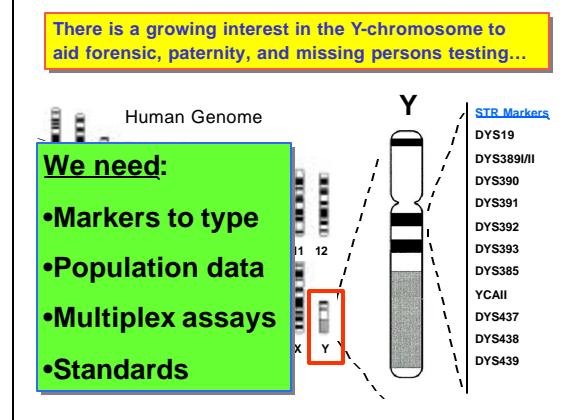


**NIST**  
National Institute of  
Standards  
Technology

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

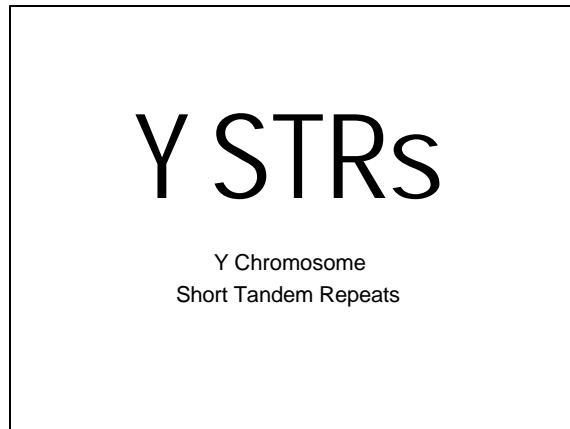
## Recent Developments in Y-Chromosome Analysis of Y-STRs and Y-SNPs

**AAFS Y Chromosome Workshop**  
February 12, 2002  
John M. Butler  
National Institute of Standards and Technology



### Outline of Presentation

- Standardizing Information on Y Chromosome Markers
  - STRBase and Other Internet Resources
- Development of New Y STR Multiplexes
  - Primer Design Strategies
  - NIST Y STR 20plex Results
- Y SNP Typing Technologies
  - Y SNP Multiplex Assays
- NIST SRM 2395 with Y STR and Y SNP Data



### History of Y STR Marker Discovery

- 1992 - DYS19 (Roewer et al.)
- 1994 - YCAI a/b, YCAII a/b, YCAIII a/b, DXYS156 (Mathias et al.)
- 1996 - DYS389I/II, DYS390, DYS391, DYS392, DYS393 (Roewer et al.)
- 1996 - DYF371, DYS425, DYS426 (Jobling et al.)
- 1997 - DYS288, DYS388 (Kayser et al.)
- 1998 - DYS385 a/b (Schneider et al.)
- 1999 - A7.1, A7.2, A10, C4, H4 (White et al.)
- 2000 - DYS434, DYS435, DYS436, DYS437, DYS438, DYS439 (Ayub et al.)
- 2000 - G09411, G10123 (de Knijff unpublished)
- 2001 - DYS441, DYS442 (Iida et al.)
- 2002 - DYS446, DYS447, DYS448, DYS449, DYS450, DYS452, DYS453, DYS454, DYS455, DYS456, DYS458, DYS459, DYS463, DYS464 (Redd et al.)

### History of Y STR Marker Discovery

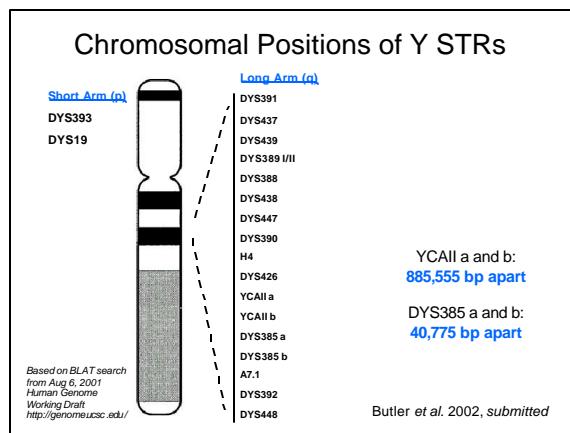
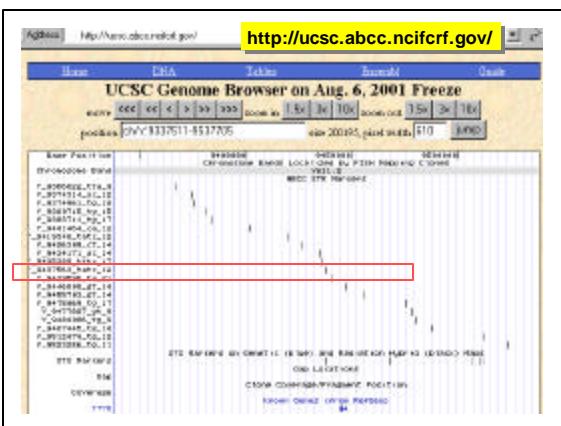
- 1992 - DYS19 (Roewer et al.)
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- 1996 - DYS389I/II, DYS390, DYS391, DYS392, DYS393 (Roewer et al.)
- 1996 - DYF371, DYS425, DYS426 (Jobling et al.)
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- 2001 - DYS441, DYS442 (Iida et al.)
- 2002 - DYS446, DYS447, DYS448, DYS449, DYS450, DYS452, DYS453, DYS454, DYS455, DYS456, DYS458, DYS459, DYS463, DYS464 (Redd et al.)

**Blue labeled markers are in YSTR 20plex assay**

### Y STR Typing of Duplicated Regions

### Human Genome Data

- Human Genome Project has enlarged knowledge of Y chromosome...
- Public human genome sequence available at <http://genome.ucsc.edu> ("Golden Path")
- Entire Y chromosome sequence can be downloaded -- **51 Mbytes (last half is all "Ns" from heterochromatin region)**
- ABCC STR sets – total number of Y STRs that might be polymorphic
- We can position all Y STR markers on current Y chromosome sequence



### Internet Resources for Y Chromosome Information

<http://www.ystr.org/usa/>   <http://www.ystr.org/europe/>   <http://www.ystr.org/asia/>

<http://www.medfac.leidenuniv.nl/lfd/>   <http://ycc.biosci.arizona.edu/>

<http://www.cstl.nist.gov/biotech/strbase/>

These data can be used in basic research and application of short tandem repeat (STR) markers in human identity testing. The authors are solely responsible for the information herein.

