



NIST
National
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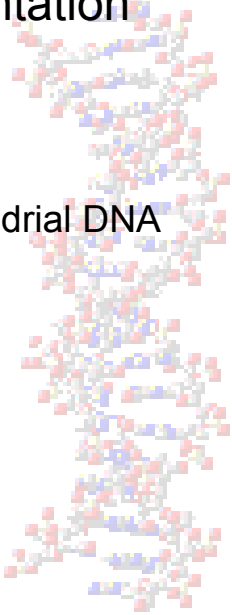
...working with industry to develop and apply technology, measurements and standards

Multiplexed Assays for Probing Y Chromosome and Mitochondrial Markers

5th Annual DNA Forensics Meeting
June 27-28, 2002
Peter M. Vallone
National Institute of Standards and Technology

Outline of Presentation

- Multiplexing
- Assays and Instrumentation
- Y Chromosome and Mitochondrial DNA
- Primer design strategy
- Results
 - mtSNP 10 plex
 - Y SNP 5 plex
 - Y STR multiplexes



Multiplexing

Probing multiple loci/markers simultaneously

Multiple strands of short DNA bind to template DNA and chemistry occurs (PCR, primer extension, hybridization, etc)

What are the Advantages of Multiplexing?

Obtain more information per unit time

Reduce the amount of limited forensic sample used

Save on reagents; enzyme, buffers, DNA oligomers

Reduces labor

Streamlines data analysis

For certain markers it is essential (SNPs, YSTRs)

Coincides with high capacity instrumentation

What are the Challenges of Multiplexing?

Only guidelines exist for designing multiplexes

More markers = increased complexity

Testing a robust multiplex

Inclusion of useful markers in the multiplex

What Type of Genetic Variation?

- Length Variation

short tandem repeats (STRs)

CTAGTCGT(GATA)(GATA)(GATA)GCGATCGT

- Sequence Variation

single nucleotide polymorphisms (SNPs)

insertions/deletions

GCTAGTCGATGCTC(G/A)GCGTATGCTGTAGC

What Assays are we Multiplexing?

Polymerase chain reaction (PCR)

Amplification of specific region of the human genome

Typically used for STR and SNP

Use **Capillary Electrophoresis** for detection

Primer Extension reaction (minisequencing)

Typically used for SNP markers

Use **Capillary Electrophoresis** and

Mass Spectrometry for detection

NIST Goals for Multiplex Assays

Working with collaborators who have markers of forensic interest

By using our multiplex assays collaborators can type markers and evaluate forensic utility

Further understanding of multiplex assays

Publish assay details for others to evaluate (commercial and research)

Multiplexing


Assays and Instrumentation

Y Chromosome and Mitochondrial DNA

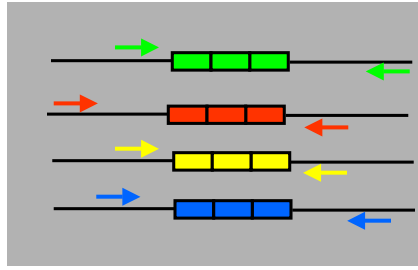
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Multiplex PCR

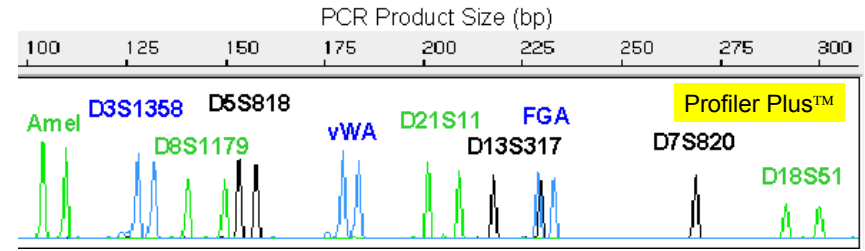


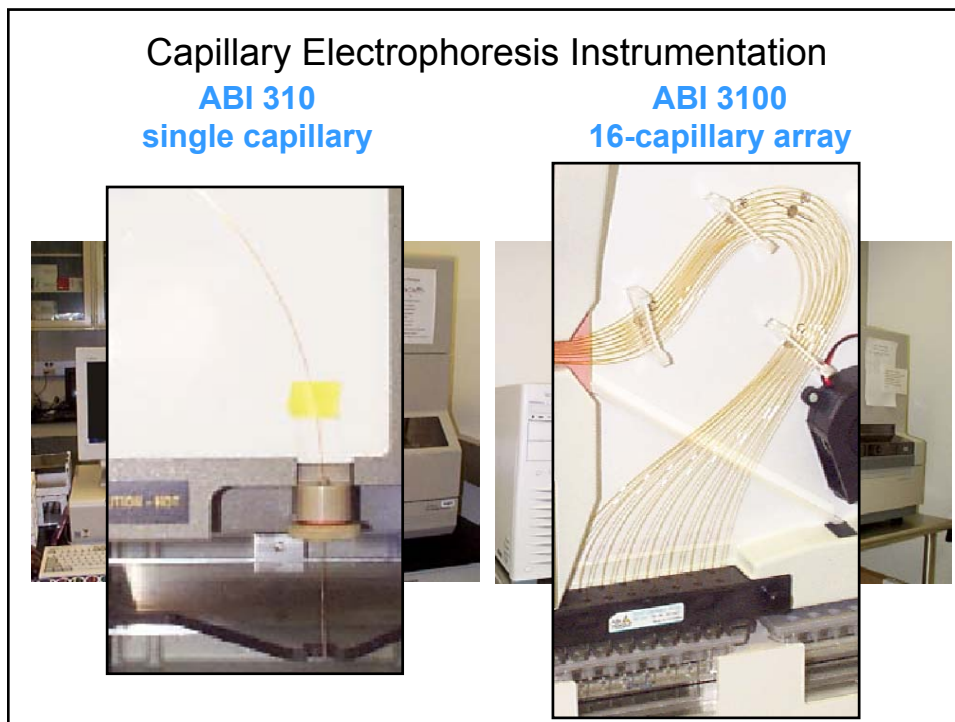
Multiple primer pairs target more than one specific site on the DNA strand

Compatible primers are the key to successful multiplex PCR

Commercial kits are available for targeting and simultaneously amplifying 16 markers

PCR Product Size (bp)





ABI PRISM® SNaPshot™ Multiplex System

Primer extension assay that utilizes fluorescently labeled ddNTPs



Analysis of fragment size and fluorescent label identity by CE allows typing of multiple SNPs

Multiplexed amplicons or pooled singleplex PCR amplicons can be used as templates

Primer design must be done by user!

