Introducing TrueAllele® Casework at the New York State Police

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TA User Seminar 9/18/13

TrueAllele® Users Group
September 18, 2013

Peer-Reviewed Publications:

1. JFS 2004   **Validation Study of the TrueAllele® Automated Data Review System.**

2. JFS 2011   **Validating TrueAllele® DNA Mixture Interpretation.**

3. JFS 2013   **New York State TrueAllele® Casework Validation Study.**

STATE OF NEW YORK
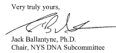DNA SUBCOMMITTEE
OF THE
COMMISSION ON FORENSIC SCIENCE

Approved by DNA Subcommittee of New York State Commission on Forensic Science May 2011

Jose Baltazar, Ph.D., Chairman
University of Central Florida

Eric Buel, Ph.D.
Vermont Forensic Laboratory

George Carmody, Ph.D.
Carleton University, Ottawa

Ranajit Chakraborty, Ph.D.
University of Texas, Houston

Charles Hirsch, M.D.
New York City Chief Medical Examiner

Mark Batzer, Ph.D.
Louisiana State University

Jeani Walsh, Ph.D.
New York State Department of Health

Sean Byrne, Acting Commissioner
Chair, Commission on Forensic Science
Division of Criminal Justice Services
4 Tower Place, 10th Floor
Albany, New York 12203-3764

Dear Commissioner Byrne:

Pursuant to Executive Law §995-b (13b) the DNA Subcommittee will assess and evaluate all DNA methodologies proposed to be used for forensic analysis and make recommendations to the Commission.

At the May 20, 2011 meeting the DNA Subcommittee reviewed and evaluated the New York State Police TrueAllele® Validation developed by New York State Police and Cybergenetics Corp. The DNA Subcommittee offers a binding recommendation to the Commission on Forensic Science that its use by NYSP Forensic Investigation Center be approved for forensic casework.
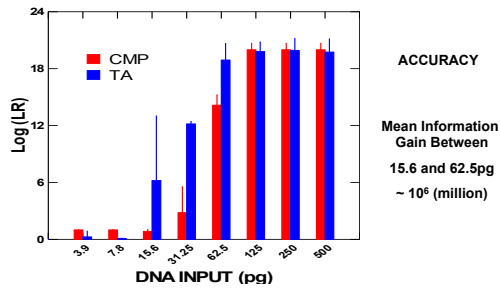
Very truly yours,

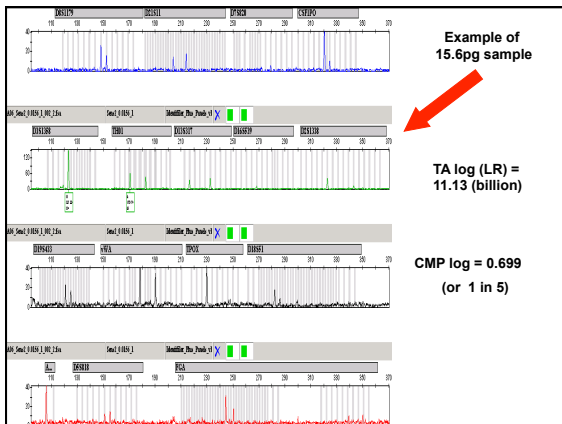Jack Ballantyne, Ph.D.
Chair, NYS DNA Subcommittee

cc: Gina L. Bianchi, Esq., Deputy Commissioner & Counsel, DCJS
NYS DNA Subcommittee Members
NYS Commission on Forensic Science Members

Validation and Implementation

- **LT-DNA Performance**
- **Two and Three Person Mixtures**
- **MCMC Run Times**
- **Report Writing/ DNA Conclusions**

Comparison of mean conditional match probability (CMP) and TrueAllele single source match statistics as a function of DNA input. Data include two amplified sets of serially diluted single source samples (n = 32). All TrueAllele samples were solved in duplicate with 25K/25K burn-in and read out cycles. Error bars represent one standard deviation.