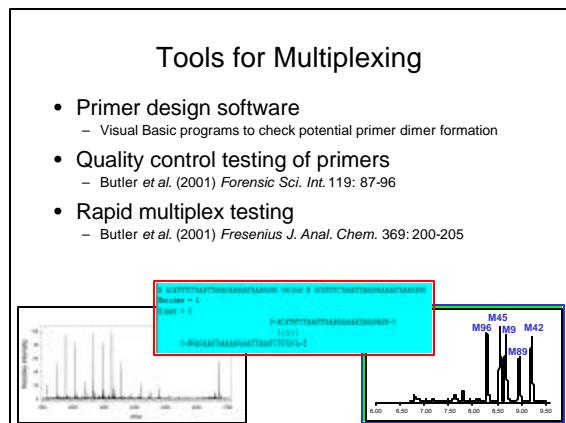
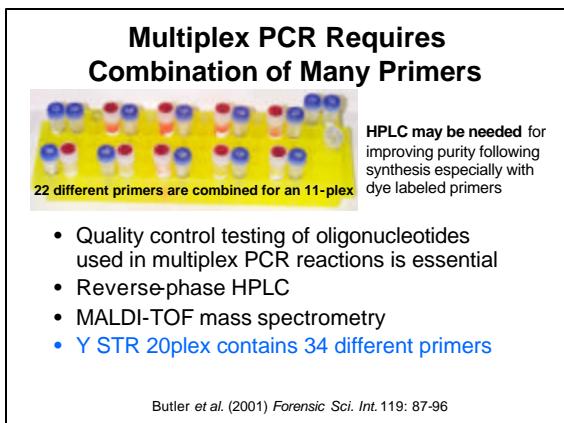
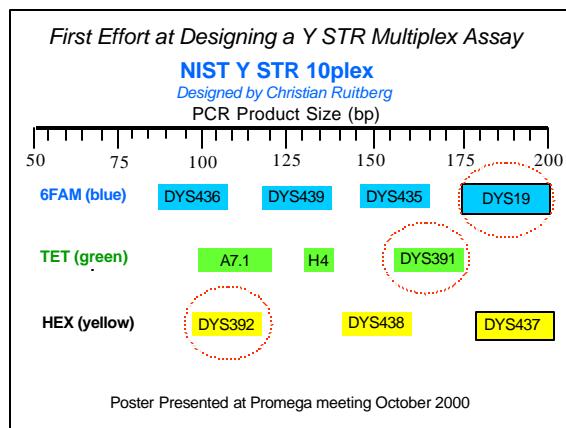
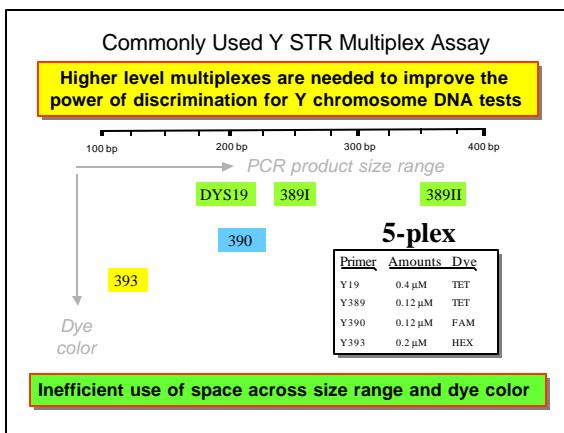
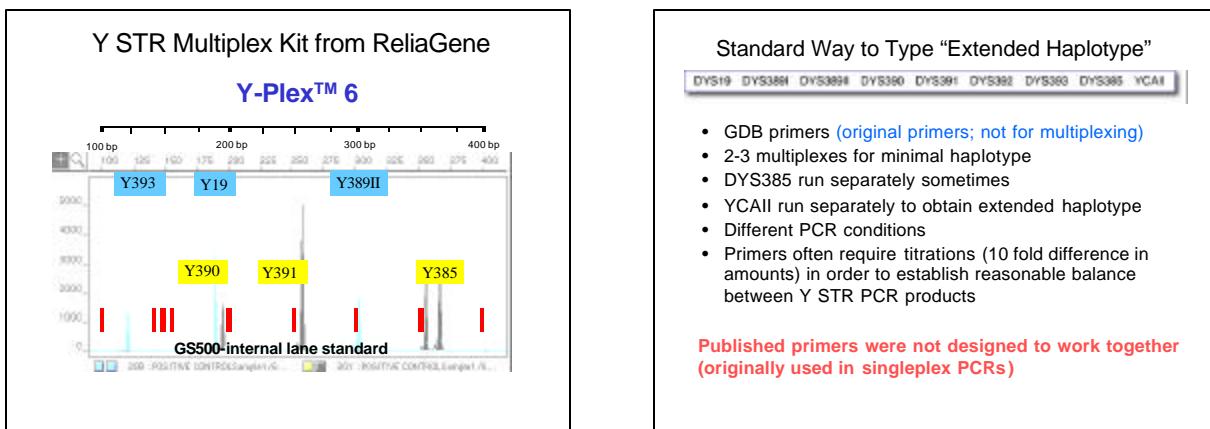
### STRBase

**Short Tandem Repeat DNA Internet Database**

<http://www.cstl.nist.gov/biotech/strbase>

**Y-Chromosome STR Information Available**

- ❖ Over 200 publications on Y STRs & SNPs cataloged
- ❖ Allele information on 16 Y STR loci
- ❖ Downloadable PowerPoint on Y STRs and Y SNPs
- ❖ Links to other Y-chromosome sites
- ❖ Information on new Y STR multiplexes developed at NIST



