NIST Update
Applied Genetics Group

SWGDAM
17 July 2014

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Applied Genetics Group
Biomolecular Measurement Division

NIST
National Institute of Standards and Technology
U.S. Department of Commerce

Applied Genetics Group (06)

Group Leader
Peter Vallone

Advancing technology and traceability through quality genetic measurements to aid work in Forensic and Clinical Genetics

A core competency of our group is the application of *nucleic acid-based methods*
PCR – Genotyping – Sequencing – Real-time PCR – Digital PCR - DNA based SRMs

Forensic Genetics ⟷ Clinical Genetics


Mike Coble


Becky Hill


Erica Butts


Katherine Gettings
Postdoc


Kevin Kiesler


Margaret Kline


Jo Lynne Harenza
Postdoc


Ross Haynes


Dave Duewer
Data analysis support


Patti Rohmiller
Office Manager


Simone Gittelson
Guest Researcher

Recent focus areas: DNA mixture interpretation, update of SRM2391c, digital PCR, RDNA, & next generation sequencing

Topics

- **SRM 2391c**
- **Candidate SRM 2372a**
- **Rapid DNA**
- **Next-generation sequencing**
- Y STRs
- DNA mixture interpretation
- Upcoming talks/workshops

SRM 2391c: PCR-Based DNA Profiling Standard

- Components A through D are DNA extracts in liquid form
- Components E and F are DNA spotted on 903 paper or FTA paper
- Certified values are for STR alleles based on length polymorphisms observed using capillary electrophoresis

Lab 1 ⟷ Lab 2

Helps meet QAS Std. 9.5.5 and ISO 17025

Standard Reference Material

Genomic DNAs characterized for the expanded CODIS core loci and Y-STRs

Calibration with SRMs enables confidence in comparisons of results between laboratories

Certified, Reference, & Information Values of SRM 2391c

- **Certified Values**: Value for which NIST has the highest confidence in its accuracy in that all known or suspected sources of bias have been investigated or taken into account
  2 or more methods are used to compare values (i.e. Sanger sequencing, genotyping with multiple sets of primers)
- **Reference Values**: High-confidence estimate of the true value but where all possible sources of bias have not been fully investigated by NIST
  Genotyping with only 2 sets of primers to compare
- **Information Values**: Data that may be of interest and use to the SRM user, but insufficient information is available to access the confidence of the assignment
  Genotyping of only 1 kit is available

Current Values for STR Loci

Certified Values

Autosomal STR (24)	Y STR (17)	X STR (0)
D1S1656	DYS19	None
D2S1338	DYS385a	
D2S441	DYS385b	
D3S1358	DYS389I	
D5S818	DYS389II	
D7S820	DYS390	
D8S1179	DYS391	
D8S1115	DYS392	
D10S1248	DYS393	
D12S391	DYS437	
D13S317	DYS438	
D16S539	DYS439	
D18S51	DYS448	
D19S433	DYS456	
D21S11	DYS458	
D22S1045	DYS635	
CSF1PO	Y GATA H4	
FGA		
Penta D		
Penta E		
SE33		
TH01		
TPOX		
vWA		

Reference Values

Autosomal STR (23)	Y STR (0)	X STR (0)
D1GATA113	None	None
D1S1627		
D1S1677		
D2S1776		
D3S3053		
D3S4529		
D4S2364		
D4S2408		
D5S2500		
D6S1017		
D6S474		
D9S1122		
D9S2157		
D10S1435		
D17S1301		
D17S974		
D18S853		
D20S1082		
D20S482		
F13A01		
F13B		
FESFPS		
LPL		

Information Values

Autosomal STR (1)	Y STR (0)	X STR (0)
Penta C	None	None

STR Typing kits and Primer Mixes

100% Concordance with all kits

Current

Kit Provider			
Thermo Fisher (12)	Promega Corp. (8)	Qiagen Inc. (2)	Primer Mixes (2)
Identifiler	PowerPlex 16	ESSplex	26plex
Identifiler Plus	PowerPlex 16 HS	IDplex	miniSTRs
NGM	PowerPlex ESX 17		
NGM SElect	PowerPlex ESI 17		
COfiler	PowerPlex ES		
Profiler	PowerPlex S5		
Profiler Plus	PowerPlex Y		
Profiler Plus ID	FFFL		
SGM Plus			
SEfiler			
MiniFiler			
Yfiler			

