A Comparison of the Deconvolution and Likelihood Ratio (LRs) produced using a continuous probabilistic software from low-level samples when amplifying the entire extract or splitting the extract

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February 17, 2017

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Research Funding by the NIST Special Programs Office and the NIST Law Enforcement Standards Office

Brief Review
(not comprehensive)

Back in the LCN days…

ELSEVIER

Forensic Science International
112 (2000) 17–40

Forensic Science International

www.elsevier.com/locate/forsciint

An investigation of the rigor of interpretation rules for STRs derived from less than 100 pg of DNA

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Received 9 December 1999; received in revised form 12 February 2000; accepted 13 February 2000

The need for replicate testing and consensus profiles

Table 3
Results from an actual case showing derivation of the consensus result[a]

Sample	Amel	VWA	THO	D8	FG	D21	D18	D19	D3	D16	D2
R_1	XY	16,19	6,7	12,14	20,24	28,30	12,F	13,17	15,16	11,13	17,20
R_2	XY	16,19	6,F	12,14	20,24,25	28,30	12,F	13,17	15,16	11,13	17,20
Consensus	XY	16,19	6,F	12,14	20,24	28,30	12,F	13,17	15,16	11,13	17,20
Suspect	XY	16,19	6,7	12,14	20,24	28,30	12,12	13,17	15,16	11,13	17,20
Negative 1	X	14	–	14,15	–	–	–	15	15	–	–
Negative 2	X	14	–	–	–	–	–	14	16	5	–

[a] See Table 1 for full locus designations.

Gill et al. (2000)

Low-template Mixtures

Validation of Testing and Interpretation Protocols for Low Template DNA Samples Using AmpFℓSTR® Identifiler®

ONLINE
CMJ
CROATIAN MEDICAL JOURNAL
Vol. 50, No 3 (2009)

Theresa Caragine[1], Rebecca Mikulasovich[1], Jeannie Tamariz[1], Ewelina Bajda[1], James Sebestyen[1], Howard Baum[2], Mechthild Prinz[1]

[1]Office of Chief Medical Examiner of the City of New York, The Department of Forensic Biology, New York, NY, USA

[2]Office of Forensic Sciences, New Jersey State Police, New Jersey, NJ, USA

TABLE 4. Detection of repeating minor component alleles in 100 pg mixtures*

LOCI	D8	D21	D7	CSF	D3	THO1	D13	D16	D2	D19	vWA	TPOX	D18	Amel	D5	FGA	Total repeating alleles
150a			●				○	N/A	○		●	○	○		N/A		2
150b								N/A	○		●	○	●	N/A	N/A	○	2
149c								N/A					●		○		1
149d													○				0
149e		N/A	○					N/A	●		N/A					N/A	1
149f			○	N/A		○	N/A	N/A			N/A	○		○	N/A	N/A	0
120a	○		●	○	●			●	N/A			●		●	N/A		5
120b			○		●	○			N/A		●	●	○		N/A	N/A	○	3
119c			○						○								○	0
119d		○	●	○		●				○	○		●	○			●	4
119e		N/A	○	○	●	●	N/A	○			N/A	○	○	●			N/A	3
119f							N/A	N/A			N/A		○			N/A	N/A	0
110a	●	●	●	○	●		●	N/A				●	●	●	N/A	○		9
110b	○	●	●	●	●	●	○	N/A	○	●			○	○	N/A	N/A	●	7
19c	○	○				○		○							●			1
19d		●	○	●	○		●	○	○	○	●	●	●		○	●		9
19e	○	N/A	●	○	●	●	N/A	●	○	N/A	●	●			●	N/A		8
19f	○	●	○	●	○	○	N/A	N/A		N/A	○	●			N/A	N/A		8
15a	●	●	●	●	●	●	●	N/A	○	●	●	●	●	●	N/A	●		13
15b	●	●	●	●	●	●	●	N/A	●	●	●	●	●	N/A	N/A	●		13
15g	●	●	●	N/A	●	●	●	●		●	●	N/A	●	●	●	●		13
14c	●	●	●		●	●		●	○	●	●	○	●	●	●			9
14d	●	●	●	○	●	●	●	●	○	●	●	●	●	●	●	●		14
14e	●	N/A	●	○	●	●	N/A	●	●	N/A	●	○	●	●	●	N/A		10
14f	●		●		●	●	N/A	N/A	●	N/A	●	●	●		N/A	N/A		8
13a	●	●	●	●	●	●	●	N/A	●	●	●	●	●	●	N/A	●		14
13b	●	●	●	●	●	●	●	N/A	●	●	●	●	●	N/A	N/A	●		13
13g	●	●	●	N/A	●	●	●	●		●	●	N/A	●	●	●	●		13
12c	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●		13
12d	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●		16
12e	●	N/A	●	●	●	●	N/A	●	○	N/A	●	○	●	●	●	N/A		9
12f	●	●	●	●	●	●	N/A	N/A	●	N/A	●	●	●	●	N/A	N/A		11