## Assay Development Goals

*Discussion with Mecki Prinz December 2000*

- Single tube amplification of all loci in minimal (9-loci) or extended (11-loci) European Y STR haplotypes
- Incorporation of additional polymorphic markers recently published
- No female amplification products (avoid X homology)
- Spacing between loci in same color to allow additional undiscovered alleles to be accommodated
- Similar concentration of primers to produce balanced amplification products
- Sensitivity to <500 pg male DNA with 28 cycle PCR (similar behavior to current STR kits)

The first demonstration of our Y STR 20plex was on July 5, 2001

## Summary of Y STR Multiplex Assays

#	Locus	Ref. Allele	NIST 20plex	NIST 10plex	Y-PLEX 6	Gusmao 5plex
1	DYS19	15	253 bp	196 bp	193 bp	196 bp
2	DYS389I	12	155 bp			249 bp
3	DYS389II	29	275 bp		302 bp	369 bp
4	DYS390	24	217 bp		195 bp	216 bp
5	DYS391	11	109 bp	172 bp	253 bp	
6	DYS392	13	305 bp	114 bp		
7	DYS393	12	121 bp		116 bp	120 bp
8,9	DYS385	11	258 bp		356 bp	
10,11	YCAII	23	159 bp			
12	DYS388	12	157 bp			
13	DYS426	12	98 bp			
14	DYS437	16	194 bp		193 bp	
15	DYS438	10	320 bp		154 bp	
16	DYS439	20	226 bp		135 bp	
17	A7.1	10	113 bp		112 bp	
18	H4	12	138 bp		137 bp	
19	DYS447	23	212 bp			
20	DYS448	23	311 bp			
21	DYS435	9			143 bp	
22	DYS436	12			92 bp	

## New Y STRs

New Y STRs	Core Repeat	Alleles
DYS446	CTCTT	9
DYS447	TAATA	8
DYS448	AGAGAT	7
DYS449	TTTC	10
DYS450	TTTTA	4
DYS452	TATAC	7
DYS453	AAAT	5
DYS454	AATA	3
DYS455	AATA	5
DYS456	GATA	6
DYS458	GAAA	8
DYS459	TAAA	9
DYS463	AARGG	9
DYS464	CCTT	41

Discovered by Mike Hammer's Group at the University of Arizona

14 Y STRs  
8 tetras  
5 pentas  
1 hexa

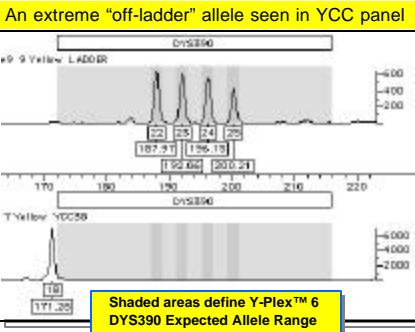
Will be included in future multiplex assays

Redd et al. (submitted)

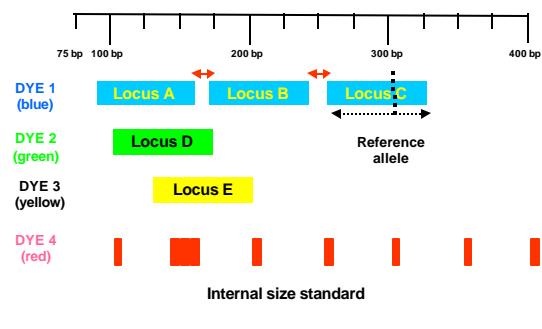
## Development Strategy for Y STR Multiplexes

- Careful definition of allele ranges
  - Literature searches of over 200 papers to locate all known alleles
  - Evaluation of diverse population samples to search for rare alleles (M. Hammer cell lines)
  - Permits markers to be packed together more closely in a single dye color
- Efforts to avoid polymorphic nucleotides in primer binding sites
  - Alignment of multiple GenBank entries
  - Permits primers to be designed with less risk of null alleles
- Incorporation of newly developed NIST multiplex assay design and testing tools

## Need to Define Allele Range Well



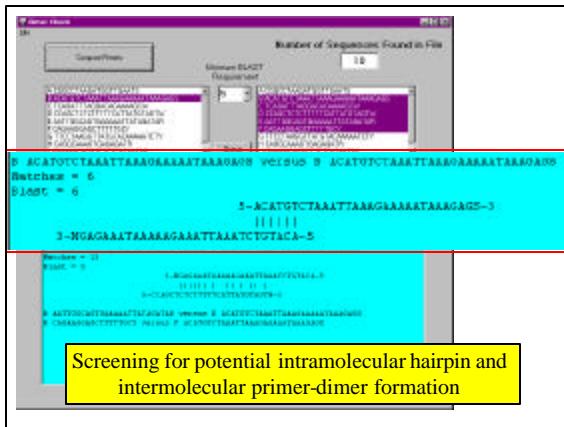
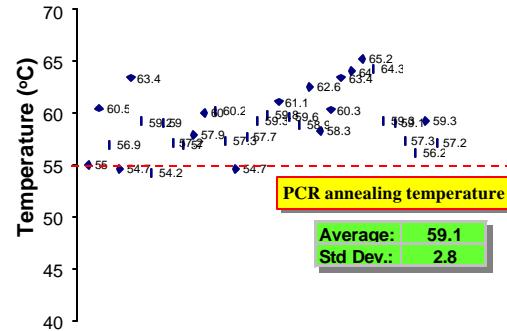
## Multiplex Design Schematic



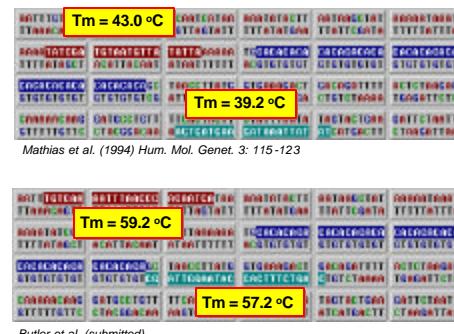
## Intelligent Primer Design

- Overall balance in calculated primer Tm
  - Check for primer-primer interaction
- Examples
- YCAII
    - improved primer Tm compared to commonly used set
  - DYS391
    - efforts to avoid X homology
  - DYS19
    - moving primers in an effort to improve efficiency resulted in discovery of duplicated region of the Y