Primer Extension with SNaPshot™

SNP Primer is extended by one base unit

“tail” used to vary electrophoretic mobility

Oligonucleotide primer 18-28 bases

5' → 3'

SNP

Fluorescently labeled ddNTPs + polymerase

PCR Amplified DNA Template

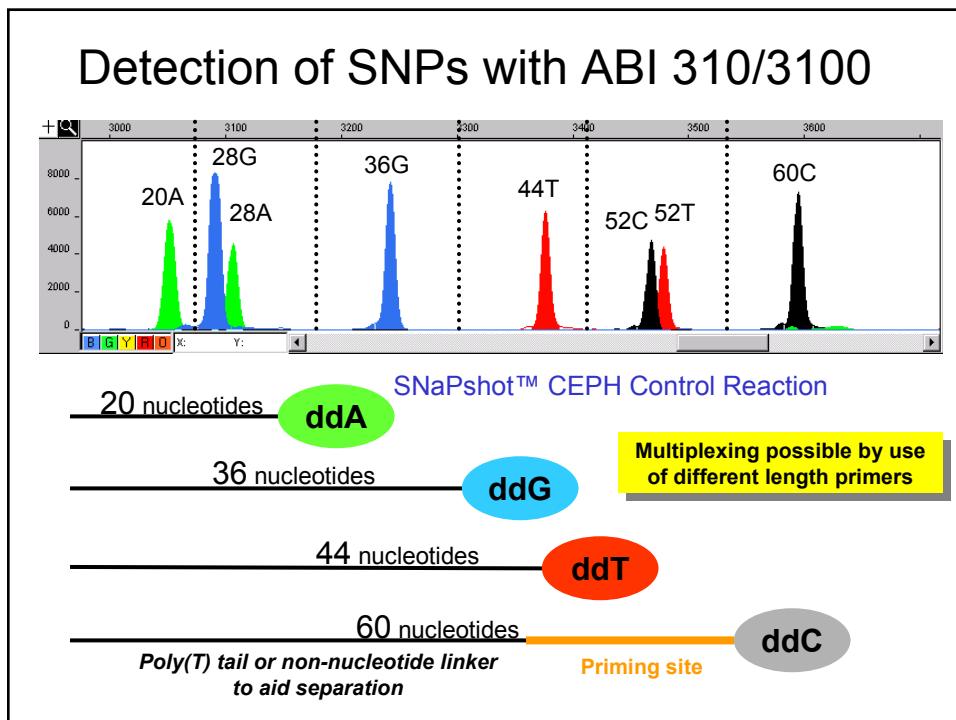
ddNTP	Dye label	Color
A	dR6G	Green
C	dTAMRA	Black
G	dR110	Blue
T	dROX	Red

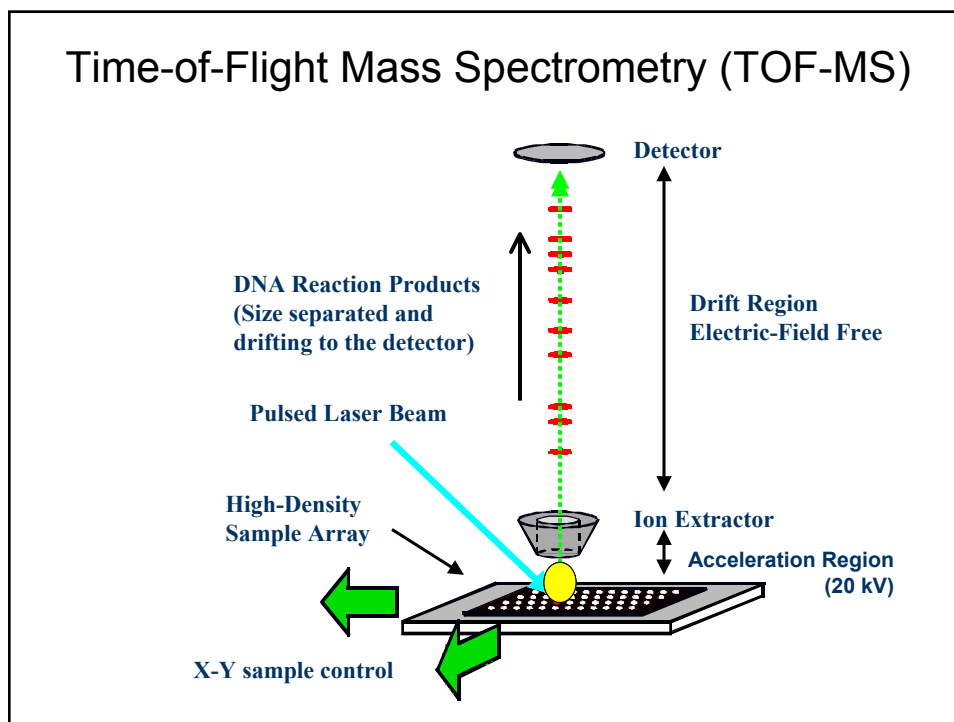
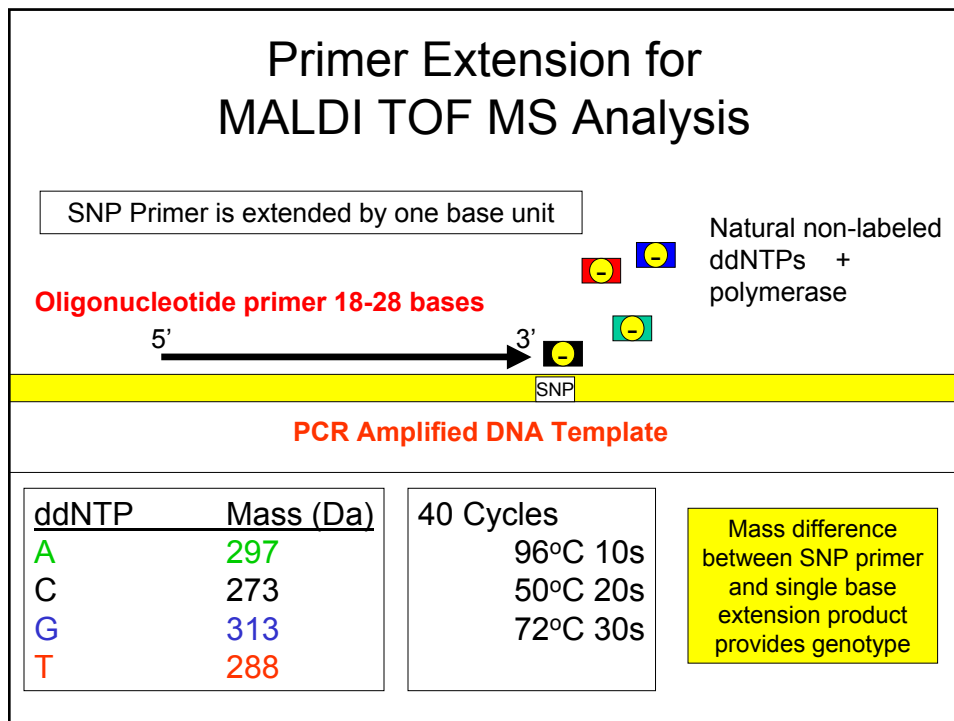
25 Cycles

