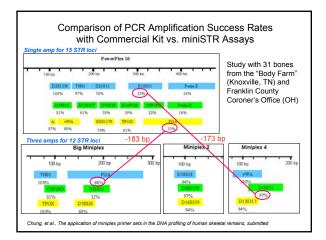
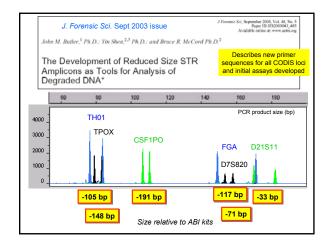


February 20, 2004





Reduc	tion in PCR Product Size
Locus TH01 FGA	Size Difference (relative to ABI kits) -105 bp -71 bp
CSF1PO	-191 bp
D21S11 TPOX	-33 bp -148 bp
D7S820	-117 bp
	Not as much size reduction as other STR loci

How C	los	se Can a Stable Pri STR Repeat	mer be Designed to the Region?
Locus		Distance 3'end from Repeat	Comment
CSF1PO	F	14	partial repeat just 5' of repeat
	R	6	
FGA	F	~	
	R	(23)	partial repeat just 3' of repeat
TH01	F		
	R	1	
TPOX	F	-4	
	R	5	
VWA	F	0	
	R	0	
D3S1358	F	-1	
	R	-1	
D5S818	F	4	
	R	-5	
D7S820	F	<u>A</u>	
	R	(65)	polyA stretch just 3' of repeat

STR Locus	GenBank Accession	GenBank Allele	Allele Range	Allele Spread
CSF1PO	X14720	12	6-16	40 bp
FGA	M64982	21	12.2-51.2	156 bp
TH01	D00269	9	3-14	44 bp
TPOX	M68651	11	5-14	36 bp
vWA	M25858	18	10-25	60 bp
D3S1358	NT_005997	18	8-20	48 bp
D5S818	AC008512	11	7-16	36 bp
D7S820	AC004848	13	5-15	40 bp
D8S1179	AF216671	13	7-19	48 bp
D13S317	AL353628	11	5-16	44 bp
D16S539	AC024591	11	5-15	40 br
D18S51	AP001534	18	7-27	80 bp
D21S11	AP000433	29	24-38.2	58 bp
Penta D	AP001752	13	2.2-17	73 bp
Penta E	AC027004	5	5-24	95 bp
D2S1338	AC010136	20	15-28	52 bp

Why go beyond CODIS loci

"STRs have proven to be highly successful [for mass disasters] in the past e.g. Waco disaster and various air disasters. However, even if the DNA is high quality there are occasions when there are insufficient family members available to achieve a high level of confidence with an association."

Gill, P., Werrett, D.J., Budowle, B. and Guerrieri, R. (2004) An assessment of whether SNPs will replace STRs in national DNA databases-Joint considerations of the DNA working group of the European Network of Forensis Science Institutes (ENFS) and the Scientific Working Group on DNA Analysis Methods (SWGDAM). Science&Justice, 44(1), in press.

Why go beyond CODIS loci

"To achieve this purpose, either new STRs could be developed, or alternatively, existing STRs could be supplemented with a SNP panel."

"There also efforts for modifying existing STR panels by decreasing the size amplicons by designing new primers."

Gill, P., Werrett, D.J., Budowle, B. and Guerrieri, R. (2004) An assessment of whether SNPs will replace STRs in national DNA databases-Joint considerations of the DNA working group of the European Network of Forensis Csicnee hstltutes (ENFS) and the Scientific Working Group on DNA Analysis Methods (SWGDAM). Science&Justice, 44(1), in press.