## Y STR 20plex Primers (Predicted T<sub>m</sub>)

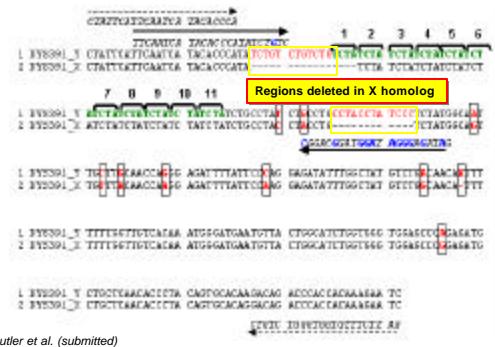


## YCAII: Improving Primer T<sub>m</sub>

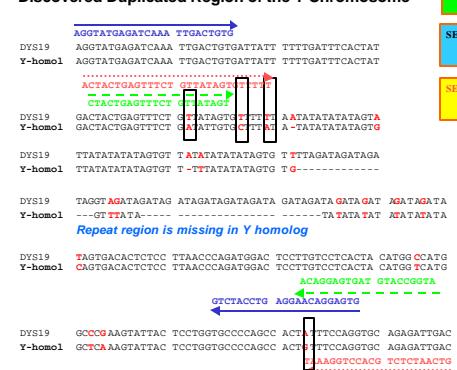


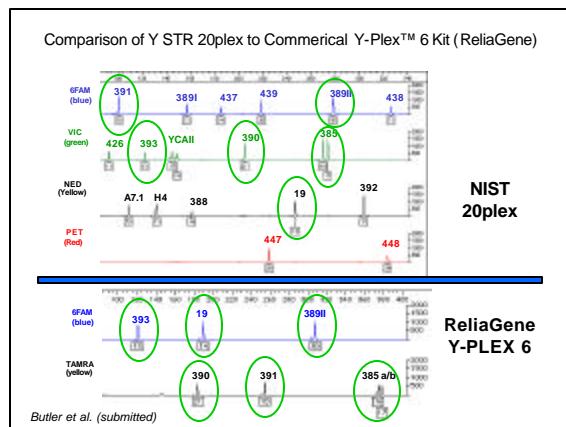
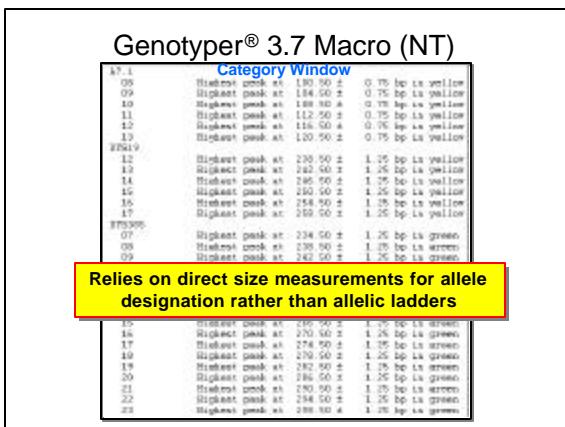
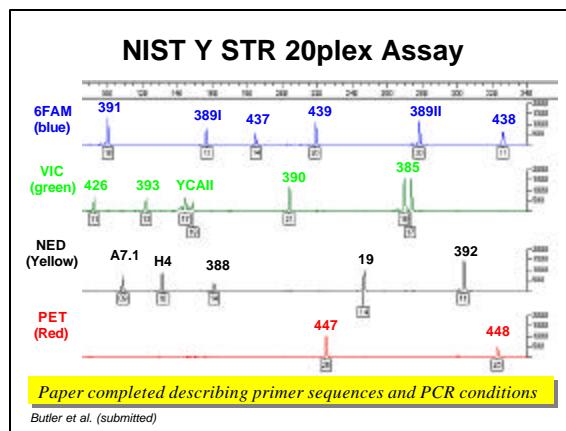
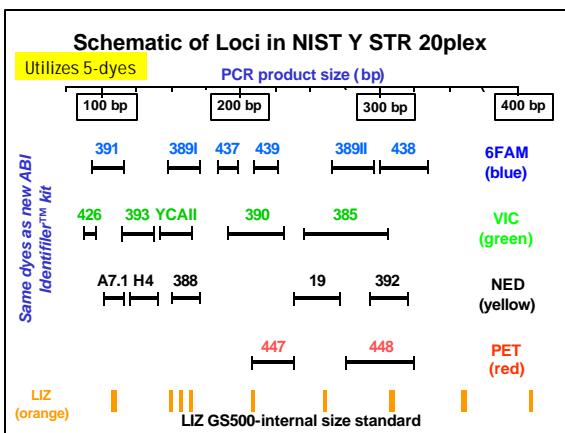
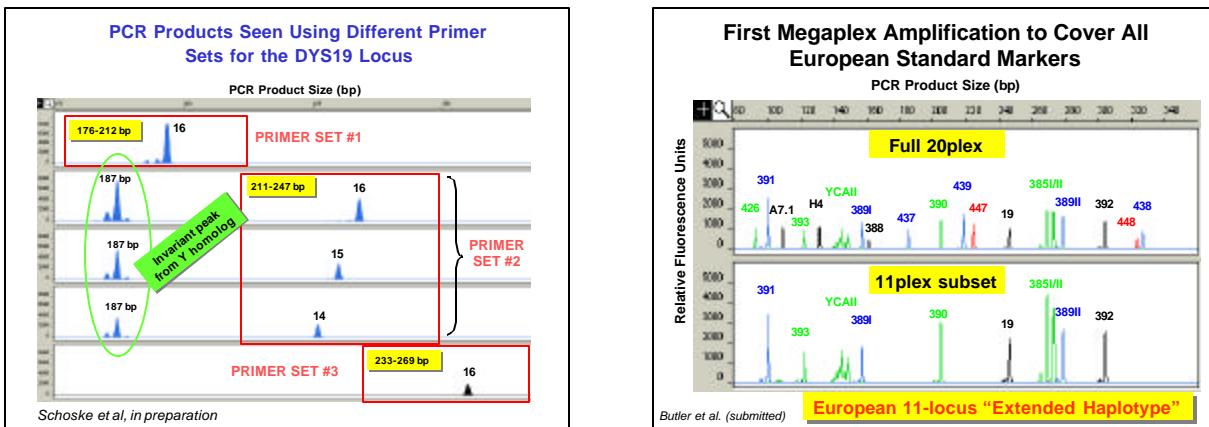
## DYS391: Avoiding the X Homolog