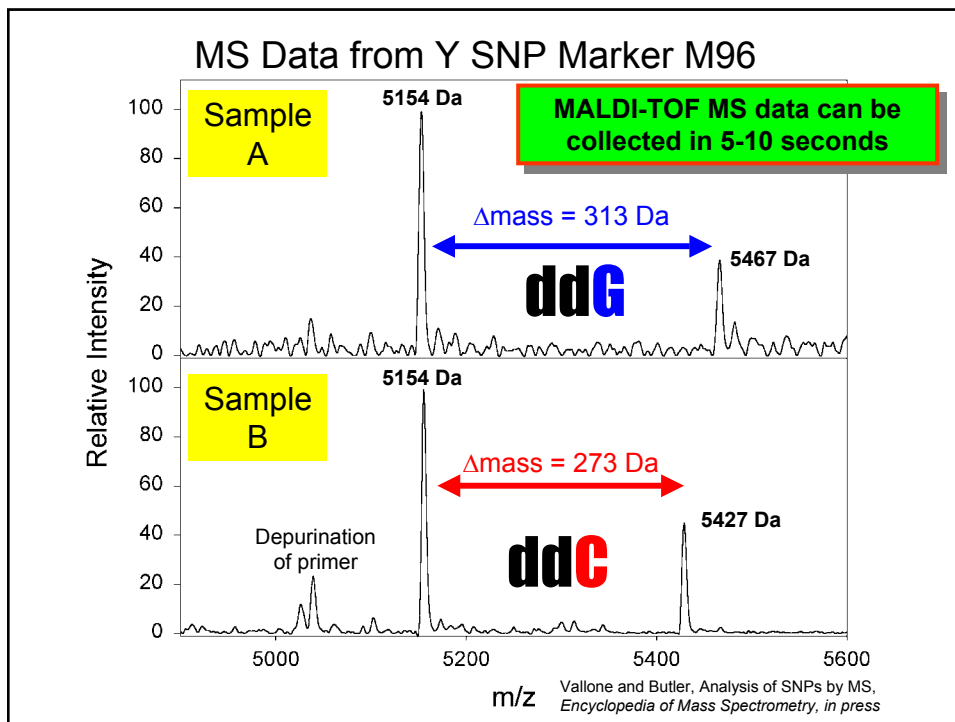
96°C 10s

50°C 5s

60°C 30s







Multiplexing

Assays and Instrumentation

Y Chromosome and Mitochondrial DNA

Primer design strategy

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Markers of Interest

- Mitochondrial DNA (mtDNA)
 - maternally inherited
 - polymorphic control region (D-loop)
 - ~1000's of copies per cell
- Y chromosome
 - paternally inherited
 - variety of Y STR and Y SNP markers
 - ***haplotype rather than genotype***



Require large databases because recombination does not occur

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Stand Alone Primer3

Sending multiple sequences over the web for primer selection can be tedious

The Primer3 web output is fine for the screen viewing or printing but not for organizing in spreadsheets

Primer3 is publicly available and can be run (in batch!) on a Unix, Linux, or Mac (OSX) computer

Developed a program that formats files for Primer3 input

Reference sequences that are stored in Excel can be quickly formatted for Primer3

Example input
format for
Primer3

```
PRIMER_SEQUENCE_ID=M9
SEQUENCE=GCAGCATATAAACTTTCAGGACCCTGAAATACAGAAGCTG
CAAAGAAACGGCCTAAGATGGTTGAATNCTCTTTATTTTTCTTTAATTTAG
ACATGTTCAAACGTTCAATGTCTTACATACTTAGTTATGTAAGTAAGGTAG
CGCTTACTTCATTATGCATTTCAACTCAAAAAAAAAATTCCTTTGTGAAAT
GTTGAAATATTTTTCTAATCTGTTTCACGAGCTTCAAAAATGAGGAAAAAA
GATTCAGTTTACATTTACAGCAAATGCCTCTTTTTAATCGGATTTATGTTT
ACTTAACATTTACAGTACATTTACGCTTGAGCAAAGTTAGGTTTT
PRIMER_COMMENT=(340 bp); G to C at position 68
PRIMER_MISPRIMING_LIBRARY=/Users/vallone/Desktop/primer3/misprM9
PRIMER_MAX_MISPRIMING=8
PRIMER_PAIR_MAX_MISPRIMING=20
EXCLUDED_REGION=38,60
PRIMER_PRODUCT_SIZE_RANGE=90-150
PRIMER_PRODUCT_OPT_SIZE=105
PRIMER_MIN_SIZE=18
PRIMER_MAX_SIZE=27
PRIMER_OPT_SIZE=20
PRIMER_OPT_TM=60
PRIMER_MIN_TM=57
PRIMER_MAX_TM=63
PRIMER_NUM_RETURN=1
PRIMER_EXPLAIN_FLAG=1
PRIMER_LIBERAL_BASE=1
=
PRIMER_SEQUENCE_ID=M42
SEQUENCE=AAAGCGAGAGATTCAATCCAGGATGACAGAATGCGTTCAC
CTTTAAAGGGATTAAGAAGTATAATACAGTCTGTATTATTAGATCACCC
AGAGACACACAAAACAAGAACCCTGAATTGAATTAGTGGTATACTAATAG
ACTGCTTTTACAGCTCAAAATTTTACAGTCAATTCAGCTCAATTTTACAG
```