ACCURACY

Mean Information Gain Between

15.6 and 62.5pg

~ 10^6 (million)

Example of 15.6pg sample

TA log (LR) = 11.13 (billion)

CMP log = 0.699

(or 1 in 5)

Dot plot showing the specificity of TrueAllele Casework as a function of DNA input. Reference samples include one known donor and 19 non-donors from each LT-DNA sensitivity set. Mean values from all replicated single unknown requests are pooled (n = 32). Error bars represent one standard deviation; dashed line is set at zero.

SPECIFICITY

**Average donor
log (LR) = 11.78
w/in group σ = 1.71**

**Average non-donor
log (LR) = -19.25
w/in group σ = 2.68**
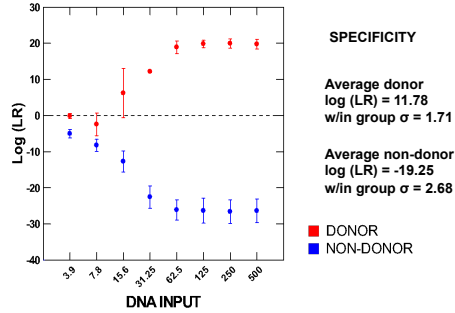
■ DONOR
■ NON-DONOR

Mean log(LR) values for known donor and non-donor reference samples with separation in log units for both combined sensitivity sets. Values from all replicated single unknown donor requests are pooled (n = 32).

DNA INPUT (pg)	Mean Donor Log(LR)	Mean Non-Donor Log(LR)	Mean Donor/Non-Donor Separation (log units)	Minimum Donor/Non-Donor Separation (log units)
3.9	-0.127	-5.025	4.898	1.649
7.8	-2.430	-8.239	5.809	0.637 *
15.6	6.203	-12.718	18.921	8.586
31.25	12.172	-22.551	34.723	25.104
62.5	18.911	-26.131	45.042	34.785
125	19.813	-26.324	46.137	35.165
250	19.925	-26.637	46.562	34.098
500	19.749	-26.382	46.131	35.176

*** Log(LR) for non-donor exceeded log(LR) for known donor: sample set 2 (7.8pg).
All non-donors generated negative log(LR) match statistics.**

Mean log(LR) match scores as a function of DNA input and replicate amplification. Data include two amplified sets of serially diluted single source samples (n = 32). All TrueAllele samples were solved in duplicate with 25K/25K burn-in and read out cycles. Error bars represent one standard deviation; dashed line set at zero.
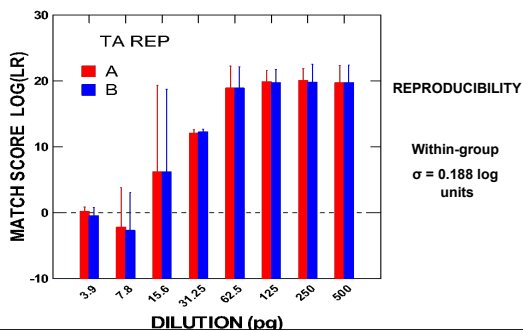
TA REP
■ A
■ B

REPRODUCIBILITY

**Within-group
σ = 0.188 log
units**

Comparison of log (LR) match information as a function of mixture ratio. Mean values from two separate two person mixture sets are shown below; all TrueAllele samples were solved in duplicate with TA1 and TA2 denoting the separately inferred contributors for the two person mixture sets. Error bars represent one standard deviation.
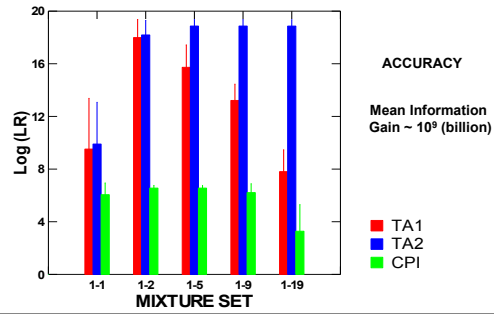
ACCURACY

Mean Information Gain ~ 10^9 (billion)

■ TA1
■ TA2
■ CPI

Dot plot showing the specificity of TrueAllele Casework by reference sample. Mean values from the two person mixture set 1 are shown below; reference donors 4 and 18 (far right) were used in the creation of all mixture ratios from this mixture set. Error bars represent one standard deviation; dashed line is set at zero.