Why go beyond CODIS loci

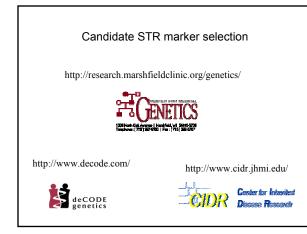
- Desirable to have markers unlinked from CODIS loci (different chromosomes) for some applications
- Small size ranges to aid amplification from degraded DNA samples

Characterization of New miniSTR Loci

- Candidate STR marker selection
- · Chromosomal locations and marker characteristics
- · PCR primer design
- · Initial testing results
- · Population testing
- · Allelic ladder construction
- · Miniplex assay performance

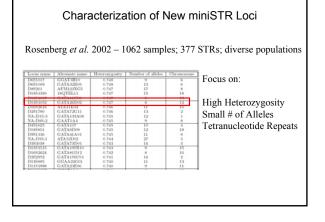
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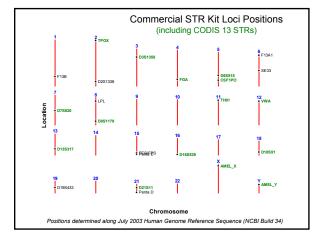
	SCIENCE VOL 298 20 DECEMBER 2002
	Genetic Structure
	of Human Populations
	Noah A. Rosenberg, ¹⁺ Jonathan K. Pritchard, ² James L. Weber, ³ Howard M. Cann, ⁴ Kenneth K. Kidd, ³ Lev A. Zhivotovsky, ⁶ Marcus W. Feldman ²
I: Am J Phys Ar	affropol. 2003 Nov;122(3):259-68. Redain Anders, Links
A PROPERTY OF A	tion of human evolutionary tree using polymorphic autosomal microsatellites.
	soor A, Ismail M, Khaliq S, Mohyuddin A, Hameed A, Mazhar K, Rehman S, Siddiqi S, Papaioannou M, valli-Sforza I, L., Mehdi SQ.

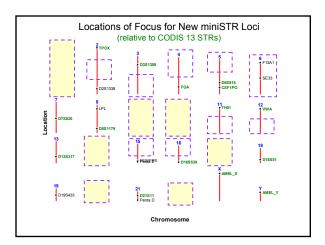
Rosent	oerg et al.	2002 - 1	062 sampl	les; 377	STRs; diverse population
Locus name D6S1017	Alternate name CCAT3H10	Heterozygosity 0.748	Number of alleles	Chromosome	Focus on:
D681017 D681009	GGAT3H10 GATA32B03	0.748	13	2	rocus on.
D88261	AFM123XG5	0.745	13		
D18S1390	18QTEL11	0.747	15	18	
D13S1807	GATA11C08	0.747	9	13	
D1251052	GATA26D02	0.747	8	12	High Heterozygosity
D1682616	ATA41E04	0.746	11	16	
D2S1780	GATA72G11	0.746	13	2	Small # of Alleles
NA-D18-3 NA-D88-2	GATA133A08 GAAT1A4	0.745	12	1	Sman # Of Ancies
D481625	GATA107	0.745	9	8	Totronualaatida Danaat
D18S851	GATA6D09	0.745	12	18	Tetranucleotide Repeat
D8S1136	GATA41A01	0.745	11	8	
NA-D58-1	ATA52D02	0.744	27	5	
D353038	GATA73D01	0.743	14	3	
D1581515	GATA197B10	0.743	9	15	1
D16S2624 D2S2972	GATA81D12 GATA176C01	0.742	8 14	16	
D13S895	GGAA22C01	0.741	14	13	
D1151998	CATA23E06	0.740	9	11	
		0.140			4



Characterization of New miniSTR Loci

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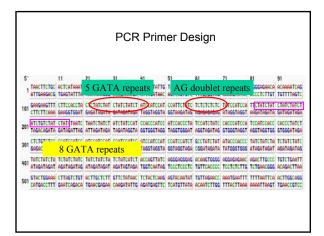