Primer3 Parameters

Desired Tm Range for PCR Primers

Minimum: 57, Maximum: 63, Optimum: 60, Max Tm Difference: 12.0

Desired Size Range for PCR Primers

Minimum: 18, Maximum: 27, Optimum: 20

Primers to Return: 2

Set Parameters

Primer3 Defaults - see Peter Vallone if you want to change these

Max 3' Stability: 9.0

Max 3' Mispriming: 12.0

Pair Max Mispriming: 12.0

Primer GC %: 20.0 - 80.0

Max Self Comp: 8.0

Max 3' Comp: 3.0

Max # N's: 0

Max Poly-X: 3.0

Ct (nM): 50.0

Salt Conc (mM) - KCl: 50.0

Can help utilize all the tools that Primer3 provides

Non-Specific Interactions

Primers that interact with non-specific (undesired) regions of a genome OR with each other can degrade PCR performance

Screening for alternate genomic binding regions can be accomplished using **BLAST** <http://www.ncbi.nlm.nih.gov>

Screening for potential primer-dimer interactions is accomplished using in house software - **AutoDimer**

AutoDimer Check

Screening for potential intramolecular hairpin
and intermolecular primer-dimer formation

PCR Assay Design

If primer pairs meet criteria

Obtain primer pairs and test singleplex PCR
(QC all primers with MS/CE/HPLC)

Begin initial testing of multiplex PCR
Start with a PCR mix containing
1.0 μM of each primer pair

Evaluate amplicon yields, presence and balance

Vary primer pair concentrations, [polymerase], number of
cycles, [Mg^{++}], [dNTPs], BSA

Redesign and retest failing loci

Multiplexing

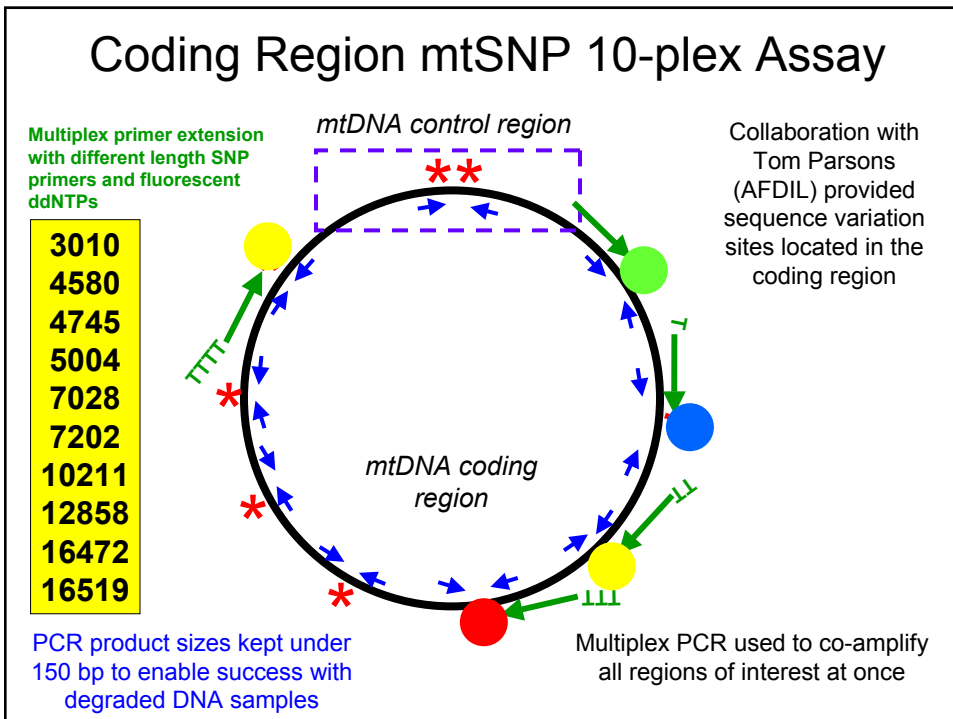

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Tailed SNP primers allows for multiplexing in the SNaPshot assay

Sequences for 10 SNP primers

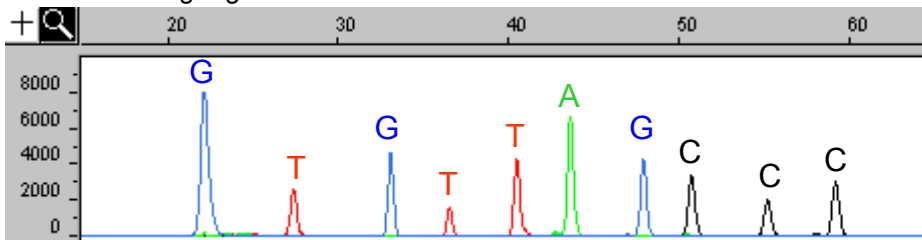
TCAGAAGTGAAAGGGGGC	18/na
TTTTTTTTGTTGGATCAGGACATCCC	19/26
TTTTTTTTTACTAAGAAGATTTTATGGA	20/30
TTTTTTTTTTTTAGACCCAGCTACGCAAATC	20/34
TTTTTTTTTTTTTTGACACGTACTACGTTGTAGC	20/38
TTTTTTTTTTTTTTTTCCACAACACTTTCTCGGCCT	20/42
TTTTTTTTTTTTTTTTTGTGGGCTATTTAGGCTTTATG	22/46
TTTTTTTTTTTTTTTTTTGCAGCCATTCAAGCAATCCTATA	23/50
TTTTTTTTTTTTTTTTTTTTGTTAGAACTGGAATAAAAGCTAG	25/54
TTTTTTTTTTTTTTTTTTTTTTGAACCATAACCAATACTACCAATCA	25/58

Template binding sequence – black
 Tailed sequence for fragment separation - red

mtSNP 10-plex run on ABI 3100 (SNaPshot™ assay)