SPECIFICITY

Average donor
log (LR) = 12.72
σ = 5.18

Average non-donor
log (LR) = -22.82
σ = 5.52
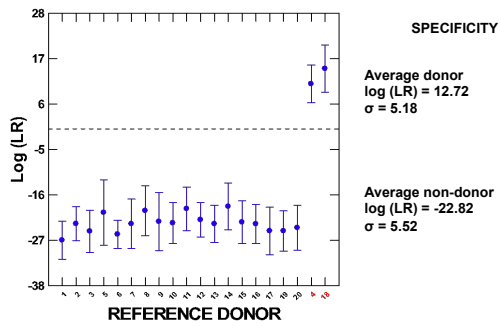
Dot plot showing the specificity of TrueAllele Casework by reference sample. Mean values from the two person mixture set 2 are shown below; reference donors 10 and 17 (far right) were used in the creation of all mixture ratios from this mixture set. Error bars represent one standard deviation; dashed line is set at zero.

SPECIFICITY

Average donor
log (LR) = 14.77
σ = 4.41

Average non-donor
log (LR) = -23.09
σ = 5.88

4

Two Person Mixture Specificity Data Extended to 3,888,000 comparisons

False positives = 18

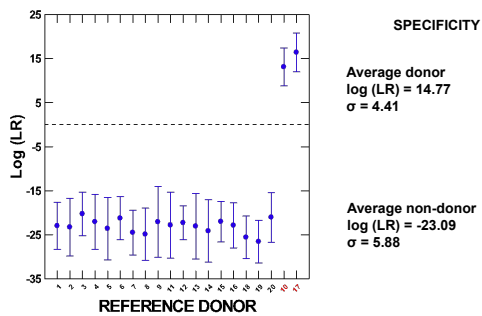False inclusion rate = 0.00046%

Max log(LR) = 2.03

Comparison of log(LR) match information as a function of mixture ratio. Mean values from two separate three-person mixture sets are shown below; all TrueAllele samples were solved in duplicate with TA1, TA2, and TA3 referring to the separate contributors for the three person mixture sets. Error bars represent one standard deviation.

ACCURACY

Mean Information Gain ~ 10^5 (100K)

Dot plot showing the specificity of TrueAllele Casework by reference sample. Mean values from the three person mixture set 1 are shown below; reference donors 12, 16, and 19 (far right) were used in the creation of all mixture ratios from this mixture set. Error bars represent one standard deviation; dashed line is set at zero.

SPECIFICITY

Average donor log(LR) = 8.91 σ = 5.24

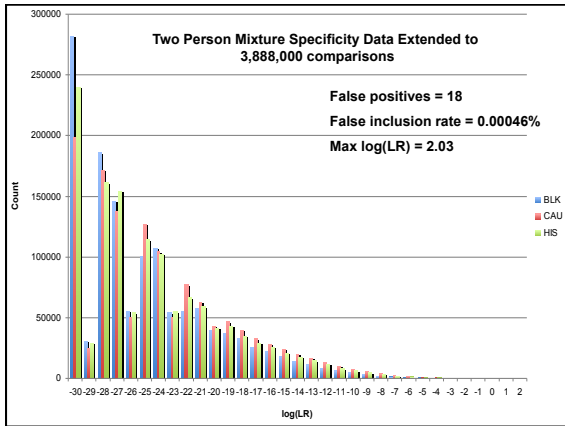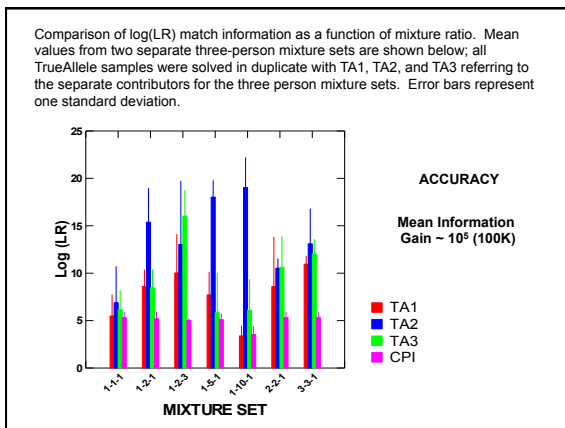**Average non-donor log(LR) = -19.26 σ = 5.62**