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5'		11	21	31	41	51	61	71	81	91
1	TARCTTCTGC ATTGRAGACS	ACTCATAAAT TGAGTATTTA	ATTATTTCCC TRATARAGGG	TGTCTTTGCT ACAGARACGA	TRAGCTATTG ATTCGATARC	TCRGTCRCRG RGTCRGTGTC	ARGCTCCATC TTCGAGGTAG	TTTTCATATG RARAGTATAC	TGSGAGAACA ACCCTCTTGT	ACAAAATCAG
101	GARGARGTTT	CTTCCACCTA GRAGGTGGAT	CTCTATCTAT GRGATAGATA		ATCCATCCAT TAGGTAGGTA	CCATTCTATC GGTAAGATAG	TCTCTCTCTC RGRGRGRGRG	TATCCATCCA ATAGGTAGGT	TICTATCTAT REGATEGATE	CTATCTATCT
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381	CTCTCTCTCTC GRGRC	8 GAT	А гере			CCATCCATCT GGTAGGTAGA		ATACCCACCC TATEGETEES	TATCTATCTA ATAGATAGAT	TCTATCTATC AGATAGATAG
401	TATCTATCTA ATAGATAGAT	TCTATCTATC AGATAGATAG	TATCTATCTA	TCTATCATCT	ACCAGTTATC TGGTCAATAG				AGACTTGCCC TCTGAACGGG	TETCTERAT
581	GTACTEGAAA CATGACCTTT	CTTRETCTET GRATCAGACA	ACTTECTCTT TERACEAGAA	GTTCTATAAC CRAGATATTG					TTTTRATTCR RARATTRAGT	

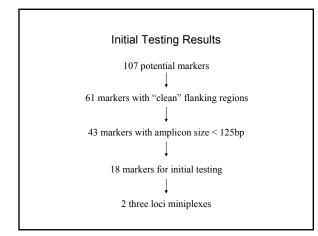


				PCR Primer Design					D2S441		
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101	GAAGAGATTC CTTCTCTAAG	TTAAGACCCA Aattctgggt	CGGCCAGAAA GCCGGTCTTT	GTTGGGTAAA Caacccattt	GACTAGAGTC CTGATCTCAG		GCAGGTGAAA Cgtccacttt	GGAGTGCAAG CCTCACGTTC		AGAGATTCT TCTCTAAGA	
201	TTCCTGAGCC AAGGACTCGG	CTAATGCACC Gattacgtgg	CAACATTCTA GTTGTAAGAT	ACAAAAGGCT Tgttttccga	GTAACAAGGG Cattgttccc		CATGAGCCAG Gtactcggtc		TCATCTATGA Agtagatact	AAACTTCTA TTTGAAGAT	
301	CTATCTATCT Gatagataga				CTATATCATA Gatatagtat			CAATTTAAAA Gttaaatttt	GATTAATCAT Ctaattagta		
401	GAAGGAGAGT CTTCCTCTCA	GAAGATTTTT Cttctaaaaa	GTGATGTTAA Cactacaatt	ATAAGAATGA Tattcttact	TTATACTAAA Aatatgattt		ATATGTTATT Tatacaataa		TGTGGTGGCT Acaccaccga		
501	ATCCCAGAAC TAGGGTCTTG	TTTGGGAGGC AAACCCTCCG	CAAGGCTTGT GTTCCGAACA	GGATCACTTG CCTAGTGAAC	AGCCCAGAAG TCGGGTCTTC		GCCTGGGCAA CGGACCCGTT			ACAAAAAAT Tgttttta	