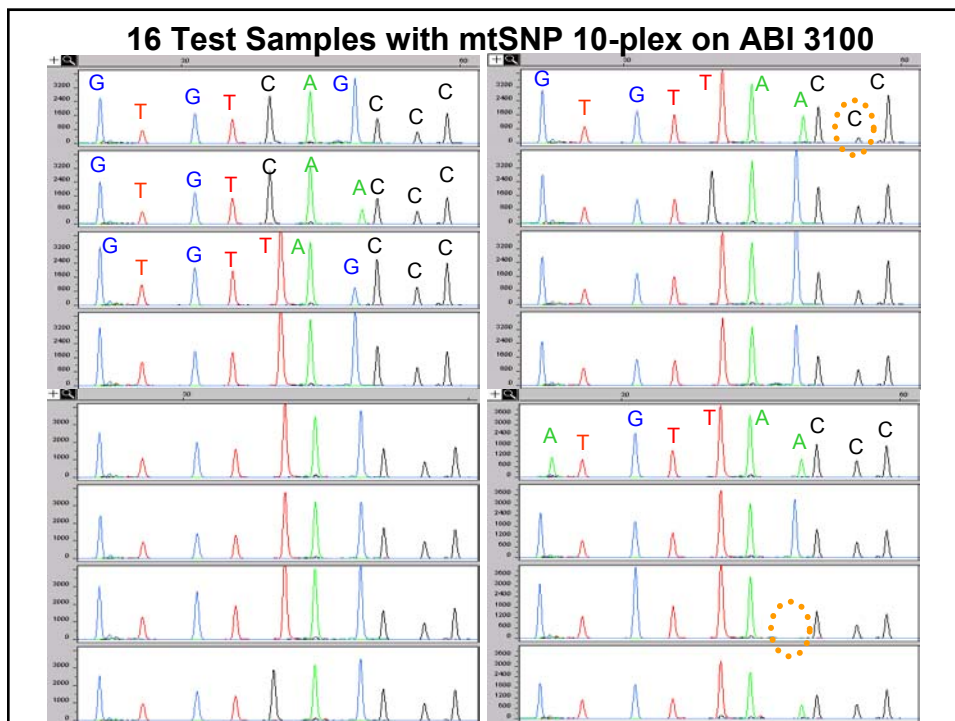
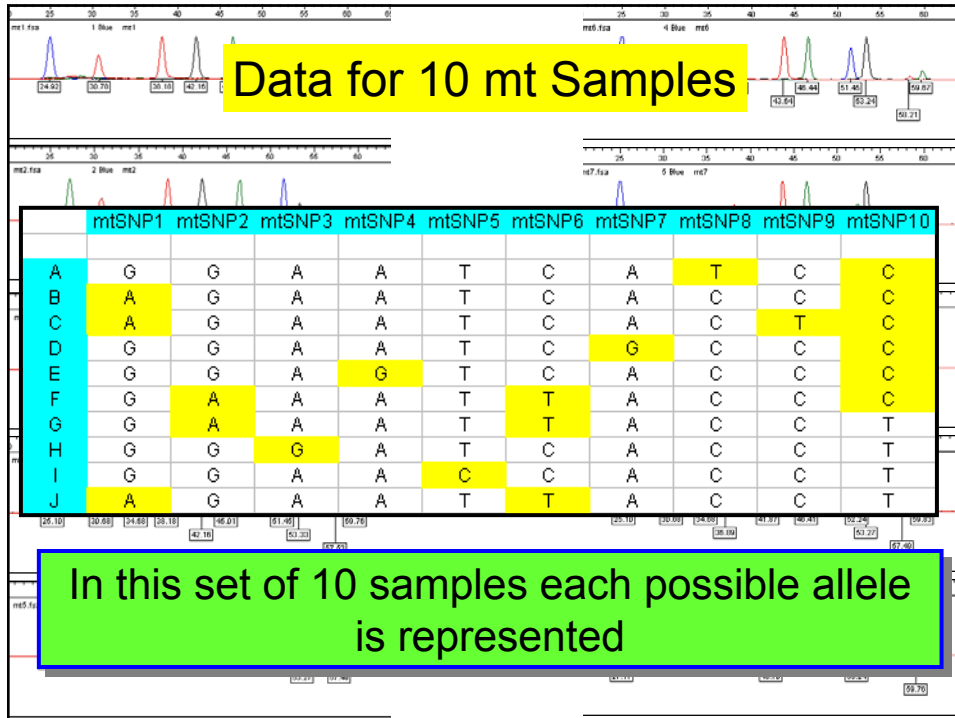
Multiplex PCR and Multiplex SNP Detection

mtDNA coding region SNPs




SNP types

Sizing performed by comparison to GS120 LIZ internal size standard (not shown)

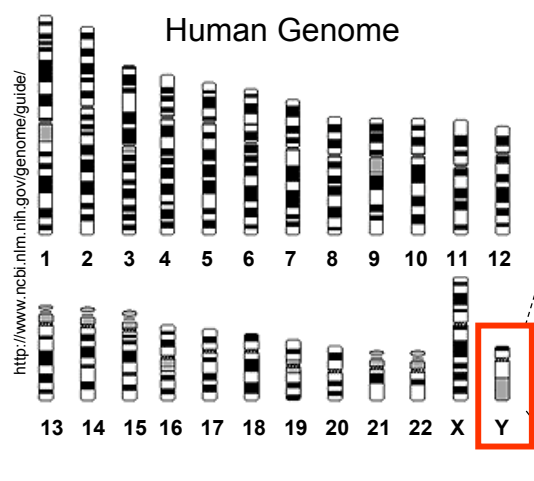


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There is a growing interest in the Y-chromosome to aid forensic, paternity, and missing persons testing...