Dot plot showing the specificity of TrueAllele Casework by reference sample. Mean values from the three person mixture set 2 are shown below; reference donors 3, 11, and 14 (far right) were used in the creation of all mixture ratios from this mixture set. Error bars represent one standard deviation; dashed line is set at zero.
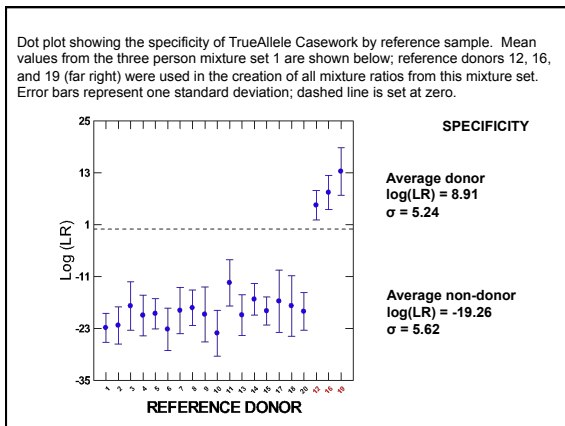
SPECIFICITY

Average donor
log(LR) = 7.54
σ = 3.56

Average non-donor
log(LR) = -17.62
σ = 5.51

Three Person Mixture Specificity Data Extended to 3,024,000 comparisons

False positives = 79

False inclusion rate = 0.00261%

Max log(LR) = 1.87

Comparison of mean log(LR) match statistics as a function of varied MCMC cycle time and DNA input. Data from the 25K requests were taken from Study 2 (Sensitivity); error bars represent one standard deviation.

MCMC TIME
5K
10K
15K
25K
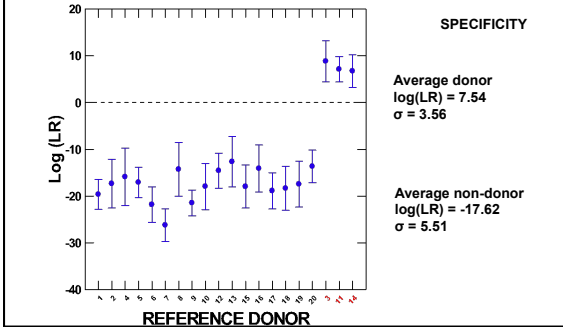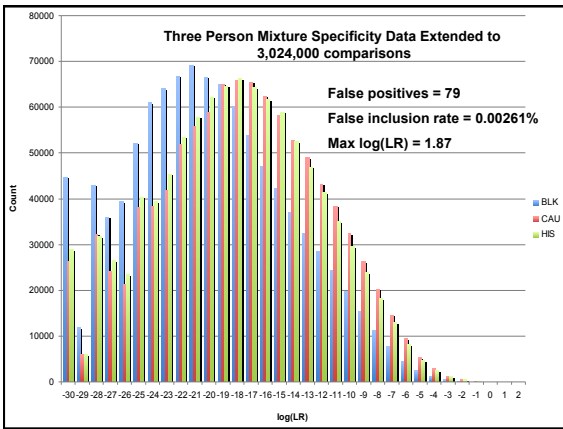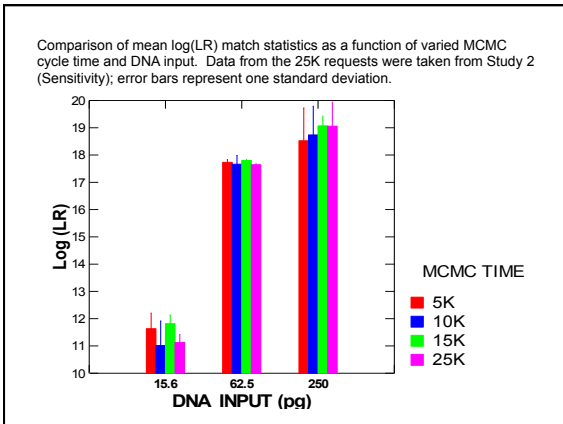
Comparison of log(LR) match statistics resulting from extended cycle times and grouped by mixture set (n = 36). Error bars represent one standard deviation.
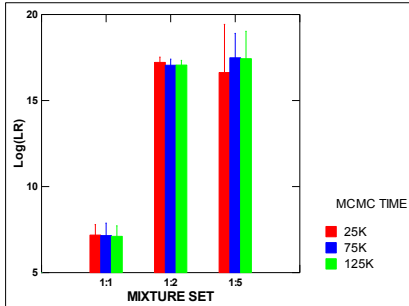
TrueAllele® Casework Report Writing