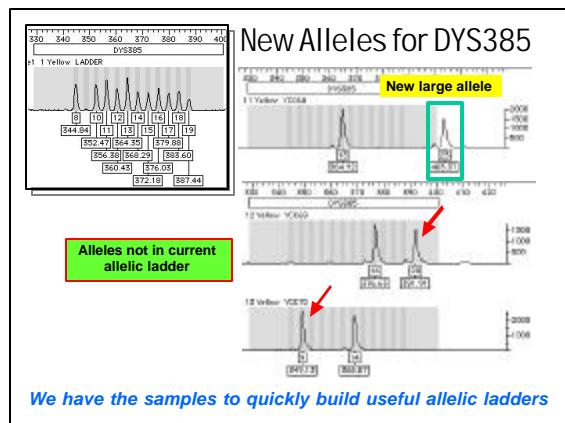
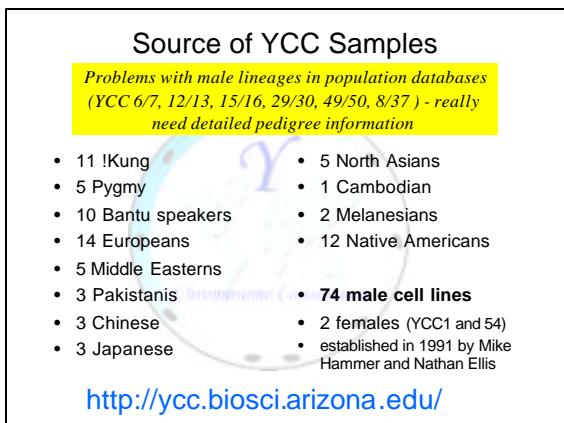
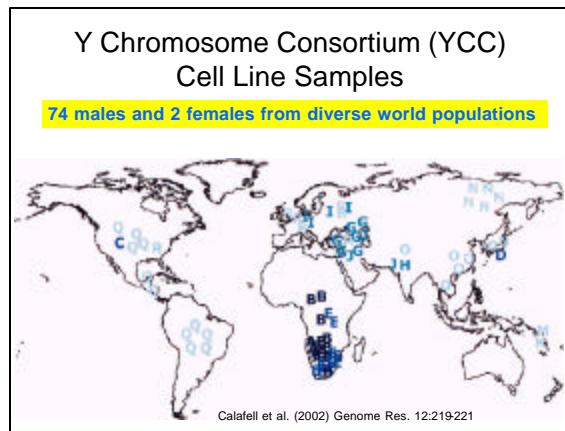
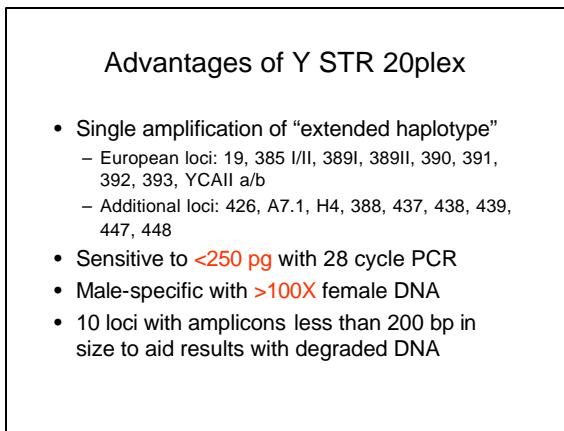
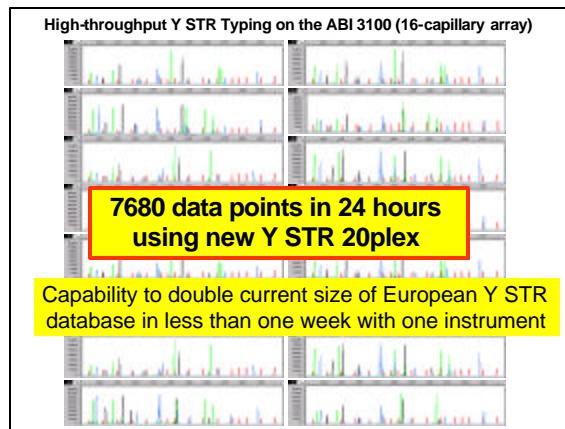
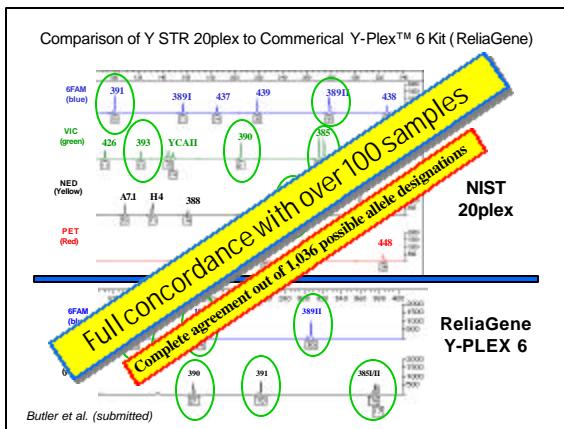
*Female artifact problems seen with published and Y-PLEX 6 primers*