Human Genome

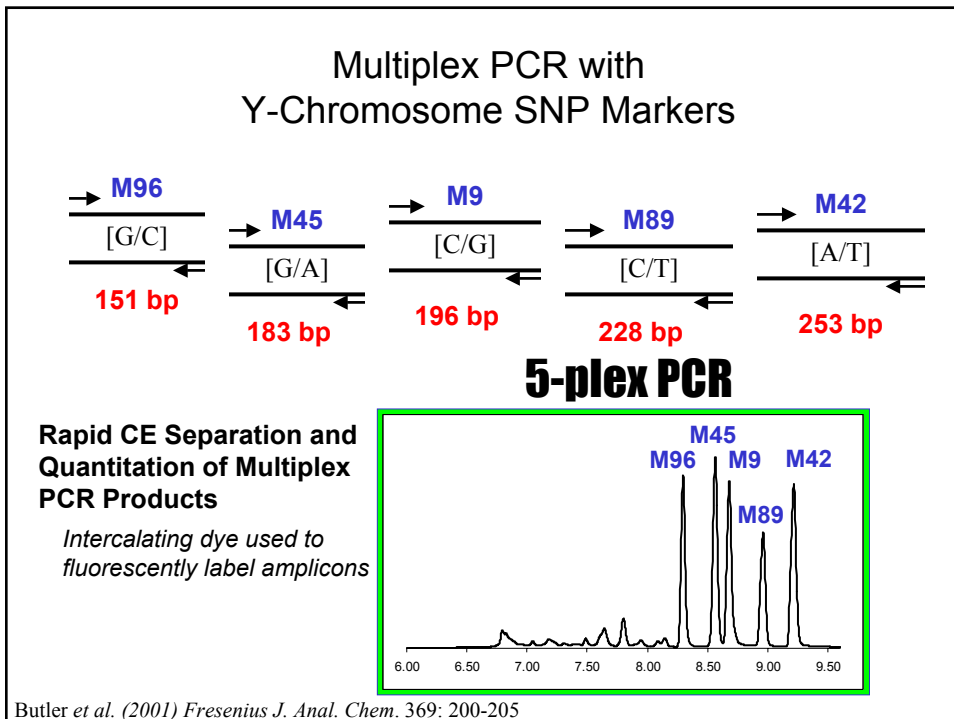
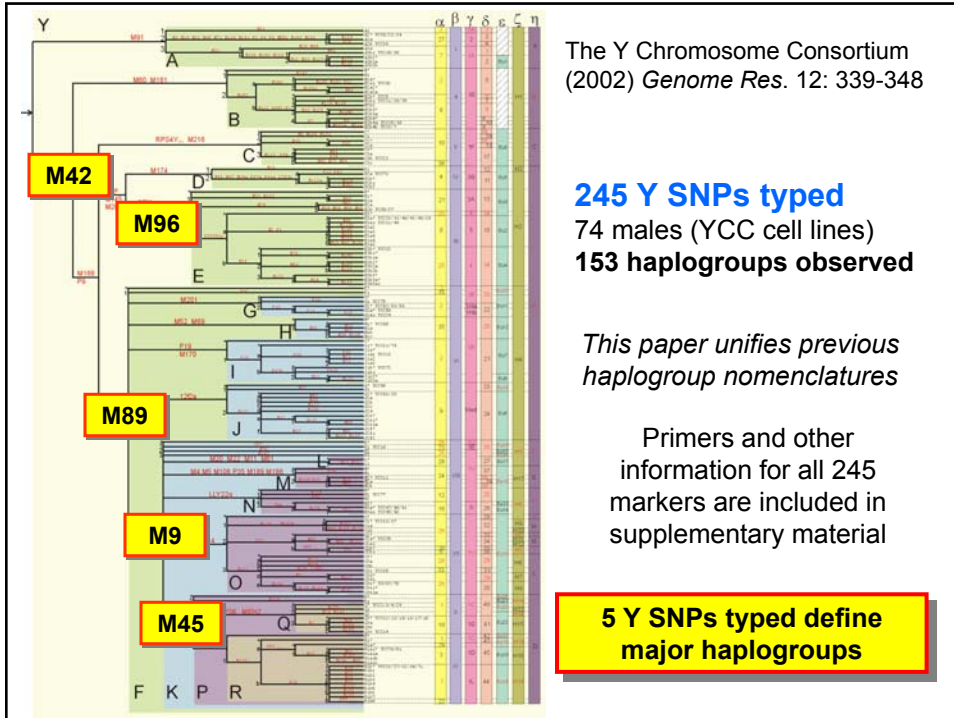


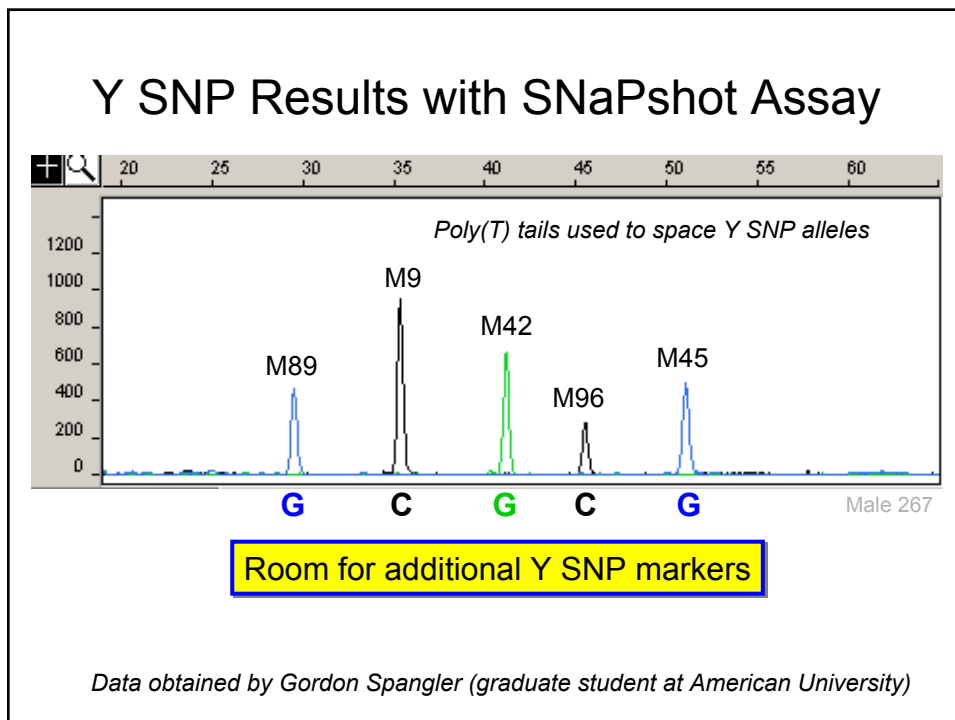
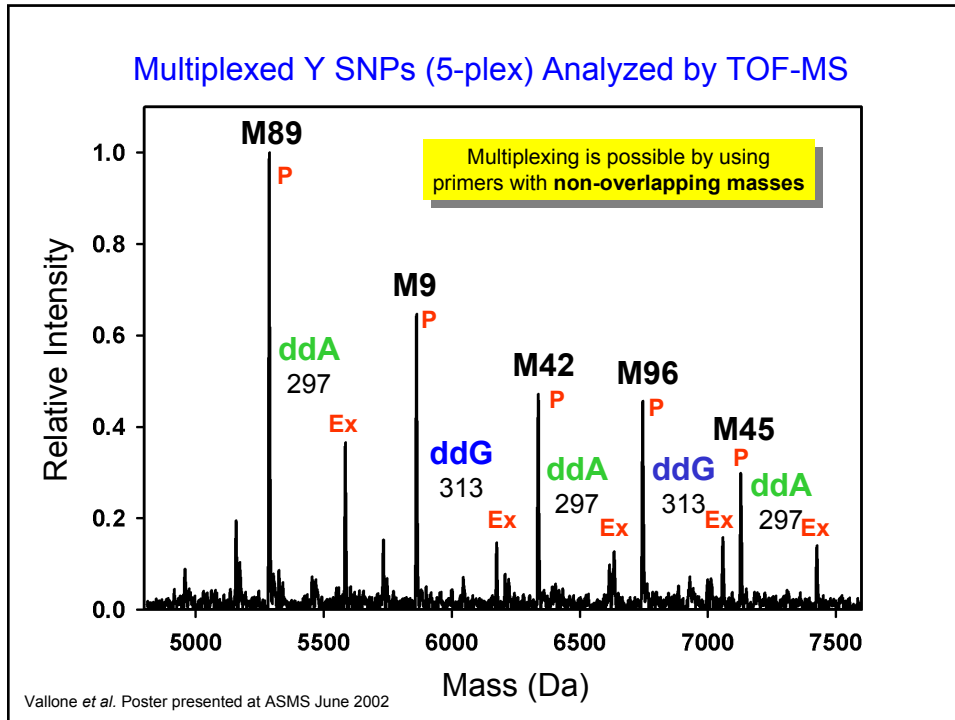
<http://www.ncbi.nlm.nih.gov/genome/guide/>