Update

Kit Provider			
Thermo Fisher (14)	Promega Corp. (16)	Qiagen Inc. (9)	Primer Mixes (3)
Identifiler	PowerPlex 16	ESSplex	26plex
Identifiler Plus	PowerPlex 16 HS	IDplex	miniSTRs
NGM	PowerPlex ESX 17	ESSplex SE	RM Y STRs
NGM SElect	PowerPlex ESI 17	ESSplex SE Plus	
COfiler	PowerPlex ES	ESSplex SE GO!	
Profiler	PowerPlex S5	IDplex Plus	
Profiler Plus	PowerPlex Y	IDplex GO!	
Profiler Plus ID	FFFL	Argus X-12	
SGM Plus	PowerPlex ESI 17 Pro	DIPplex	
SEfiler	PowerPlex ESX 17 Fast		
MiniFiler	PowerPlex ESI 17 Fast		
Yfiler	PowerPlex 18D		
GlobalFiler	PowerPlex 21		
Yfiler Plus	PowerPlex CS7		
	PowerPlex Fusion		
	PowerPlex Y23		

Updated Values for STR Loci

All certified loci have been fully sequenced

Certified Values		
Autosomal STR (25)	Y STR (29)	X STR (0)
D1S1656	DYS19	None
D2S1338	DYS385a	
D2S441	DYS385b	
D3S1358	DYS389I	
D5S818	DYS389II	
D6S1043	DYS390	
D7S820	DYS391	
D8S1179	DYS392	
D8S1115	DYS393	
D10S1248	DYS437	
D12S391	DYS438	
D13S317	DYS439	
D16S539	DYS448	
D18S51	DYS456	
D19S433	DYS458	
D21S11	DYS635	
D22S1045	Y GATA H4	
CSF1PO	DYS449	
FGA	DYS460	
Penta D	DYS481	
Penta E	DYS518	
SE33	DYS533	
TH01	DYS549	
TPOX	DYS570	
vWA	DYS576	
	DYS627	
	DYS643	
	DYF387S1a	
	DYF387S1b	

Reference Values		
Autosomal STR (23)	Y STR (0)	X STR (0)
D1GATA113	None	None
D1S1627		
D1S1677		
D2S1776		
D3S3053		
D3S4529		
D4S2364		
D4S2408		
D5S2500		
D6S1017		
D6S474		
D9S1122		
D9S2157		
D10S1435		
D17S1301		
D17S974		
D18S853		
D20S1082		
D20S482		
F13A01		
F13B		
FESFPS		
LPL		

Information Values		
Autosomal STR (1)	Y STR (0)	X STR (12)
Penta C	None	DXS7132
		DXS7423
		DXS8378
		DXS10074
		DXS10079
		DXS10101
		DXS10103
		DXS10134
		DXS10135
		DXS10146
		DXS10148
		HPRTB

Argus X-12 kit

*Other Information Value Considerations:
- DIPplex kit (InDel markers)
- PGM and MiSeq IISNPs

New Y-STR loci in commercial kits (Yfiler Plus & PPY23)

Update to be completed by Oct. 2014

Digital PCR (dPCR) and SRM 2372a

Next Certification Method

- The next generation of SRM 2372 (SRM 2372a) will be certified for "copy/target number"
- Digital PCR allows for the calculation of the absolute concentration without the use of an external calibrant

Migrating away from UV based measurements for DNA quantitation

- A sample is partitioned so that individual nucleic acid targets within the sample are localized
  - Microfluidic (Fluidigm BioMark)
  - Emulsion/droplet PCR (Bio-Rad QX100, RainDance)
- Each partition will contain a negative or positive PCR reaction

Instruments available for dPCR at NIST

Chamber Digital - cdPCR

Droplet Digital - ddPCR

Fluidigm BioMark

BIO-RAD QX100

Fluidigm BioMark

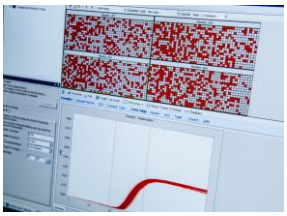
Chamber Digital PCR

- Fluidic module transfers PCR mastermix onto chip
- 'Reader' performs thermal cycling and fluorescence detection (real-time PCR)

Fluidigm Digital Array

12.765 = 765 chambers × 12 panels (samples)

48.770 = 770 chambers × 48 panels (samples)

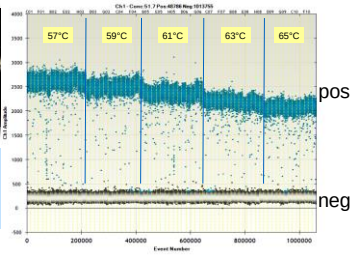


- Well volumes
  6 nL (12 sample)
  0.85 nL (48 samples)
- TaqMan compatible chemistry
- FAM-VIC dye detection