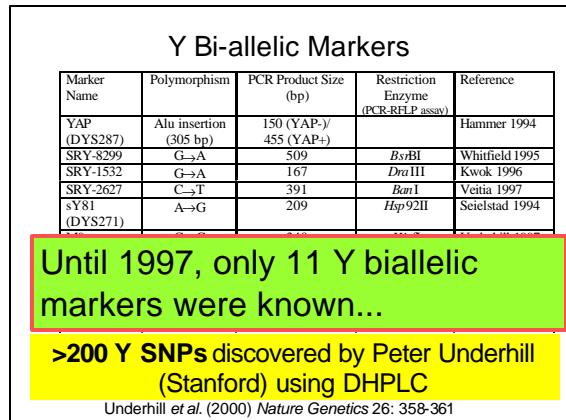
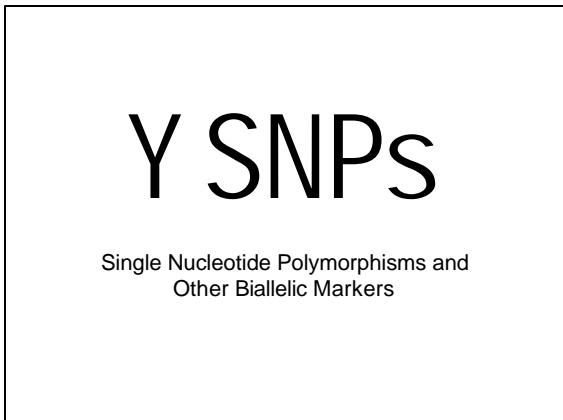
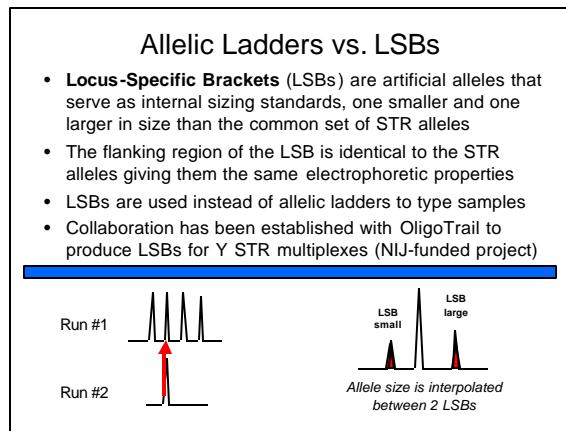
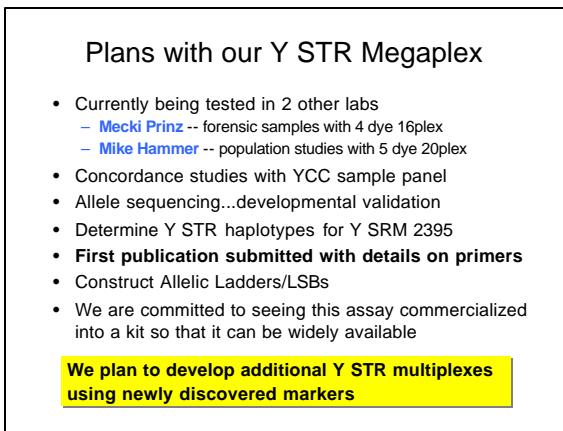
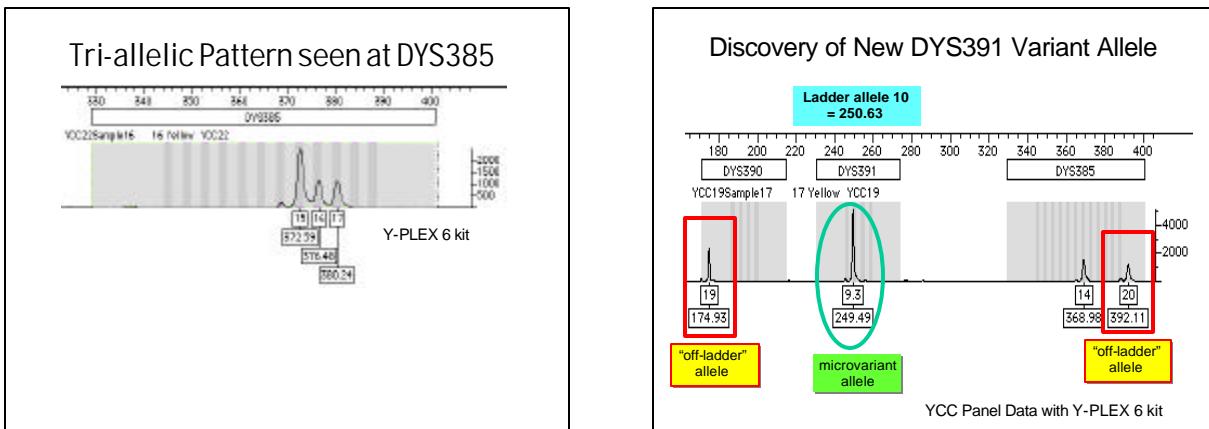


