm suspected)

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xtractio

Differential



- Through centrifugation, sample is separated into two general fractions.
 - Epithelial (all non-sperm cells)
 - Sperm
- Helps alleviate the possibility of the female donor overwhelming the male profile.



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Quantification



How much DNA do we have?

• Typically reported in nanograms (ng)

 QuantValues
 DNATotals

 Auto Conc:
 0.0949ng/uL
 Auto DNA:
 3.6062ng

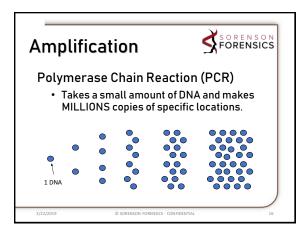
 Auto/Y:
 1.1
 Y DNA:
 3.4124ng

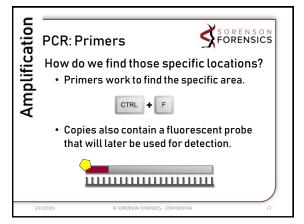
 Y Conc:
 0.0898ng/uL
 Y DNA:
 3.4124ng

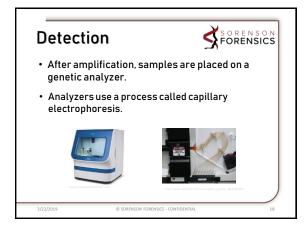
What do these numbers mean?

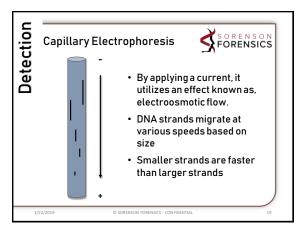
1,000,000,000 ng = 1 g The DNA from one cell = ~0,006ng. 3.6062/0.006=601 cells

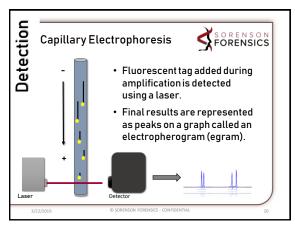
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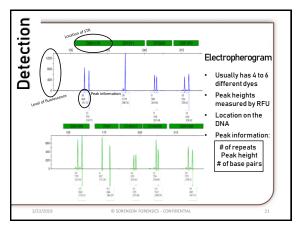


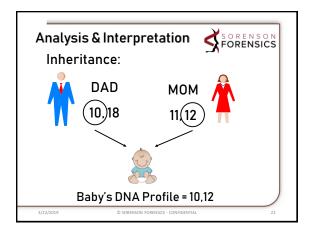


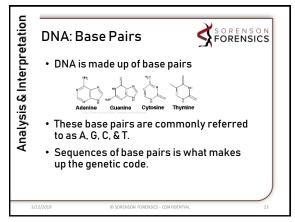


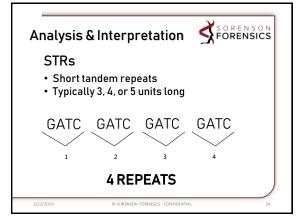


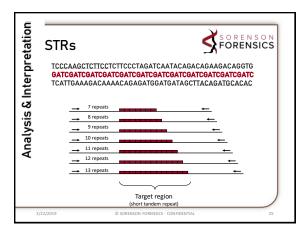


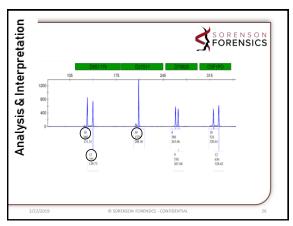


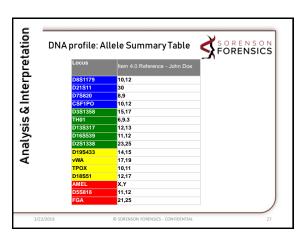


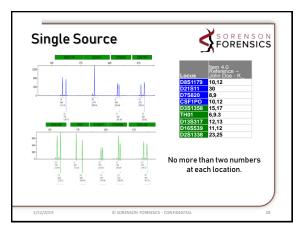


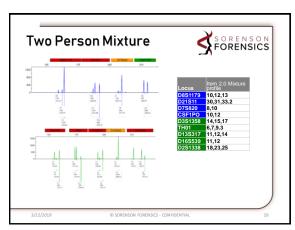


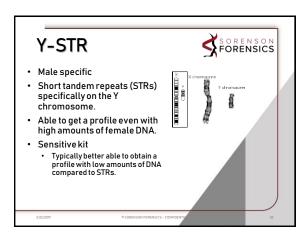


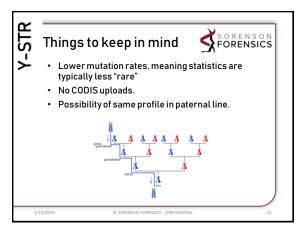


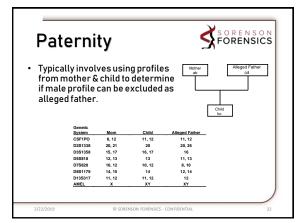












Things to keep in mind • Possible reasons for genetically dissimilar parent-child relationship • Mutation • Null Allele • Motherless profile cases are typically more difficult to determine. • Possibility that related individuals can't be excluded.