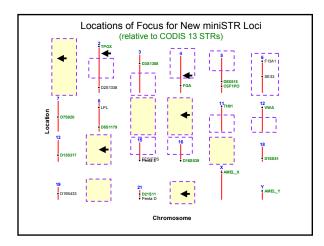
				PCR	Prime	er Des	sign		D2S4	41
5'		11	21	31	41	51	61	71	81	91
1	CAGCTATACA GTCGATATGT	GAAGCTTCCT CTTCGAAGGA	GAACCCAGTC CTTGGGTCAG	CTCTTGGGGT Gagaacccca	TTGAGGGAAG Aactcccttc		TCAGCATTCC AgtCgtaagg	TTCCTCCAGG AAGGAGGTCC	GTATTAATGG Cataattacc	
101	GAAGAGATTC Cttctctaag			otteeetooo <mark>op A</mark>			ACAGETGAAA Actit		AGAAGGTAAG TCTTCCATTC	
201	TTCCTGAGCC AAGGACTCGG		v00v011v10	NYDDDDWWY	MINNYNNWW	VINVNMNNI	GTACTCGGTC		TCATCTATGA Agtagatact	
301							CACTTAGCTC GTGAATCGAG			
401	GAAGGAGAGT CTTCCTCTCA	GAAGATTTTT Cttctaaaaa	GTGATGTTAA Cactacaatt				ATATGTTATT Tatacaataa			TAAGCCTGTI Attcggaca
501	ATCCCAGAAC Tagggtcttg	TTTGGGAGGC AAACCCTCCG	CAAGGCTTGT GTTCCGAACA	GGATCACTTG CCTAGTGAAC			GCCTGGGCAA CGGACCCGTT			ACAAAAAAT Tgtttttai

Characterization of New miniSTR Loci Candidate STR marker selection Chromosomal locations and marker characteristics PCR primer design Initial testing results Population testing Allelic ladder construction Miniplex assay performance

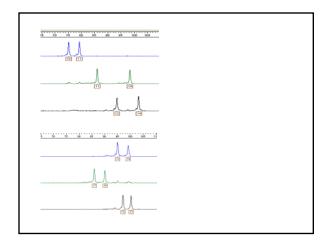
M.D. Coble Talk at AAFS, Dallas, TX

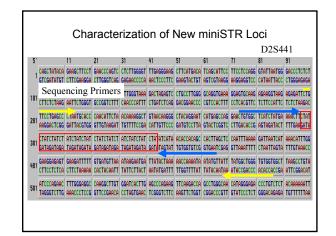


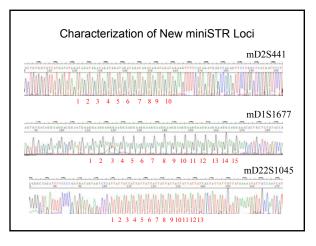
Initial Testing Results	
Miniplex01- mD10S1248 - FAM mD14S1434 - VIC mD22S1045 - NED	
Miniplex02- mD4S2364 - FAM mD2S441 - VIC mD1S1677 - NED	