*100 pg mixtures of 4 buccal sample were prepared in ratios of 1:9:9:11 as indicated (11 minutes not shown). Designations of "a," "b," "c," "d," "e," "f," and "g" correspond to the combination of samples used to prepare the mixtures. All mixture samples were amplified in triplicate. Loci for each sample concentration were assigned a closed circle if a minor component allele repeated in 2 of the 3 amplification replicates, or an open circle if a minor allele was observed in only one replicate. "N/A" was assigned to loci for which the mixture components shared genotypes.

Extreme ratios

Caragine et al. (2009)

Profile comparison and statistical evaluation

For the purposes of statistical evaluation for single-source or deduced major component profiles when calculating the random match probability, only the assigned alleles that meet the interpretation requirements should be used. For loci assigned a "Z," only one allele is considered and the random match probability is calculated as 2p. For mixtures where the profile of the major component cannot be determined, a known sample may be compared and qualitative conclusions can be drawn. If the known sample's alleles are labeled at all loci where DNA alleles are repeating, the probability of exclusion of the individual from the mixture may be calculated using the Random Man Not Excluded method.

Used "2p" for "Z" calls (only one allele present)

[The] phenomena of allelic drop-in and dropout must be taken into account when evaluating the weight of the missing allele(s). Statistical methods to achieve this purpose are in the process of being refined and validated for forensic casework (33,34). In the absence of such validated statistical methods, qualitative results may still be provided. Once likelihood ratio methods are validated, they could also be applied to the scenarios described above.

Caragine et al. (2009)

Forensic Science International: Genetics 5 (2011) 376–380

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

Analysis and interpretation of mixed profiles generated by 34 cycle SGM Plus® amplification

Jon H. Wetton *, John Lee-Edghill, Emily Archer, Valerie C. Tucker, Andrew J. Hopwood, Jonathan Whitaker, Gillian Tully

Forensic Science Service, 2960 Trident Court, Birmingham Business Park, Solihull B37 7YN, UK

Well-trained reporting officers could reliably detect and report LCN mixtures

Probabilistic Genotyping (I)

Forensic Science International: Genetics 6 (2012) 697–707

Contents lists available at SciVerse ScienceDirect

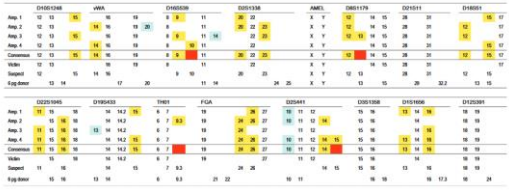
Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

Assessment of mock cases involving complex low template DNA mixtures: A descriptive study

Corina C.G. Benschop, Hinda Haned, Tanja J.P. de Blaeij, Alexander J. Meulenbroek, Titia Sijen *

Department of Human Biological Traces, Netherlands Forensic Institute, P.O. Box 24044, 2490 AA The Hague, The Netherlands



Reporting Officers and Prob Gen (LRmix)
LT-DNA mixture interpretation is feasible

Probabilistic Genotyping (II)

Science & Justice

Volume 53, Issue 2, June 2013, Pages 103–114

DNA mixture genotyping by probabilistic computer interpretation of binomially-sampled laser captured cell populations: Combining quantitative data for greater identification information

Jack Ballantyne[a, b], Erin K. Hanson[a], Mark W. Perlin[c]

Laser Capture Microdissection

Probabilistic Genotyping (III)