Statistics



Typically three major types of statistics performed

- Random Match Probability (RMP)
 - · Used for single source samples
- Combined Probability of Inclusion (CPI)
 - Used for mixtures that can't be deconvoluted.
- · Likelihood Ratios
 - Can be used on a wide range of profile types.
 - Currently being used in our laboratory for Y-STRs & Paternity.

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Statistics Random Match Probability



Item 1.0 (Fabric – Sperm Fraction):

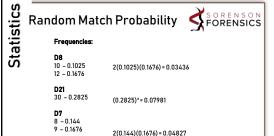
A DNA profile that genetically types as male was obtained from this item. This DNA profile matches the DNA profile obtained from Reference – John Doe. The frequency of cocurrence of this profile among unrelated individuals in the U.S. population is estimated to be:

One in 226 quadrillion for Caucasians One in 151 quintillion for African Americans One in 4.28 quintillion for Hispanics

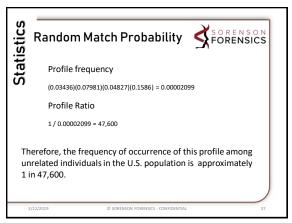
What does that mean?

· The probably of randomly selecting a nonrelated person from a population who also matches our profile.

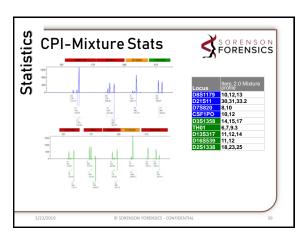
35

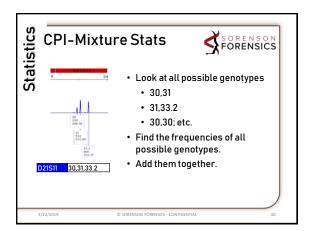


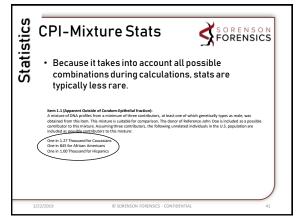
2(0.144)(0.1676) = 0.04827 **CSF** 10 - 0.2202 12 - 0.3601 2(0.2202)(0.3601) = 0.1586



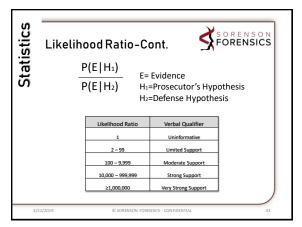
CPI-Mixture Stats • Similar wording & logic to RMP Item 1.1 (Apparent Outside of Condom-Epithelial frostain). Anishus of Other public from a minimum of three contributors, at least one of which genetically types as made, was obtained from this item. This mixture is suitable for comparison. The donor of Reference-John Doe is included as a possible contributor to this mixture. Assuming three contributors, the following urrelated individuals in the U.S. population are included as a possible contributor to this mixture. One in 1.27 Thousand for Cucustians One in 1.05 for African Americans One in 1.05 for Afric

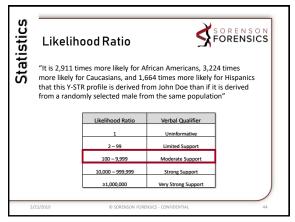




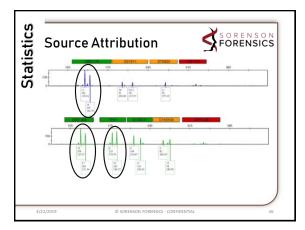


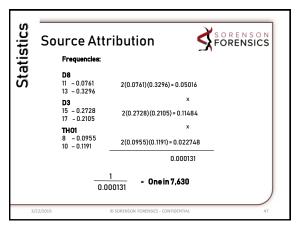
Likelihood Ratio "It is 2,911 times more likely for African Americans, 3,224 times more likely for Caucasians, and 1,664 times more likely for Hispanics that this V-STR profile is derived from John Doe than if it is derived from a randomly selected male from the same population" What does that mean? Based on the evidence, how likely it is for one hypothesis to be correct vs. another.

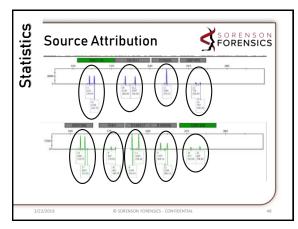


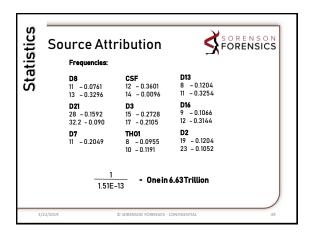


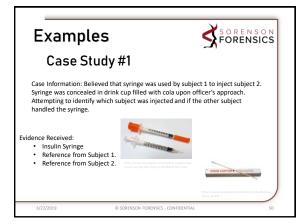
Source Attribution What makes one statistics more rare than other? Possible number of individuals in sample. Ability to deconvolute a profile. Quality of the profile. Lab thresholds and guidelines met.