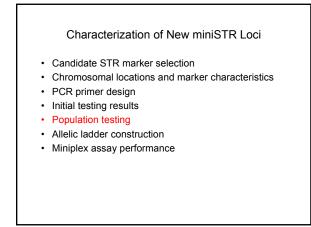


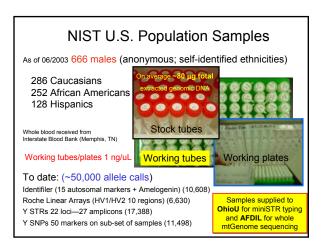
0					miniSTR		
		Allele Size		Ref.	Primer distance	Amplicon	1
Marker Name	Het	Range	(Motif)	Repeat	from repeat	Size	
D10S1248	0.77	20 bp	TETRA	13	1	102	
GGAA23C05N		00	GGAA		0		1
D1461424	0.72	20 hn	TETDA	10	1	00	Miniplex01
GATA168F06	0.72	20 DP	GATA	10	0	00	
	0.77	18 bp		13		105	
A1A37D06			AIA		6		
D1S1677	0.74	35 bp	TETRA	15	0	103	
GGAA22G10N			GGAA		0		
D2S441	0 74	18 bn	TETRA	12	0	92	Miniplex02
GATA8F03	0.74	op	GATA	12	0	52	minpiex
				_			
D4S2364	0.64	18 bp	TETRA	7	2	78	
	D10S1248 GGA23C05N D14S1434 GATA168F06 D22S1045 ATA37D06 D1S1677 GGAA22G10N D2S441 GATA8F03	D1051248 0.77 GGAA23C05N 0.72 D14S1434 0.72 GATA168F06 0.77 ATA37D06 0.74 GGAA22G10N 0.74 D2S441 0.74 GATA8F03 0.74	Marker Name Het Rance D1051248 0.77 20 bp GGAA23C05N 0.77 20 bp D1451434 0.72 20 bp GATA168F06 0.77 18 bp D1551545 0.77 18 bp GGAA23C010N 0.74 35 bp GGAA23C010N 0.74 18 bp D25441 0.74 18 bp	Marker Name Hat Rance (Motif) D1051248 0.77 20 bp TETRA GGAA23C05N 0.72 20 bp TETRA GGAA23C05N 0.72 20 bp TETRA GATA168F06 0.72 20 bp TETRA GATA37D06 0.77 18 bp TRI ATA37D06 0.74 35 bp TETRA GGAA22G10N 0.74 18 bp TETRA GATA8F03 0.74 18 bp TETRA GATA8F03 0.74 18 bp TETRA	Markar Nama Hat Bance (Motif) Raseat D1081248 0.77 20 bp TETRA 13 GGAA23005N GGAA GGAA GGAA D1481434 0.72 20 bp TETRA 10 GATA168F06 0.72 20 bp TETRA 10 GATA158F06 0.72 18 bp TRI 13 ATA37006 0.74 35 bp TETRA 15 GGAA2GTON 0.74 18 bp TETRA 15 D28441 0.74 18 bp TETRA 12 GATA8F03 0.74 18 bp TETRA 12	Marker Name Het Ranse /Motifi Repeat from repeat D1051248 0.77 20 bp TETRA 13 0 GGAA32005N 0.72 20 bp TETRA 13 0 D1451434 0.72 20 bp TETRA 10 1 GATA168F06 0.72 20 bp TETRA 10 1 GATA168F06 0.72 20 bp TETRA 10 1 GATA169F06 0.77 18 bp TRI 13 3 ATA37006 74 35 bp TETRA 15 0 GGAA22GT00 0.74 18 bp TETRA 12 0 D2S411 0.74 18 bp TETRA 12 0 GATA8F03 0 GATA 0 0 0	Markar Nama Hat Banace /Motifi Repeat from repeat Size D1051248 0.77 20 bp TETRA 13 1 102 GGAA32005N 0.77 20 bp TETRA 13 0 102 D16151248 0.77 20 bp TETRA 10 1 88 GATA168F06 0.77 20 bp TETRA 10 1 88 D2551045 0.77 18 bp TRI 13 3 105 ATA37006 74 35 bp TETRA 15 0 0 D25410 0.74 18 bp TETRA 12 0 92 GATA8F03 0.74 18 bp TETRA 12 0 92