Bio-Rad QX-100

Droplet Digital PCR

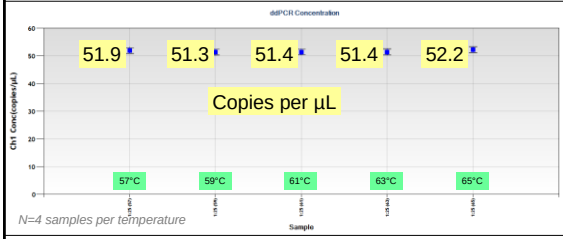
- PCR master mix and DNA template are partitioned into droplets
- 8 strip tubes - up to 96 samples/run
- Thermal cycling is performed on a standard cycler (9700, Veriti)
- Fluorescence from up to 20,000 droplets are detected in the reader (3.5 h)



Validating annealing temperatures for the validation of a digital PCR assay

BioRad QX100

Effect of annealing temperature on copy number estimate



N=4 samples per temperature

ddPCR Copies/µL original Sample to ng/µL

Convert copies/µL and calculate the DNA concentration as ng/µL:

Assay	Average ng/µL	sd
D6S474	56.3	1.2
D9S2157	55.2	0.7
HBB1	51.7	1.5
D5S2500	51.7	0.9
D14S1434	52.1	0.4
2PR4	50.6	0.9
22C3	50.0	1.2
EIF5	49.0	0.3
D1P32.3	39.7	0.8
All good assays	52.1	2.5

Rapid PCR Protocols Paper

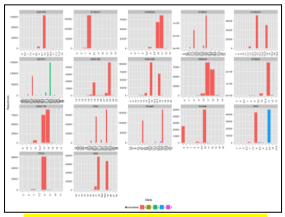
- Invited to submit articles by Dr. Bruce McCord (FIU)
- Accepted for publication in Electrophoresis

"Rapid PCR Protocols for Forensic DNA Typing on Six Thermal Cycling Platforms"

Erica L.R. Butts and Peter M. Vallone

Sequencing STRs on the MiSeq

- Early access beta version of product from Promega
- Designed for use on NGS platforms
  - Primers redesigned for NGS read lengths
  - Protocol developed for Illumina MiSeq
- Ran SRM 2391c on MiSeq
  - 100 % concordance with CE derived alleles
- Data analysis with STRaitRazor PERL script
  - Tertiary analysis in "R"



SRM 2391c Component A

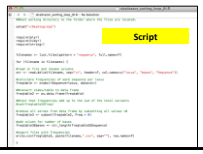
STRait Razor

STRait Razor: A length-based forensic STR allele-calling tool for use with second generation sequencing data

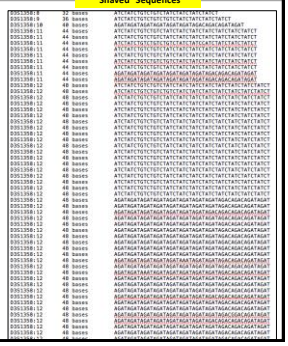
David H. Warshauer[a], David Lin[b], Kumar Hari[b], Ravi Jain[b], Carey Davis[a], Bobby LaRue[a], Jonathan L. King[a], Bruce Budowle[a,b,*]

Scripts in "R"

- Parse sequence output from STRaitRazor
- Goals
  - Confirm expected repeat structure
  - Evaluate error types and frequency



"Shaved" Sequences



Scripts in “R”

- Parse sequence output from STRaitRazor
- Goals
  - Confirm expected repeat structure
  - Evaluate error types and frequency

Allele Calls

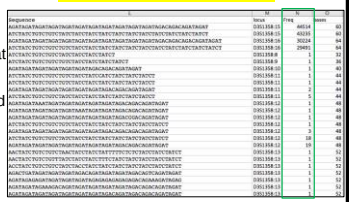
```
D3S1358:R1:D3S1358:8:1
D3S1358:R1:D3S1358:8.3:
D3S1358:R1:D3S1358:9:1
D3S1358:R1:D3S1358:10:1
D3S1358:R1:D3S1358:11:9
D3S1358:R1:D3S1358:12:44
D3S1358:R1:D3S1358:13:560
D3S1358:R1:D3S1358:14:8331
D3S1358:R1:D3S1358:14.3:2
D3S1358:R1:D3S1358:15:104737
D3S1358:R1:D3S1358:15.1:
D3S1358:R1:D3S1358:15.2:2
D3S1358:R1:D3S1358:15.3:3
D3S1358:R1:D3S1358:16:68830
D3S1358:R1:D3S1358:16.2:
D3S1358:R1:D3S1358:17:356
D3S1358:R1:D3S1358:17.1:
D3S1358:R1:D3S1358:17.2:
D3S1358:R1:D3S1358:18:1
D3S1358:R1:D3S1358:18.1:
D3S1358:R1:D3S1358:18.2:
D3S1358:R1:D3S1358:18.3:
D3S1358:R1:D3S1358:19:9
D3S1358:R1:D3S1358:20:1
D3S1358:R1:TOTAL:182888
```