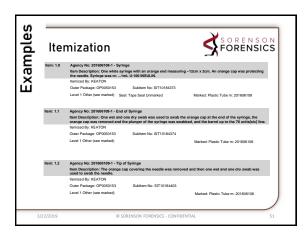


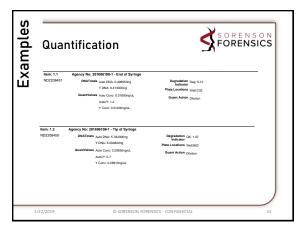


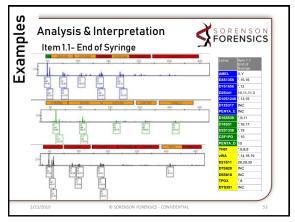


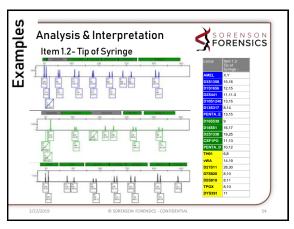




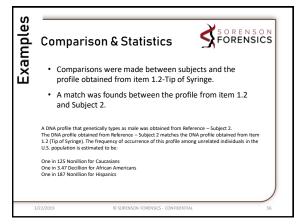


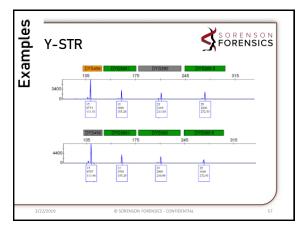


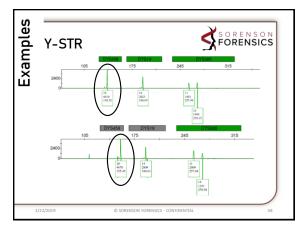


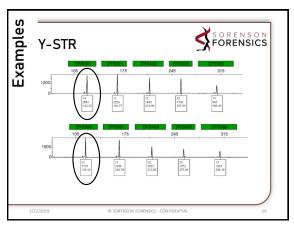


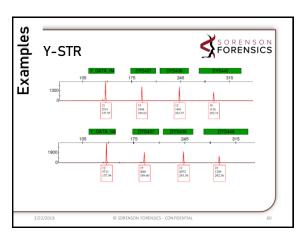


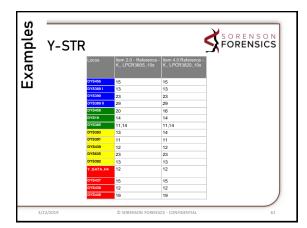


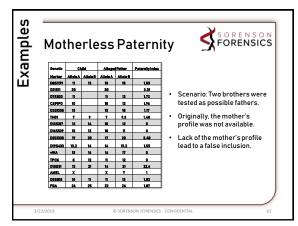


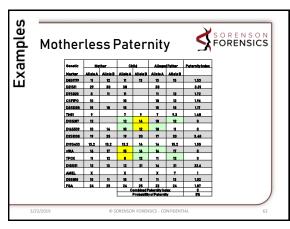


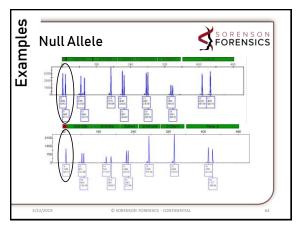


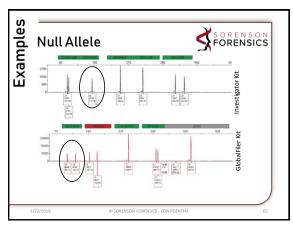








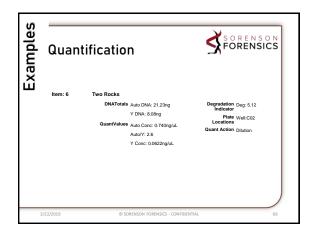


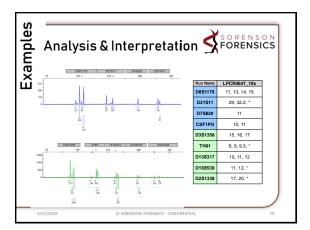


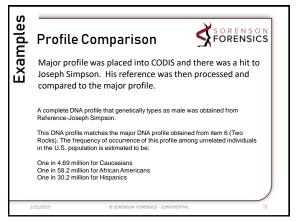


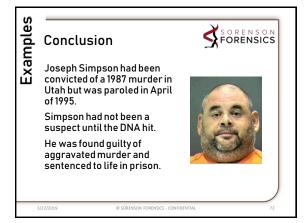












For the Future



- Probabilistic Genotyping (Probgen)
- Rapid DNA Testing
- · Next Gen. Sequencing (NGS)



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Need Help on a Case?



- · Case reviews
- Customizable level to fit specific needs
- Experienced analyst recommendations
- Preparation help for cross-examination
- · Expert witness testimony



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Need a Case Tested?



- · All case types
- Multiple turnaround time options
 - 2-3 day, 5 day, 10 day, 15 day, 30 day, 60 day
- Multiple STR and YSTR chemistries available
- Next generation sequencing (NGS) starting in 2019



3/22/201

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