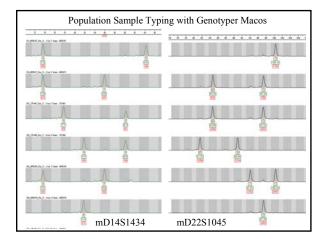


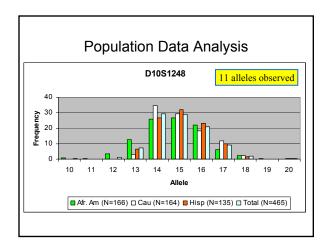


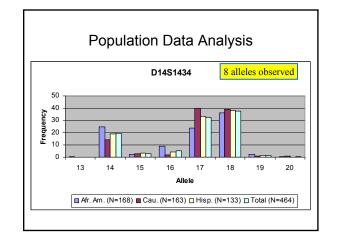


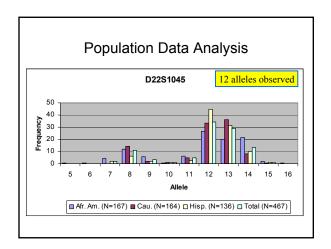








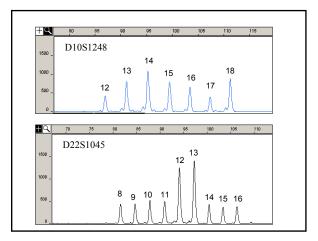




Loci	Heterozygosity	
D18S51	0.914	
FGA	0.886	
D21S1338	0.871	N = 140 Hispanics (Identifiler)
D7S820	0.864	,
VWA	0.850	
D2S1338	0.843	N = 135 Hispanics (Mini01)
D13S317	0.843	1
D16S539	0.793	
D8S1179	0.786	
D19S433	0.764	
THO1	0.764	
D3S1358	0.757	
CSF1PO	0.743	
D10S1248	0.733	
D5S818	0.729	
D22S1045	0.721	
TPOX	0.679	
D14S1434	0.662	

Characterization of New miniSTR Loci

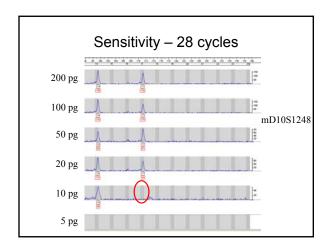
- Candidate STR marker selection
- · Chromosomal locations and marker characteristics
- PCR primer design
- · Initial testing results
- · Population testing
- Allelic ladder construction
- · Miniplex assay performance