- **Approach and Documentation Strategy**
- **Methods Section**
- **Conclusions**
- **Allele Tables Replaced with Match Table**

TrueAllele® Casework Report Writing

- **All samples analyzed with TrueAllele®**
- **Report single, standardized LR**
- **Increased reporting consistency with one common set of conclusions**
- **Dispense with language of inclusion**

Request Date: 09/04/2013   Analyst: FIC Scientist

Request Batch #: 1   Case Number: 13HL-XXXXX

Item #	Plate ID	Rule(s) Fired?	Total Donor #	Read Out Time	Known Reference(s) Used?	Convergence Accepted?	Replicate Matches w/in 2 Ban?	Comments
1A	09-01-2013-MD500	No	2	25K	No	Yes	Yes	Good contributor separation
1B	09-01-2013-MD500	No	2	25K	No	Yes	Yes	Low RFU values
1C	09-01-2013-MD500	No	2	25K	2A	Yes	Yes	Artifact peak deactivated at D8
2A	09-02-2013-05100	Ladder Interp	1	500	N/A	N/A	N/A	Ladder rejected; reference sample

Methods Section

METHODS:

- The DNA isolates were characterized through polymerase chain reaction (PCR) using the AmpF/STR® Identifiler® and/or Identifiler® Plus amplification kit(s).
- The TrueAllele® Casework system processed each evidence item in independent replicate computer runs to infer possible DNA contributor profiles from the samples.
- DNA match statistics provided herein used the population frequencies generated by the United States Federal Bureau of Investigation with a co-ancestry coefficient of 1%.
- Known reference samples were used in computer inference where appropriate.
- All evidence profiles were compared with all reference profiles to compute likelihood ratio DNA match statistics using TrueAllele® Casework version 3.3.4961.1 (23-May-2013). Comparisons resulting in no statistical match support for a given reference are listed as --- in the Match Table Results below. For DNA mixture profiles, the number of assumed contributors is listed in subscript next to the evidence item.

Single Source Match Statement

A DNA **match** was identified between the *item description* (item #) and *name* (item #). A match between this evidence item and *name* is X times more probable than a coincidental match to an unrelated person.

Mixture Match Statement

The *item description* (item #) contains a mixture of DNA from at least X donors. A DNA **match** was identified between this item and *name* (item #). A match between this evidence item and *name* is X times more probable than a coincidental match to an unrelated person.

No Match Support Statement

The item description (item #) contains a mixture of DNA from at least X donors. **No match** support was identified between this evidence item and name (item #). This profile can be used for comparison purposes in the event that additional evidence and/or control specimens are submitted in this case.

Inconclusive Statement

The *item description* (item #) contains a mixture of DNA from at least X donors. Due to insufficient genetic information, match support for *name* (item #) to this evidence item is inconclusive.

Match Table

MATCH TABLE RESULTS:

EVIDENCE ITEMS	Item 1 Buccal Swab – *Marge Simpson*	Item 2 Buccal Swab – *Peter Griffin*
Item 3: Stained cutting from Marge Simpson's dress	MATCH 258.2 quadrillion	---
Item 4: Stained cutting from Peter Griffin's shirt	---	MATCH 4.385 quintillion

--- indicates no statistical match support for a given reference.

The extracted DNA samples prepared in this case have been retained in a biological specimen bag **(biobag)**.

All evidence associated with this case will be receipted for return to the submitting agency upon completion of all examinations/analyses. It is recommended that the **biobag(s)** be stored frozen. If further analysis is required, the **biobag(s)** can be resubmitted to the laboratory.

Acknowledgements

- **Cybergenetics staff**
- **Dr. Barry Duceman**
- **NYSP TrueAllele® Working Group**

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TA User Seminar 9/18/13