Y

STR Markers

DYS19	
DYS389I/II	
DYS390	SNP
DYS391	M 09
DYS392	M 42
DYS393	M 45
DYS385	M 89
YCAII	M 96
DYS437	
DYS438	
DYS439	





Y SNP Haplotypes for 16 Test Samples

Sample ID	M9 (C/G)	M42 (A/T)	M45 (G/A)	M89 (C/T)	M96 (G/C)
Male 1	G	T	A	T	C
Male 2	G	T	A	T	C
Male 3	G	T	A	T	C
Male 4	G	T	A	T	C
Male 5	G	T	A	T	C
Male 6	G	T	A	T	C
Male 7	G	T	A	T	C
Male 8	C	T	G	C	G
Male 9	C	T	G	C	G
Male 10	C	T	G	C	G
Male 11	C	T	G	C	G
Male 12	C	T	G	C	G
Male 13	C	T	G	C	G
Male 14	G	T	G	T	C
Male 15	C	T	G	T	C
Female	-	-	-	-	-

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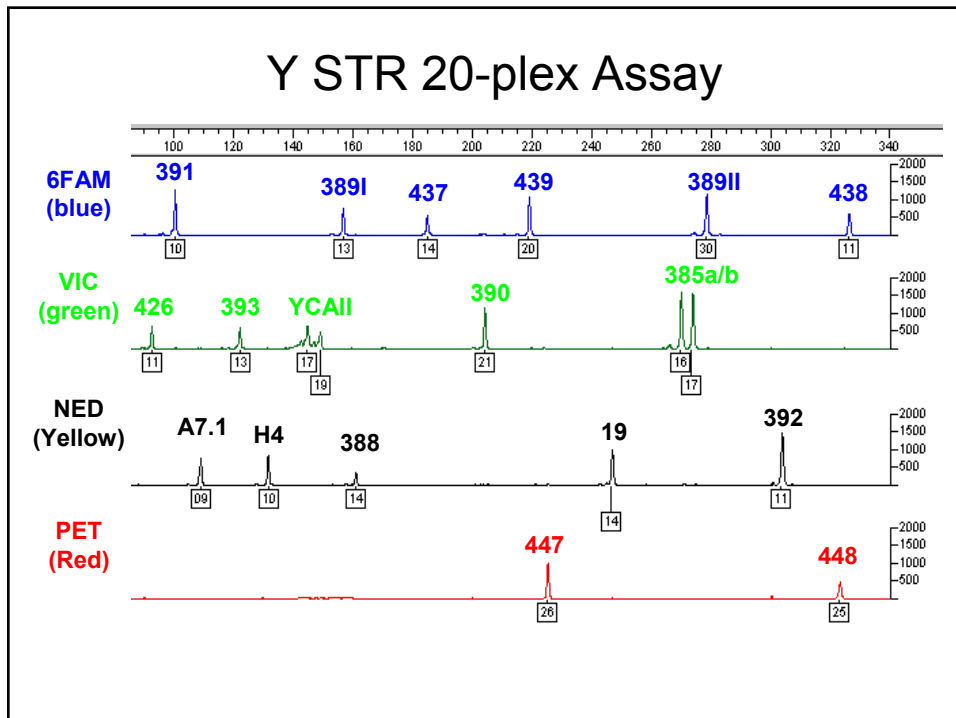
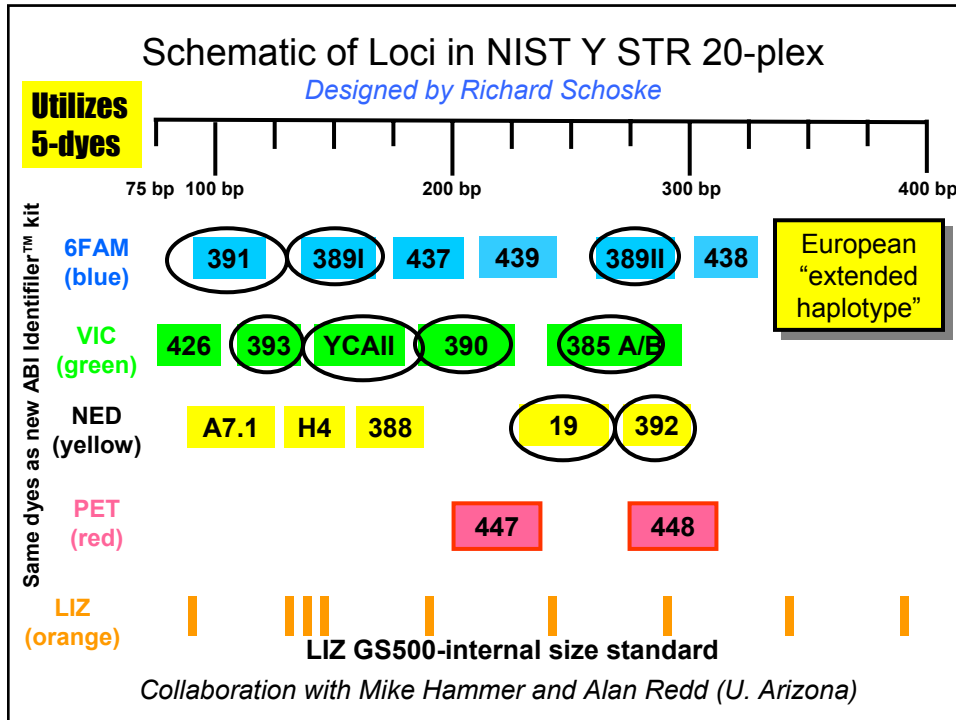
Results