Forensic Science International: Genetics 13 (2014) 82–89

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

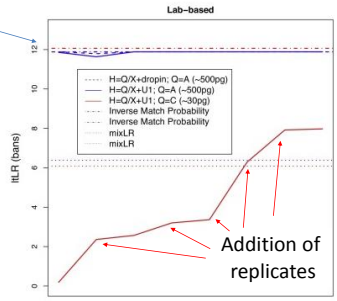
Verifying likelihoods for low template DNA profiles using multiple replicates

Christopher D. Steele [a,*], Matthew Greenhalgh [b], David J. Balding [a]

[a] UCL Genetics Institute, Darwin Building, Gower Street, London WC1E 6BT, UK
[b] Orchid Cellmark Ltd., Abingdon Business Park, Blacklands Way, Abingdon OX14 1YX, UK

Recommendation that the inverse match probability is the upper bound of the LR

IMP



LikeLTD results with joint replicate analysis

Steele et al. (2014)

Forensic Science International 264 (2016) 139–145

Contents lists available at ScienceDirect

Forensic Science International

journal homepage: www.elsevier.com/locate/forsciint

Original Research Paper

Low-template DNA: A single DNA analysis or two replicates?

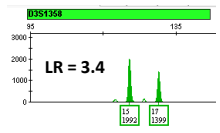
Simone Gittelson*, Carolyn R. Steffen, Michael D. Coble

National Institute of Standards and Technology, 100 Bureau Drive, Gaithersburg, MD 20899, United States

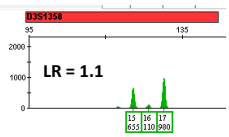
(discrete probabilistic model of interpretation)

2 replicates generally have a greater expected net gain compared to a single analysis

Joint Analysis – an example (Continuous Model)



Contrib 1	Contrib 2	Weight
15, 17	15, 15	0.620
15, 17	15, 17	0.326
15, 15	17, 17	0.054
15, 17	17, 17	0.000
15, 15	15, 17	0.000



Contrib 1	Contrib 2	Weight
15, 17	17, 17	0.897
15, 17	15, 17	0.060
17, 17	15, 15	0.042
15, 17	16, 17	0.000
17, 17	15, 17	0.000

D3S1358

[15,17]	[15,17]	0.9850387488023131
[15,17]	[17,17]	0.014229586745622698
[15,17]	[15,15]	5.573885976529381E-4
[17,17]	[15,15]	1.7427585441127485E-4

LR = 8.1

Electrophoresis 2014, *35*, 3125–3133

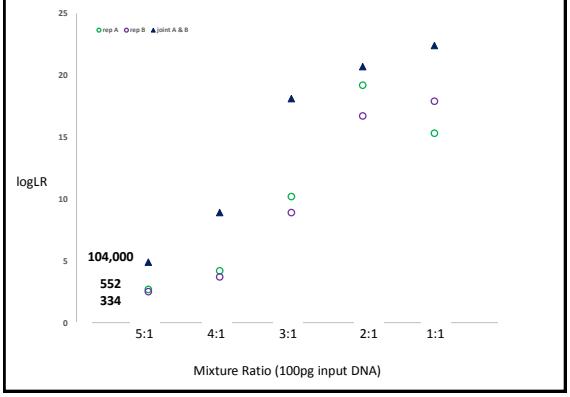
Todd W. Bille[1]
Steven M. Weitz[1]
Michael D. Coble[2]
John Buckleton[3]
Jo-Anne Bright[3]

[1]Bureau of Alcohol, Tobacco, Firearms and Explosives,

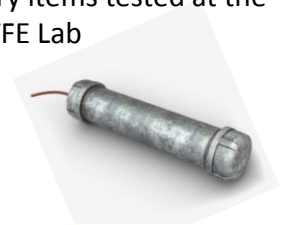
Research Article

Comparison of the performance of different models for the interpretation of low level mixed DNA profiles

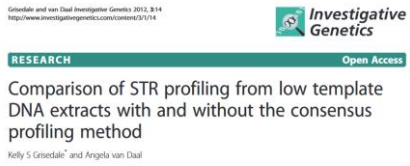
- Used two samples with low allele sharing. 2 PCR amps.
- 1:1, 2:1, 3:1, 4:1, and 5:1
- 500, 400, 300, 200, 100 pg input DNA
- CPI, RMP (2p), Discrete Model, Fully Continuous Model



Typical evidentiary items tested at the ATFE Lab



Is it better to do one amp, or split the extract and do replicates?