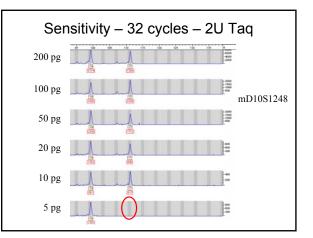


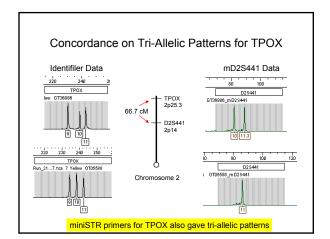
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11 Highwat peak at 97.00 t 0.00 t	cros for analysis
12 Highest peak at 91.00 t 0.00 bp in blue Dav 13 Highest peak at 91.00 t 0.00 bp in blue 100 bp in blue 14 Highest peak at 100.00 t 0.00 bp in blue 100 bp in blue 15 Highest peak at 100.00 t 0.00 bp in blue 100 bp in blue 15 Highest peak at 100.00 t 0.00 bp in blue 100 bp in blue 17 Highest peak at 111.00 t 0.00 bp in blue 100 bp in blue 19 Highest peak at 112.00 t 0.00 bp in blue 100 bp in green 19 Highest peak at 72.00 t 1.00 bp in green 100 bp in green 14 Highest peak at 92.00 t 1.00 bp in green 100 bp in green 18 Highest peak at 97.00 t 1.00 bp in green 100 bp in green 19 Highest peak at 97.00 t 1.00 bp in green 100 bp in green 19 Highest peak at 97.00 t 1.00 bp in green 100 bp in green 19 Highest peak at 97.00 t 1.00 bp in green 100 bp in green 19 Highest peak at 97.00 t 1.00 bp in green 100 bp in green <	cros for unarysis
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14 Highest peak at 99.0 f 0.0 f </td <td>e been developed</td>	e been developed
15 Highest peak at 100.0 t 0.0 to bit bit 19 Highest peak at 100.0 t 0.0 to bit bit 19 Highest peak at 110.0 t 0.0 to bit bit 18 Highest peak at 110.0 t 0.0 to bit bit 19 Highest peak at 110.0 t 0.0 to bit bit 20 Highest peak at 121.0 t 0.0 to bit bit 21 Highest peak at 121.0 t 1.00 to t pit 24 Highest peak at 72.0 t 1.00 to t pit green 14 Highest peak at 74.0 t 1.00 to t pit green 15 Highest peak at 97.0 t 1.00 to t pit green 14 Highest peak at 99.0 t 1.00 to t pit green 17 Highest peak at 99.0 t 1.00 to t green green 10 Highest peak at 99.0 t 1.00 to t green green 10 Highest peak at 99.0 t 1.00 to t green green 10 Highest peak at 99.0 t 1.00	
16 Highest peak at 107:00 ± 0.60 bp in blue 17 Highest peak at 115:00 ± 0.60 bp in blue 18 Highest peak at 115:00 ± 0.60 bp in blue 19 Highest peak at 115:00 ± 0.60 bp in blue 10 Highest peak at 123:00 ± 0.60 bp in blue 10 Highest peak at 123:00 ± 0.60 bp in blue 14 Highest peak at 70:40 ± 1.00 bp in green 14 Highest peak at 70:40 ± 1.00 bp in green 15 Highest peak at 70:20 ± 1.00 bp in green 16 Highest peak at 80:00 ± 1.00 bp in green 17 Highest peak at 90:00 ± 1.00 bp in green 18 Highest peak at 90:00 ± 1.00 bp in green 19 Highest peak at 97:70 ± 1.00 bp in green 20 Highest peak at 77:70 ± 1.00 bp in green 21 Highest peak at 77:70 ± 1.00 bp in green 220 Highest peak at 97:70 ± 1.00 bp in green 21 Highest peak at 97:70 ± 1.00 bp in green 220 Highest peak at 97:50 ± 1.00 bp in green	
17 Highest peak at 111.00 ± 0.60 bp in blue 18 Highest peak at 111.00 ± 0.60 bp in blue 10 Highest peak at 115.00 ± 0.60 bp in blue 10 Highest peak at 115.00 ± 0.60 bp in blue 10 Highest peak at 123.00 ± 0.60 bp in blue 13 Highest peak at 70.00 ± 1.00 bp in green 14 Highest peak at 70.20 ± 1.00 bp in green 15 Highest peak at 70.20 ± 1.00 bp in green 16 Highest peak at 70.20 ± 1.00 bp in green 17 Highest peak at 70.00 ± 1.00 bp in green 18 Highest peak at 90.00 ± 1.00 bp in green 19 Highest peak at 90.00 ± 1.00 bp in green 20 Highest peak at 90.00 ± 1.00 bp in green 21 Highest peak at 77.50 ± 1.00 bp in green 220 Highest peak at 77.50 ± 1.00 bp in yellow 06 Highest peak at 77.50 ± 1.00 bp in yellow 07 Highest peak at 88.70 ± 1.00 bp in yellow 08 Highest peak at 98.70 ± 1.00 bp in yellow <td></td>	
10 Highest peak at 115 00 ± 0.60 bp in blue 10 Highest peak at 115 00 ± 0.60 bp in blue 10 Highest peak at 123 00 ± 0.60 bp in blue 14 Highest peak at 123 00 ± 0.60 bp in blue 14 Highest peak at 74 00 ± 1.00 bp in green 14 Highest peak at 74 10 ± 1.00 bp in green 14 Highest peak at 90 ± 1.00 bp in green 14 Highest peak at 90 ± 1.00 bp in green 15 Highest peak at 90 ± 1.00 bp in green 16 Highest peak at 90 ± 1.00 bp in green 17 Highest peak at 90 ± 1.00 bp in green 18 Highest peak at 97 .00 ± 1.00 bp in green 19 Highest peak at 97 .00 ± 1.00 bp in green 10 Highest peak at 97 .00 ± 1.00 bp in yellow 05 Highest peak at 97 .00 ± 1.00 bp in yellow 06 Highest peak at 87 .00 ± 1.00 bp in yellow 07 Highest peak at 87 .00 ± 1.00 bp in yellow 08 Highest peak at 98 .00 ± 1.00 bp in yellow <	
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16 Highest peak at 02 10 ± 1.00 bp in green 17 Highest peak at 09.00 ± 1.00 bp in green 18 Highest peak at 09.00 ± 1.00 bp in green 10 Highest peak at 09.00 ± 1.00 bp in green 20 Highest peak at 09.00 ± 1.00 bp in green 223145 Highest peak at 07.00 ± 1.00 bp in green 223145 Highest peak at 07.00 ± 1.00 bp in yellow 06 Highest peak at 08.00 ± 1.00 bp in yellow 07 Highest peak at 08.00 ± 1.00 bp in yellow 00 Highest peak at 07.00 ± 1.00 bp in yellow 01 Highest peak at 07.00 ± 1.00 bp in yellow 11 Highest peak at 97.00 ± 1.00 bp in yellow 12 Highest peak at 97.00 ± 1.00 bp in yellow	
17 Hishbest peak at 06.00 ± 1.00 bp in green 19 Hishbest peak at 09.00 ± 1.00 bp in green 20 Hishbest peak at 09.70 ± 1.00 bp in green 20 Hishbest peak at 09.70 ± 1.00 bp in green 20 Hishbest peak at 09.70 ± 1.00 bp in green 20 Hishbest peak at 75.40 ± 1.00 bp in green 21045 Hishbest peak at 75.40 ± 1.00 bp in green 20 Hishbest peak at 75.40 ± 1.00 bp in green 21045 Hishbest peak at 07.40 ± 1.00 bp in green 20 Hishbest peak at 08.70 ± 1.00 bp in green 21045 Hishbest peak at 08.70 ± 1.00 bp in green 211 Hishbest peak at 98.70 ± 1.00 bp in green 212 Hishbest peak at 97.00 ± 1.00 bp in green 213 Hishbest peak at 97.00 ± 1.00 bp in green 214 Hishbest peak at 97.00 ± 1.00 bp in green	
10 Highest peak at 09.0 t 1.00 bpi in green 21 Highest peak at 99.0 t 1.00 bpi in green 20 Highest peak at 97.0 t 1.00 bpi in green 20 Highest peak at 97.0 t 1.00 bpi in green 20 Highest peak at 77.0 t 1.00 bpi in green 06 Highest peak at 78.0 t 1.00 bpi in yellow 07 Highest peak at 87.0 t 1.00 bpi in yellow 08 Highest peak at 97.0 t 1.00 bpi in yellow 09 Highest peak at 97.0 t 1.00 bpi in yellow 11 Highest peak at 97.0 t 1.00 bpi in yellow 12 Highest peak at 97.0 t 1.00 bpi in yellow	
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15 Highest peak at 106.40 ± 1.00 bp in yellow 16 Highest peak at 109.50 ± 1.00 bp in yellow	