D3S1358: 15,16

Scripts in “R”

- Parse sequence output from STRaitRazor
- Goals
  - Confirm expected repeat structure
  - Evaluate error types and frequency

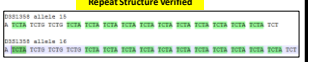
Sequences Categorized



Scripts in “R”

- Parse sequence output from STRaitRazor
- Goals
  - Confirm expected repeat structure
  - Evaluate error types and frequency

Repeat Structure Verified

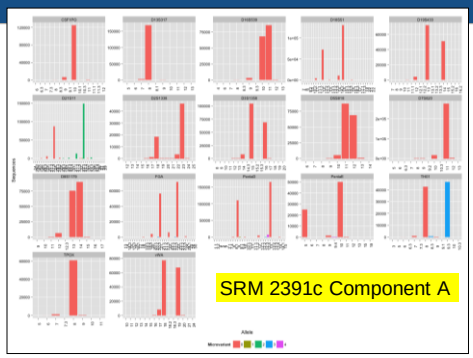


D3S1358
Summary Statistics
SRM 2391c component A

CE genotype	STRaitRazor	Total # Reads	Majority Reads	Non-majority Reads	% Non-majority Reads
15	15	104737	87749	16988	16%
16	16	68830	59715	9115	13%

# Reads - 4 Stutter	% - 4 Stutter
8331	8.0%
N/A	

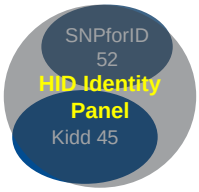
Parsing STRait Razor output in R



HID-Ion Ampliseq Identity Panel *(version 2.3)*

Run on Ion Torrent PGM

- 90 autosomal SNPs
- From Pakstis 2010, Kidd 2012, and SNPforID panels
- 30 Y-chromosome SNPs
- Upper clade branches
- RMP ≈ 4 x 10^{-36}



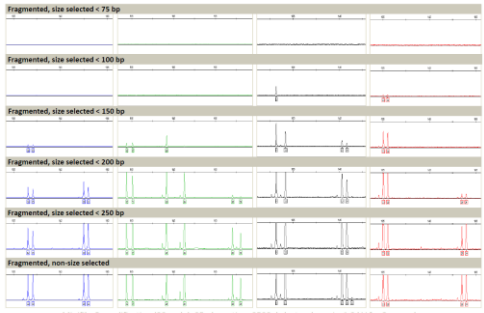
Degraded DNA Study

Assays	PGM IISNPs	MiniFiler	IdentiFiler Plus	GlobalFiler	DIPplex
DEGRADED DNA SAMPLES					
35-250 bp	X	X		X	X
35-200 bp	X	X		X	X
35-150 bp	X	X		X	X
35-100 bp	X	X		X	X
35-75 bp	X	X		X	X

DNA fragmented using Covaris instrument

Degraded DNA Study

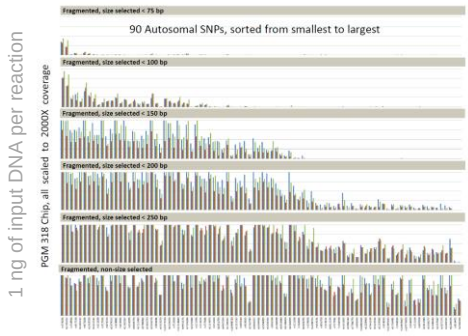
Minifiler STR Kit – 1 ng input DNA



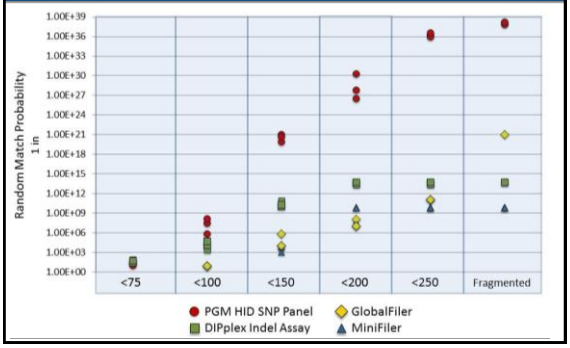
Minifiler® amplification (30 cycle), 25 µl reaction, 3500xl electrophoresis, 1.2 kV for 8 seconds
Thresholds: analytical = 100 RFU, PHR = 0.5; data scaled to 1000 RFU