Grisedale and van Daal Investigative Genetics 2012, 3:14
http://www.investigativegenetics.com/content/3/1/14

Investigative Genetics

RESEARCH Open Access

Comparison of STR profiling from low template DNA extracts with and without the consensus profiling method

Kelly S Grisedale* and Angela van Daal

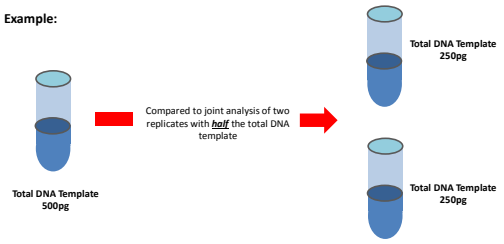
Suggests it is better to do one amp (compared to the consensus method)

Steele *et al.* (2014) Suggest replicates with PG may tilt the argument

Methods

- Two samples mixed at 1:1, 3:1, and 5:1 ratios
- DNA concentrations of 1.0, 0.5, 0.25, 0.125, 0.625 ng PCR input
- Single source and 2-person mixtures tested.
- The mixtures were tested for both "pristine" and "degraded" conditions – in the degraded examples, the "major" component was exposed to UV light to induce DNA damage.

Methods



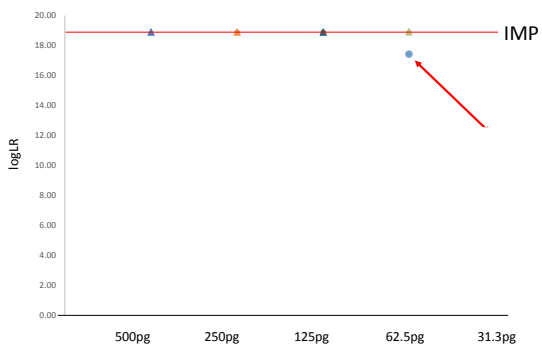
Methods

- Evidence mimicked DNA recovered from a Molotov cocktail where a single source or 2-person mixture was recovered.

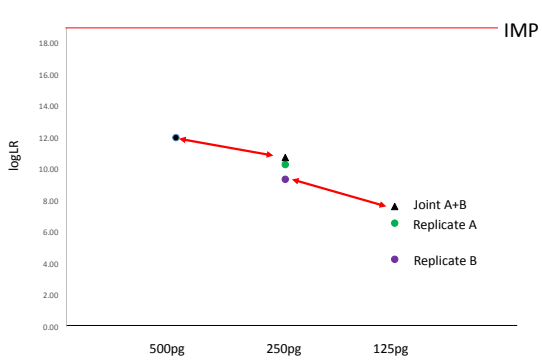
- H_1 = POI & UNK
- H_2 = UNK & UNK

Results – Single Source

Single Source "Pristine" DNA

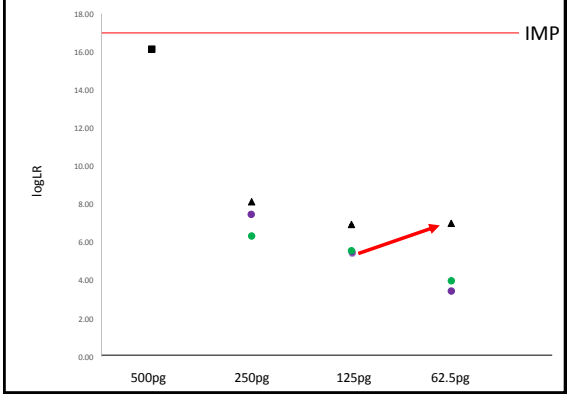


Single Source "Degraded" DNA

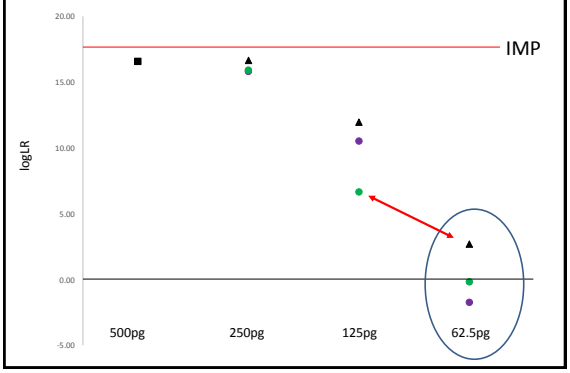


Results – 2-person Mixtures
(Pristine DNA)