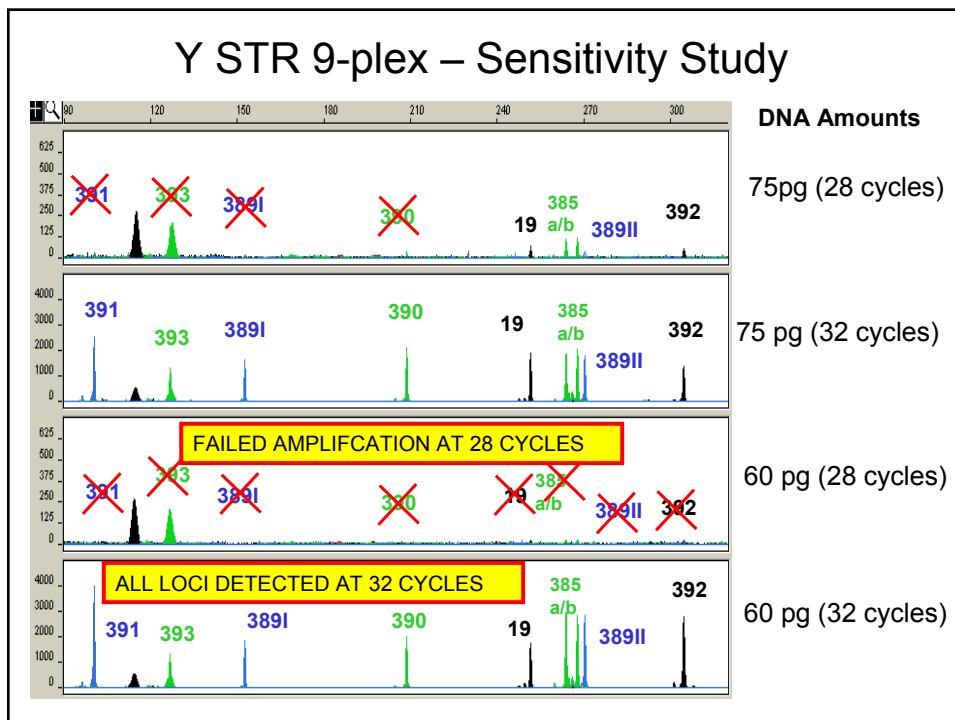
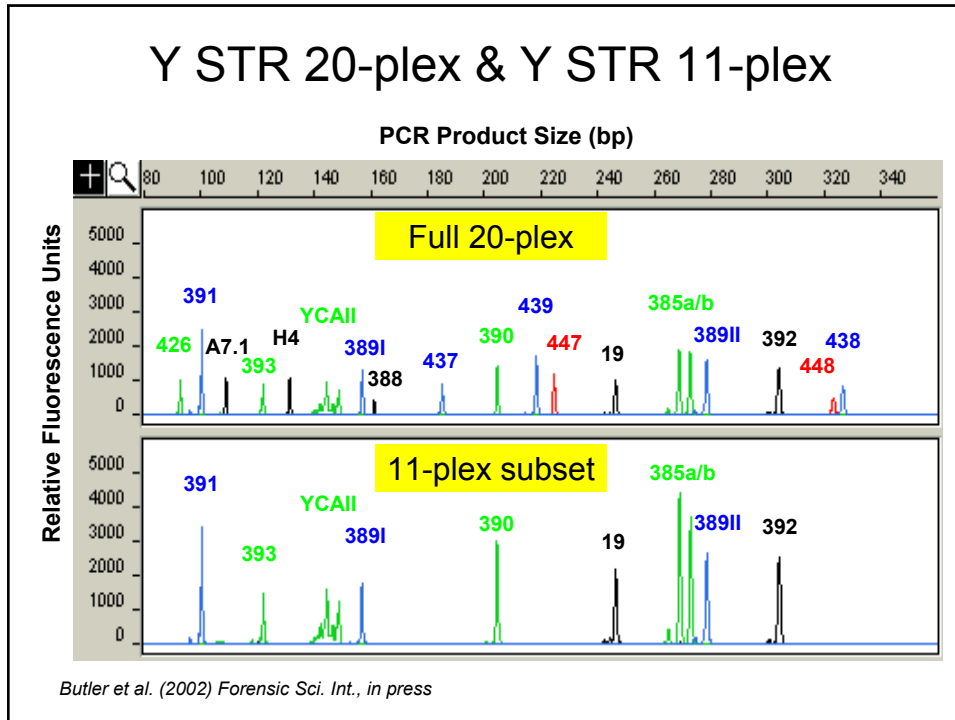
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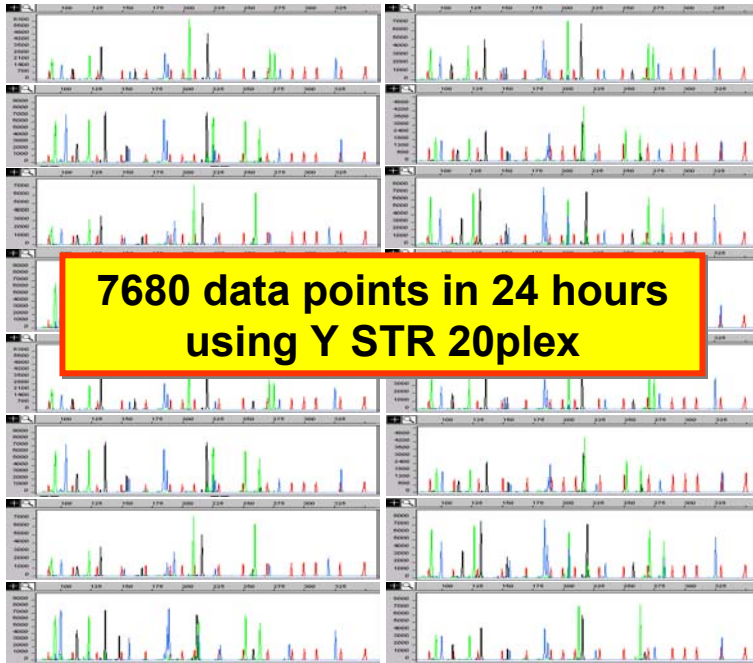
Y STR multiplexes







High-throughput Y STR Typing on the ABI 3100 (16-capillary array)



Acknowledgments



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John Butler



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