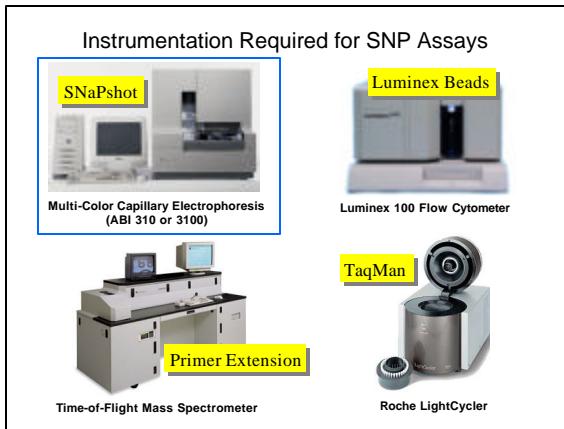
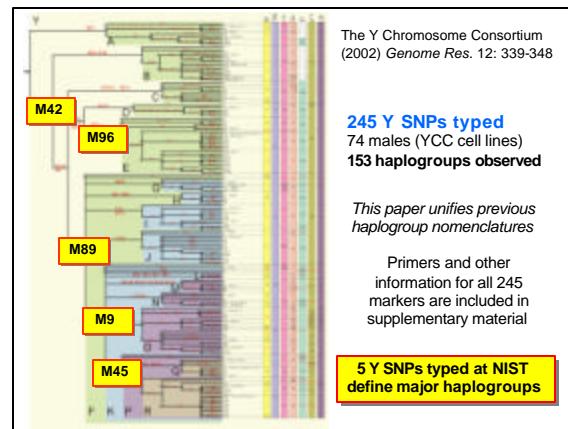
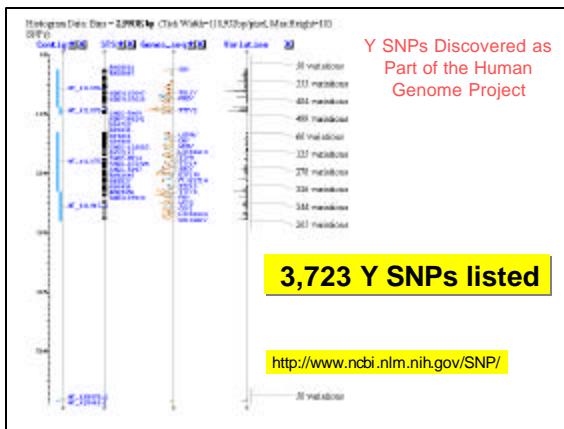
## Comparison of Various Primers on DYS19 and a Newly Discovered Duplicated Region of the Y Chromosome





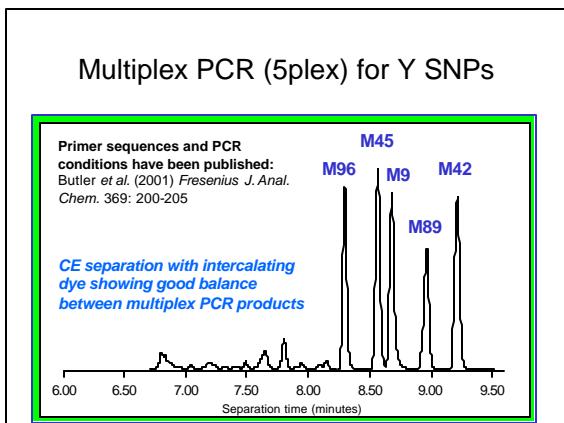






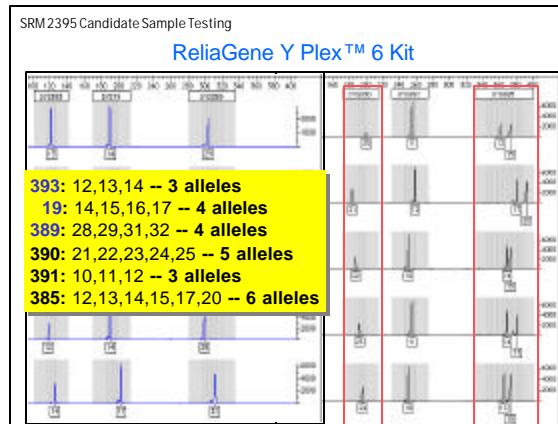
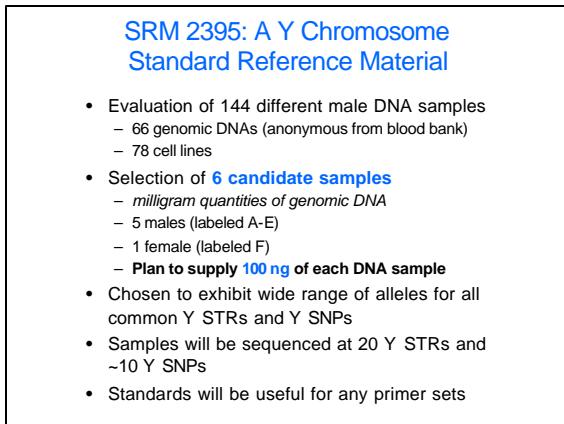
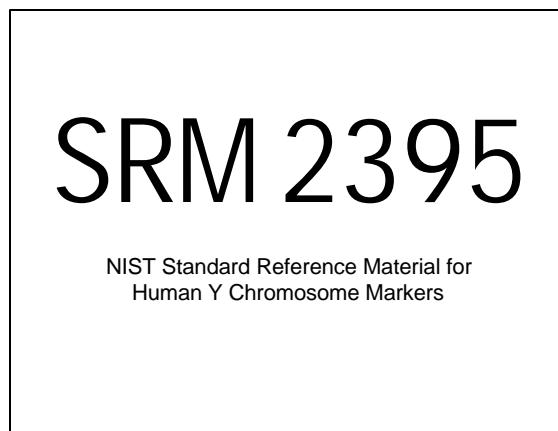
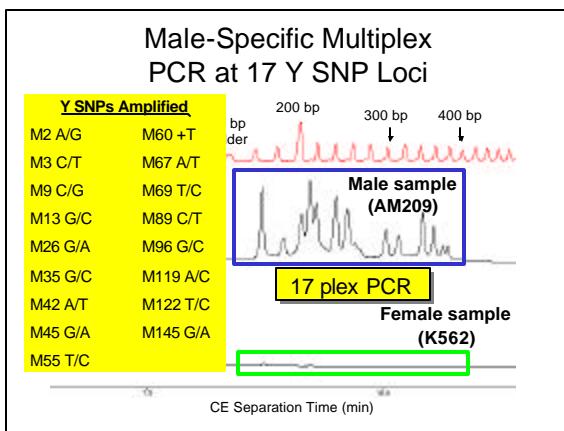
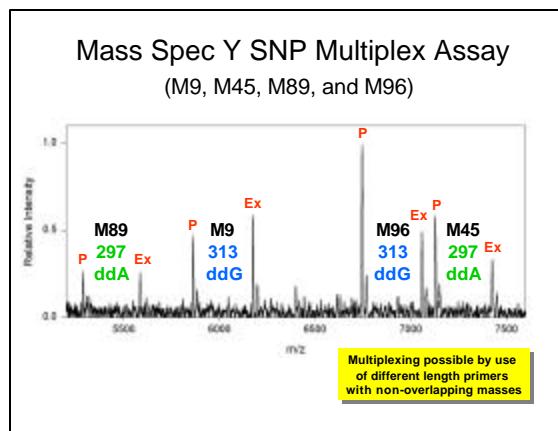
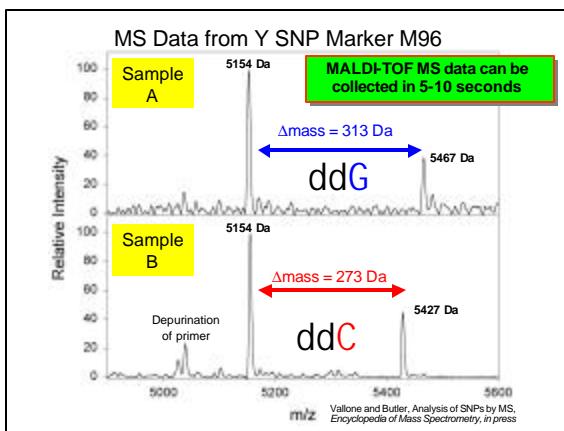
Approach to Y SNP Assays

