

## Three Match Statistics, One Verdict

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## Commonwealth vs. Foley

Apr 2006: Blairsville Dentist John Yelenic murdered

Nov 2007: Trooper Kevin Foley charged with crime



Feb 2008: Defense questions 13,000 DNA match score

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## DNA Evidence

- DNA from under victim's fingernails (Q83)
- two contributors to DNA mixture
- 93.3% victim & 6.7% unknown
- 1,000 pg DNA in 25 ul
- STR analysis with ProfilerPlus®, Cofiler®
- know victim contributor genotype (K53)
- TrueAllele® computer interpretation  
(using genotype addition method)  
infer unknown contributor genotype
- only after having inferred unknown,  
compare with suspect genotype (K2)

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## Three DNA Match Statistics

Score	Method
13 thousand	inclusion
23 million	subtraction
189 billion	addition

- Why are there different match results?
- How do mixture interpretation methods differ?
- What should we present in court?

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## Different Interpretation Methods

Data Used	inclusion	subtraction	addition
victim profile	NO	YES	YES
quantitative data	NO	NO	YES

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## Frye: General Acceptance in the Relevant Community

- Quantitative STR Peak Information
- Genotype Probability Distributions
- Computer Interpretation of STR Data
- Statistical Modeling and Computation
- Likelihood Ratio Literature
- Mixture Interpretation Admissibility
- Computer Systems for Quantitative DNA Mixture Deconvolution
- TrueAllele Casework Publications

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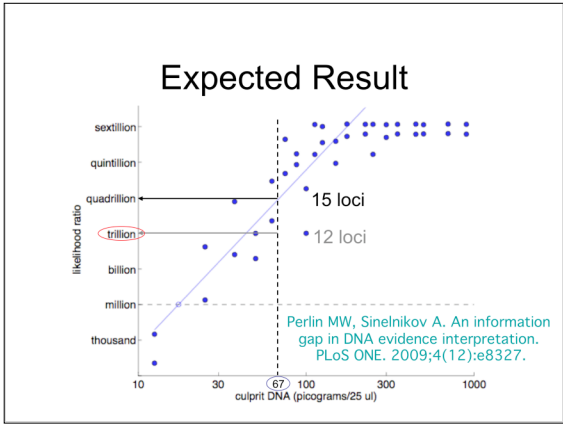
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### Expert Testimony

Dr. Perlin explained to the jury why these apparently different results were expected by DNA science. "The less informative methods ignored some of the data," said Dr. Perlin, "while the TrueAllele computation considered all of the available DNA data."

"A scientist may look at the same slide using the naked eye, a magnifying glass, or a microscope," analogized Dr. Perlin. "A computer that considers all the data is a more powerful DNA microscope."

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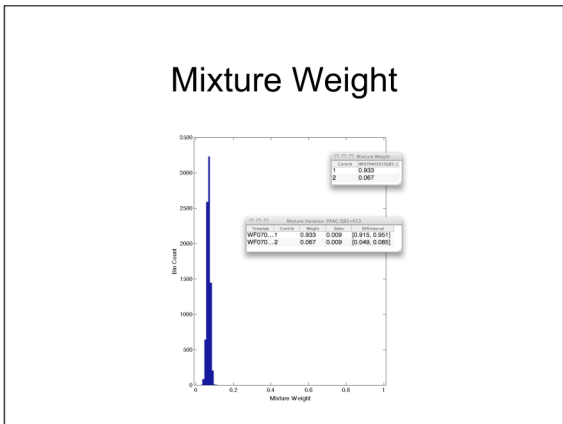
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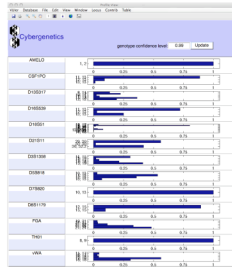
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## Inferred Genotype




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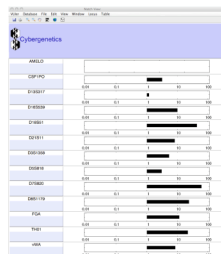
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## log(LR) Match Information




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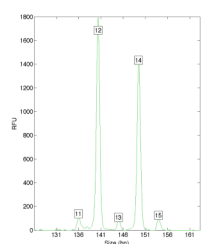
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## Locus D8S1179 Data




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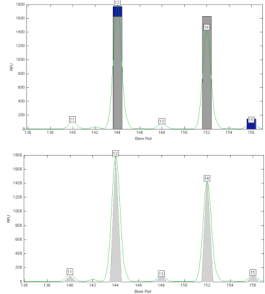
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## Explain D8S1179 Genotype




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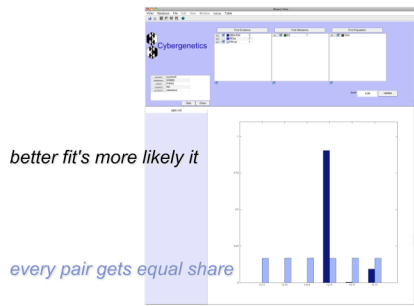
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## Likelihood Comparison




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## Generate Report

QB3 + K53 contributor 2 vs. K2 (CAI)

The LR calculation assumes one unknown contributor in the evidence with one known contributor reference relative to a Caucasian human population having a coancestry coefficient of 0.01.  
The prior LR is approximately 22.1 billion.  
The log(LR) information is 15.34.

locus	allele pair	Q	R	S	LR	log(LR)
CSF1PO	12, 13	0.091	0.0518	1	1.755	0.244
D13S317	8, 11	0.136	0.0683	1	1.990	0.299
D16S539	11, 13	0.722	0.0928	1	7.775	0.891
D18S51	12, 13	0.403	0.0354	1	22.683	1.356
D21S11	29, 30	0.561	0.0877	1	6.388	0.805
D3S1358	15, 18	0.213	0.0839	1	2.538	0.405
D5S818	12, 13	0.358	0.1077	1	3.324	0.522
D7S820	10, 13	1	0.0226	1	44.188	1.645
D8S1179	12, 15	0.895	0.0365	1	24.525	1.390
FGA	21, 24	0.483	0.0514	1	9.388	0.973
TH01	8, 9	1	0.0450	1	22.201	1.346
vWA	17, 18	0.562	0.1199	1	4.689	0.671

Locus information gain is genotype probability ratio:  
LR = after/before

Joint information is the sum of the locus information

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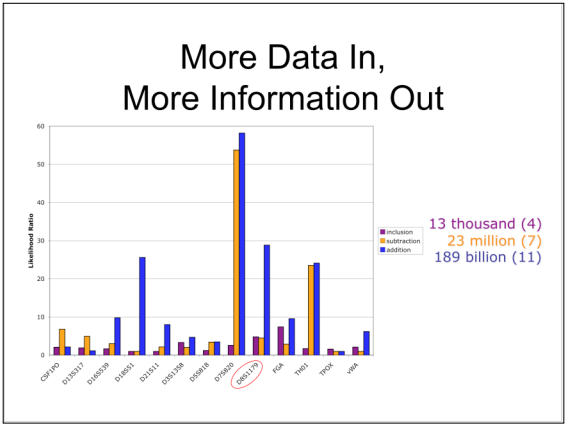
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### Case Observations

- objective review never saw suspect
- easy to testify about in court
- understandable to judge and jury
- have precedent: admitted, testified
- preserve match information in data
- rapid response to attorney
- multiple match scores presented  
all information to the triers of fact –  
nothing was withheld from the jury  
this should be standard practice

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