Degraded DNA Study

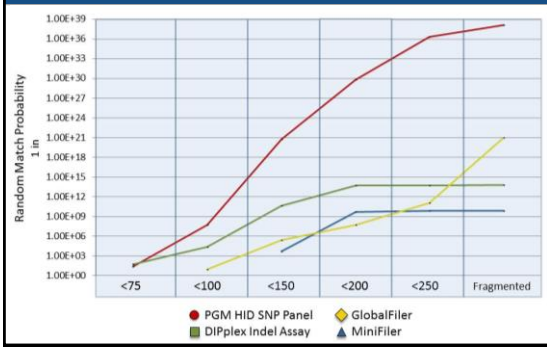
HID SNP Amplicon size range 80-220 bp



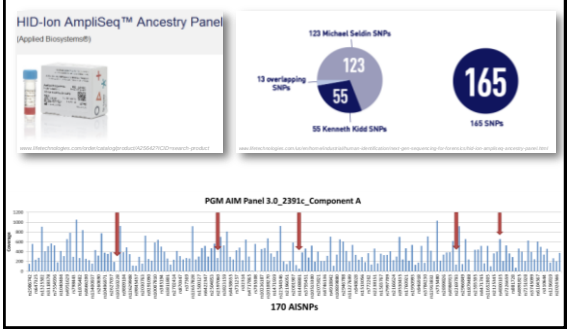
Degraded DNA Study



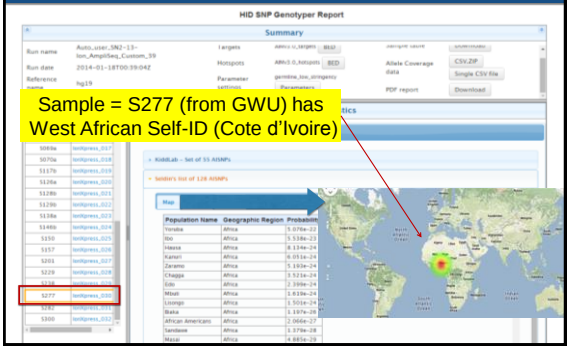
Degraded DNA Study



Ancestry SNP NGS Assay

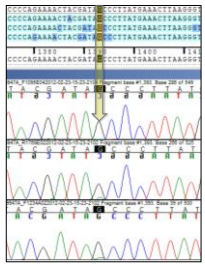


Ancestry SNP NGS Assay



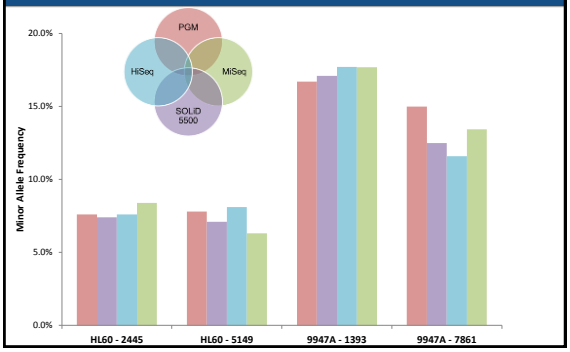
NGS Support for mtDNA Analysis

- NIST mtDNA SRM 2392 / 2392-I
- PGM & MiSeq analysis
  - 5% SNP calling threshold
  - Concordance across platforms
  - Two heteroplasmies in two components, not in previous certificates
- FSIG short communication
- Certificate update Fall 2014

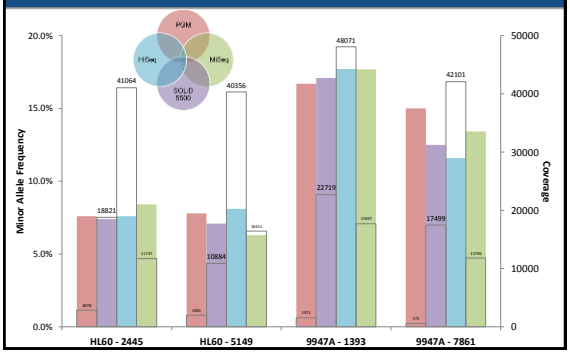


Site 1,393 (G/A)

NGS Support for mtDNA Analysis



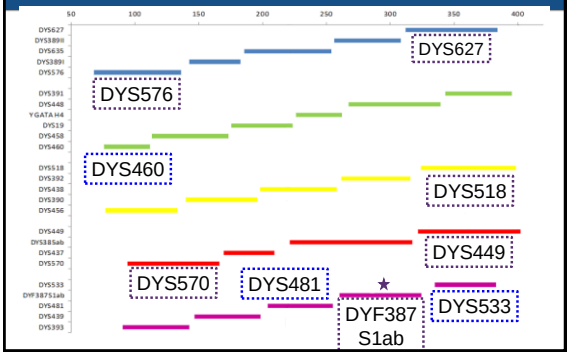
NGS Support for mtDNA Analysis



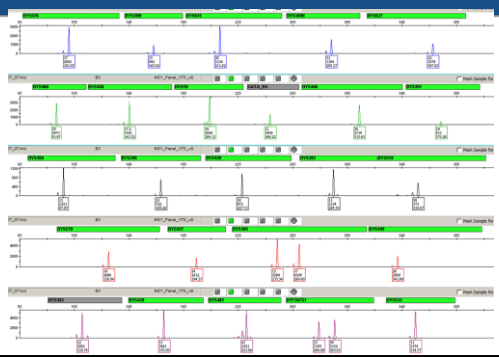
Topics

- SRM 2391c
- Candidate SRM 2372a
- Rapid DNA
- Next-generation sequencing
- **Y STRs**
- **DNA mixture interpretation**
- **Upcoming talks/workshops**