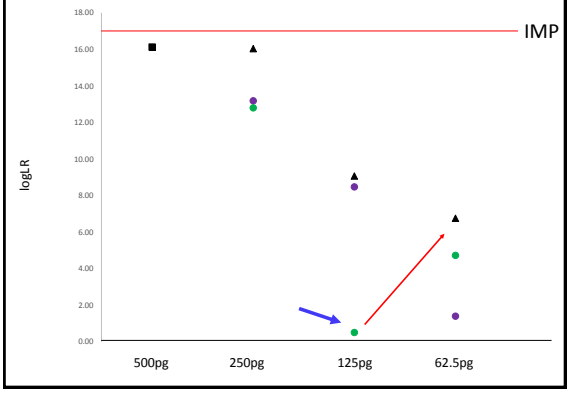
1:1 ratio 2-person, minor contributor "Pristine" DNA



3:1 ratio 2-person, minor contributor "Pristine" DNA

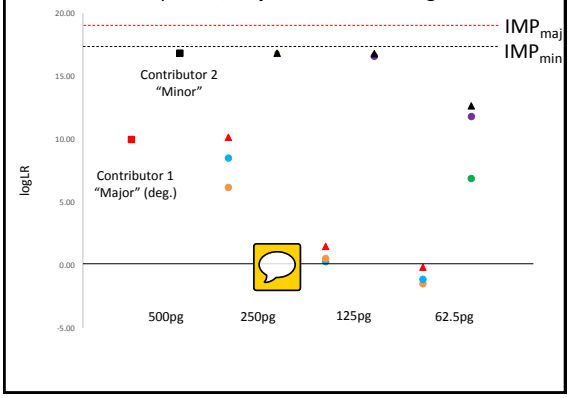


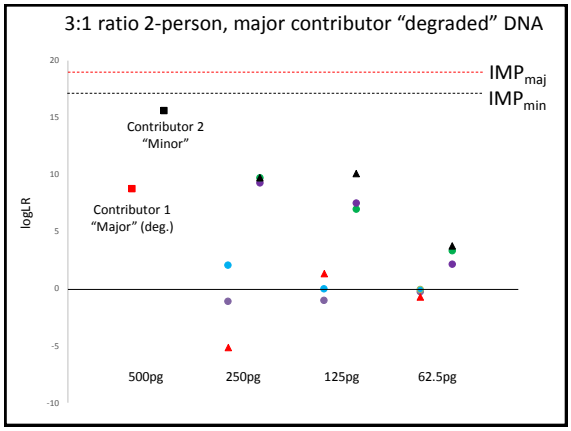
5:1 ratio 2-person, minor contributor "Pristine" DNA

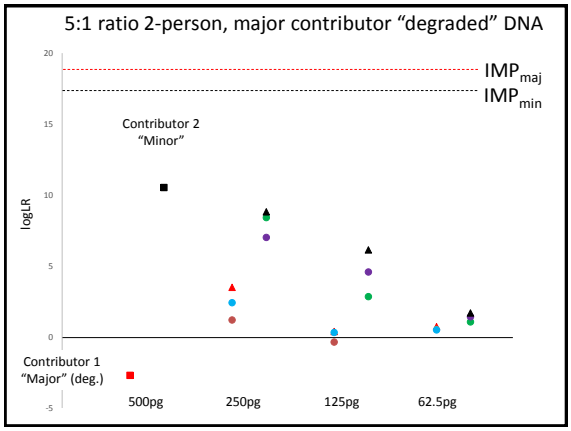


Results – 2-person Mixtures
(Degraded DNA of the major contributor)

1:1 ratio 2-person, major contributor "degraded" DNA







Conclusions

- In general, the joint analysis of replicates produces a higher LR than either of the individual replicates – but never exceeds the Inverse Match Probability.
- The analysis of a single amplification (total template of X ng) *usually* gave a higher LR than splitting the template (total DNA template of X/2 ng) and producing a joint analysis.

Conclusions

- Additional studies are planned using a range of allele sharing between the contributors and testing higher order mixtures (3 and 4 contributors).

Thank you!

Becky Steffen (NIST)

Steven Weitz (ATFE)

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