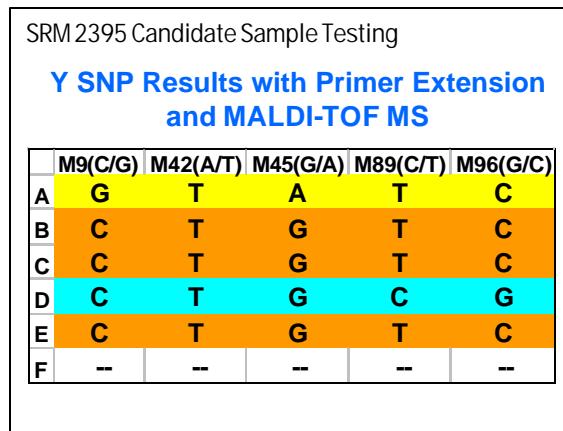
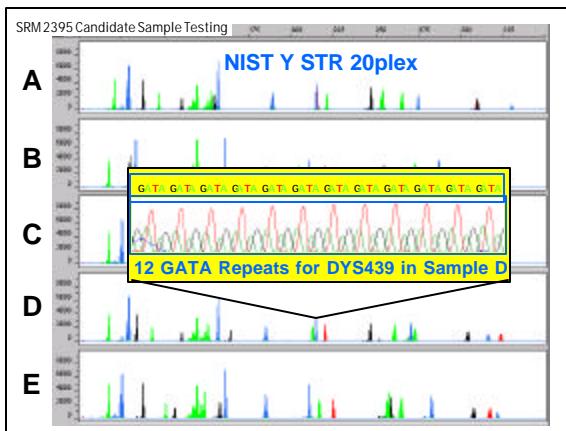
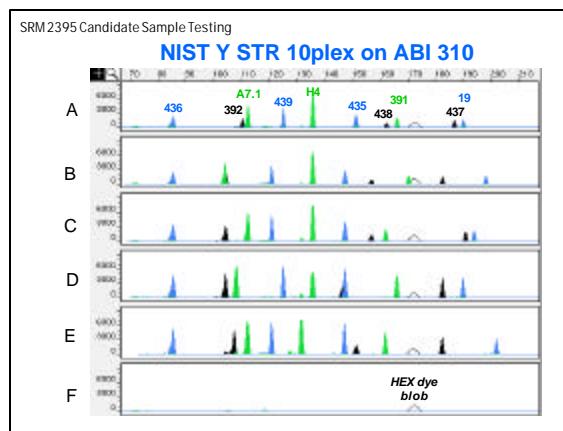
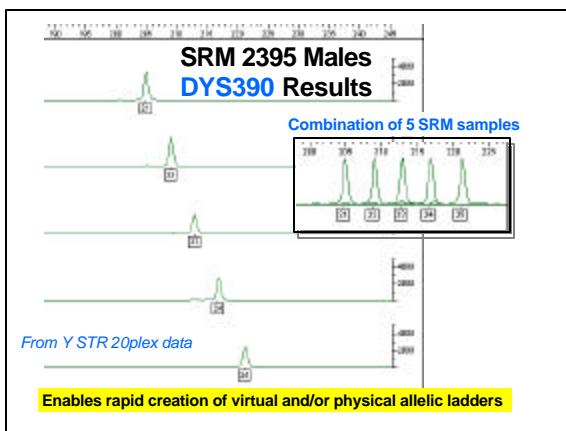
- Use branch-defining Y SNPs
- Develop multiplex PCR with optimized markers
  - M96, M42, M45, M9, M89
  - Recent *Genome Research* paper spells out best markers against the YCC panel
- Develop 10-20plex Y SNP panel with SNaPshot and mass spec approaches
  - 9plex PCR and 10plex SNaPshot assay already demonstrated with coding region mtDNA markers
  - 10plex mass spec assay from control region mtDNA following amplification of entire D-loop



Y SNP Results for 16 Standard 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	-	-	-	-	-





### Summary of Y Chromosome Work at NIST

- We are standardizing information on Y chromosome markers and making it available through **STRBase**
- We are developing new Y STR multiplex assays (**Y STR 20plex** and **Y STR 10plex**)
- We are evaluating SNP typing methodologies and developing **Y SNP assays** involving primer extension
- We are developing a Y Chromosome Standard Reference Material (**SRM 2395**)

### Acknowledgments



#### Funding:

National Institute of Justice Grant #97-LB-VX-0003

Interagency Agreement between NIJ and NIST Office of Law Enforcement Standards

#### NIST Personnel:

John Butler (Project Leader)

Pete Vallone

Margaret Kline

Jan Redman

Rich Schoske (AU)

Gordon Spangler (AU)

Christian Ruitberg (RPI)

Dave Duewer (Anal. Chem.)

#### Collaborators:

Mike Hammer and Alan Redd (U. Arizona) for Y STR sequences and samples

Mecki Prinz (NYC OCME)

Dave Carlson (Marilgen) on Y SNP work with Luminex beads

Human Genome Project participants (Jim Kent-UCSC)