Yfiler Plus (10 new loci)



Yfiler Plus



Sensitivity

Full reaction volumes (25 ul):

- 0.5 ng single amp
- 0.25 ng single amp
- 0.125 ng duplicate amp
- 0.0625 ng duplication amp
- 0.03125 ng duplicate amp

Half reaction volumes (12.5 ul):

- 0.5 ng duplicate amp
- 0.25 ng duplicate amp
- 0.125 ng duplicate amp
- 0.0625 ng duplication amp
- 0.03125 ng duplicate amp

Sensitivity – 25µL

FULL REACTION VOLUME (25 ul)

Marker	0.03125 ng		0.0625 ng		0.125 ng		0.25 ng	0.5 ng
DYS576		184	222	299	491	574	491	2308
DYS389I	96	151	344	318	1083	895	1603	2581
DYS635	195	153	198	152	379	473	1341	2481
DYS389II		115	279	176	725	648	1036	1847
DYS627	142	373	165	140	1257	591	1122	3639
DYS460		463	304	129	263	328	827	2786
DYS458		404	51	261	466	581	1091	3107
DYS19		173	220	140	335	523	1250	2697
GATA_H4	97		159	226	482	153	1898	3212
DYS448	91		154	204	500	196	2255	2489
DYS391	342		231	53	1169	721	2470	3789
DYS456	330	186	269	115	732	241	1524	2143
DYS390		232	123	87	225	331	478	1664
DYS438	144	166	207	205	557	622	999	3563
DYS392		209	53	126	700	156	840	2293
DYS518	232	118	145	185	638	411	619	2322
DYS570		92	163	300	987	327	1673	3398
DYS437	83	248	364	152	749	485	1429	2494
DYS385	109	364	303	135	525	545	1261	2608
DYS385			130		383		1539	1912
DYS449	57	91	321	218	713	482	846	3598
DYS393			485	126	172	389	2184	2353
DYS439		278	130	108	916	313	668	3488
DYS481	254		375	218	1022	588	1707	3605
DYF387S1		203	208	169	413	487	1536	2173
DYF387S1			197	192	696	428	1050	2846
DYS533	205		280	93	942	456	1987	2722

>175

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Sensitivity – 12.5µL

HALF REACTION VOLUME (12.5 ul)

Marker	0.03125 ng		0.0625 ng		0.125 ng		0.25 ng		0.5 ng	
DYS576	84	404	740	484	2271	551	3580	1773	4985	8103
DYS389I		1080	1285	2442	1064	2389	3992	2964	8646	12160
DYS635			331	911	1540	1950	3991	965	7439	5402
DYS389II		1055	717	2561	1026	1985	3080	2211	4781	8069
DYS627			1175	876	1340	2054	2944	2168	12000	4860
DYS460		785	605	1469	2961	2146	4028	2445	3443	5921
DYS458		394	262	2099	2616	1013	4972	2265	5029	6213
DYS19		835	351	1283	1886	1464	2492	2473	4532	4871
GATA_H4		245	475	1690	1766	1274	3980	1493	2813	5701
DYS448			594	1842	1131	1611	4011	2042	3175	5857
DYS391	199	398	1140	398	2861	1632	3359	3067	6691	10923
DYS456	122		121	920	1280	1391	2803	851	3190	6202
DYS390			214	673	771	1428	2059	1212	3429	4472
DYS438	321	159	656	717	2163	1269	2201	1646	5038	6472
DYS392	153		1306	446	1853	858	2242	1960	5151	5722
DYS518	367	262	844	280	771	1661	1657	997	3357	4083
DYS570	196	592	376	1165	1754	1551	3068	2200	4346	7802
DYS437	145	1152	404	325	1424	1582	6373	1199	6266	7528
DYS385	93	613	630	1672	2218	1764	3592	1671	3160	5944
DYS385		197	726	585	1434	894	3548	2302	3706	5323
DYS449	79	112	420	1727	2309	2752	4809	2858	5308	5506
DYS393	77	824	719	621	2240	1716	3786	2111	4809	6494
DYS439		286	841	1266	1449	2781	2165	2468	4563	5620
DYS481	83	618	689	1368	3258	1737	3684	3348	7554	7676
DYF387S1	51	296	842	999	2175	1016	3089	1306	3782	8096
DYF387S1		448	499	1447	1655	2940	2757	2400	4758	4924
DYS533		523	494	403	2280	952	2599	1868	5163	6819

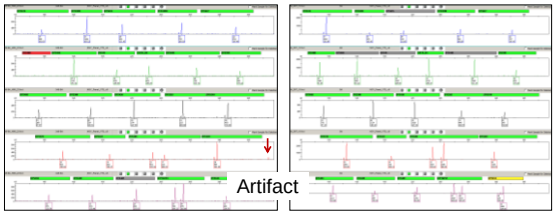
>175

<175

F/M Mixtures

200 : 1	200 ng + 1 ng	1 ng
700 : 1	200 ng + 0.3 ng	0.3 ng
2000 : 1	200 ng + 0.1 ng	0.1 ng
4000 : 1	200 ng + 0.05 ng	0.05 ng

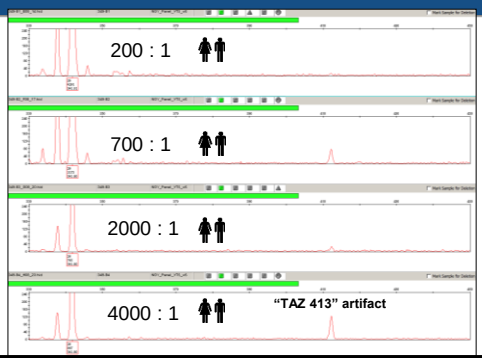
F/M Mixtures



4000 : 1
(approx. 200 ng female + 0.05 ng male)

(approx. 0.05 ng)

F/M Mixtures



Performance with unrelated males

NIST U.S. Population Samples

N = 948 males	PowerPlex Y
# haplotypes	816
discrimination capacity	0.8608
# times haplotype observed	PPY (12 loci)
1	751
2	42
3	12
4	4
5	2
6	2
7	.
8	1
9	.
10	.
11	1
12	.
13	.
14	.
15	.
16	.
17	.
18	.
19	.
20	1

Number of unique and shared haplotypes observed with various combinations of Y-STR loci across 948 U.S. population samples

N = 948 males	Yfiler	New Loci*	Yfiler Plus*
# haplotypes	930	945	946
discrimination capacity	0.9810	0.9842	0.9979
# times haplotype observed	Yfiler (17 loci)	New Loci* (10 loci)	Yfiler Plus (27 loci)
1	916	918	944
2	11	15	2
3	2	.	.
4	1	.	.
5	.	.	.
6	.	.	.
7	.	.	.
8	.	.	.
9	.	.	.
10	.	.	.
11	.	.	.
12	.	.	.
13	.	.	.
14	.	.	.
15	.	.	.
16	.	.	.
17	.	.	.
18	.	.	.
19	.	.	.
20	.	.	.

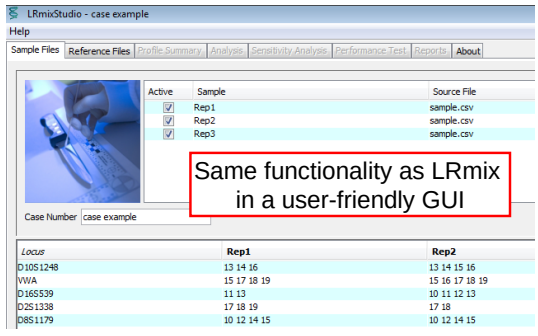
The new loci alone perform slightly better than Yfiler

(Note: Ignoring DYS460)

DNA Mixture Interpretation

- LR mix Studio (Haned and Gill)
- DNA-View Mixture Solution (Charles Brenner)
- STRmix (ESR and S. Australia collaboration)
- LikeLTD (Balding)
- Lab Retriever (Lohmueller, Rudin and Inman)
- TrueAllele (Cybergenetics)

DNA Mixture Interpretation



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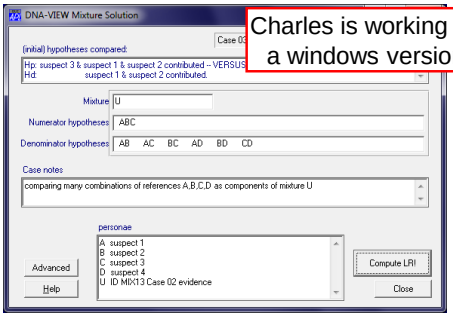
DNA Mixture Interpretation



Charles is working on a windows version

Slide courtesy of Charles Brenner

Webcasts

NIST DNA Analyst Webinar Series: Probabilistic Genotyping and Software Programs (Part 1)

Purpose:

NIST will host a series of free webinars focused on topics of interest to DNA analysts. This four-hour webinar will be held on May 28, 2014, from 1:00 pm – 5:00 pm (EDT), and will focus on probabilistic genotyping for complex low-level DNA mixtures.

Watch a recording of the webinar on this page.

Details:

Start Date: Wednesday, May 28, 2014

End Date: Wednesday, May 28, 2014

Audience: Industry, Government, Academia

http://www.nist.gov/forensics/nist-dna-analyst-webinar-series-pt1.cfm

Susan Berdine (Denver PD) – Lab Retriever
Todd Bille (ATF) – STRmix
Ate Kloosterman (Netherlands Forensic Institute) – LRmix
Craig O'Connor (NY OCME) – FST

Webcasts

Probabilistic Genotyping – Part 2
(Tentative date – September 18 (Thursday)

Planned Talks - Confirmed
TrueAllele
LikeLTD
DNA-View

(Armed Expert)
(LiRa/LiRaHT)

Webcasts

NIST DNA Analyst Webinar Series: Validation Concepts and Resources – Part 1

Aug. 6th

Purpose:
NIST will host a series of free webinars focused on topics of interest to DNA analysts. This four-hour webinar will be held on August 6, 2014, from 1:00 pm – 5:00 pm (EDT), and will focus on validation concepts and NIST software tools to assist in the validation process.

Agenda:

Details:
Start Date: Wednesday, August 6, 2014
End Date: Wednesday, August 6, 2014
Audience: Industry, Government, Academia
Format: Webinar

http://www.nist.gov/forensics/nist-dna-analyst-webinar-series-validation-concepts-and-resources-part-1.cfm

Robin Cotton, *Boston University*
John Butler, *NIST*
Mark Timken, *California Department of Justice*
Catherine Grgicak, *Boston University*
Becky Hill, *NIST*

Workshops

Almost Everything You Wanted to Know About Probabilistic Software (But Were Afraid to Ask)

Workshop Chairs:
- Charlotte Word
- Michael Coble (National Institute of Standards and Technology)

ISHI INTERNATIONAL SYMPOSIUM ON HUMAN IDENTIFICATION
PHOENIX, AZ • SEP. 29–OCT. 2, 2014

Additional Speakers:
- Dr. Charles Brenner (DNA-VIEW & UC Berkeley): DNA-VIEW Mixture Solution
- Dr. David Balding (UCL Genetics Institute): LikeLTD
- Dr. Roberto Puch-Solis (LGC Forensics): LiRa and LiRaHt
- Dr. Norah Rudin (SCIEG): Lab Retriever
- Dr. Hinda Haned (Netherlands Forensic Institute): LRmix studio
- Luigi Armogida (NicheVision): ArmedXpert™
- Jo-Anne Bright (ESR Ltd): STRmix™
- Dr. Mark Perlin (Cybergenetics): TrueAllele® Casework

Upcoming Talks / Workshops

NIST Presentations @ ISHI INTERNATIONAL SYMPOSIUM ON HUMAN IDENTIFICATION PHOENIX, AZ • SEP. 29–OCT. 2, 2014

Almost Everything You Wanted to Know About Prob
Works

Emerging Forensic Genomic Applications – Genome ID Forum 2014
Greenville, North Carolina – The Center for Advanced Forensic DNA Analysis (CAFDA) is pleased to announce the Genome ID Forum 2014 – Emerging Forensic Genomic Applications; a collaborative conference to take place on September 9 and 10 at the Hilton Greenville, North Carolina.

Vallone (NGS, digital PCR)

NGS Advances in Human Forensic Genomics
Workshop Presentation: Vallone & Gettings

STR Sequence Diversity in Population Samples and
eration"
ollaboration)

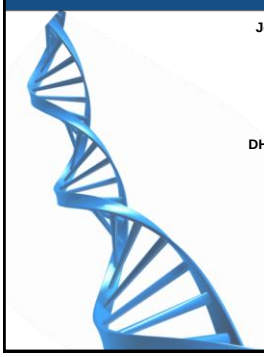
Panel: Rapid DNA and CODIS integration
Callaghan, Wendel, Vallone, Selden, Jovanovich

2014 "Future trends in forensic DNA technology" seminar series
7/30/14 Burlington, VT
8/6/14 Crystal City, VA

HID
NIST presenting on Yfiler Plus and PGM SNP assays

biometric CONSORTIUM
Global Identity Summit
Rapid DNA Session Sept 17, 2014

Acknowledgements



Jo Lynne Harenza, Ph.D. (R scripts)

David Duewer, Ph.D.

Funding

FBI: DNA as a Biometric

DHS: Rapid DNA and Kinship support

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Michael.Coble@nist.gov