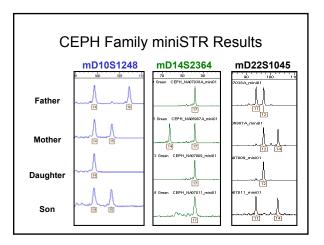
Characterization of New miniSTR Loci

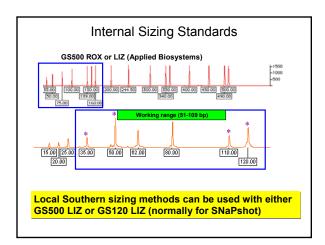
- Candidate STR marker selection
- · Chromosomal locations and marker characteristics
- PCR primer design
- Initial testing results
- · Population testing
- Allelic ladder construction
- Miniplex assay performance
 - Sensitivity
 - Inheritance with family samples
 - Allele sizing precision
 - Locus stutter percentage characterization
 - Analysis on real-world samples

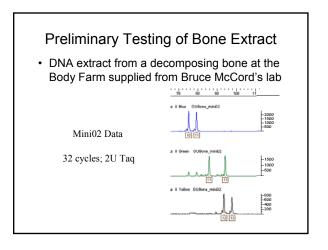












M.D. Coble Talk at AAFS, Dallas, TX

February 20, 2004

"STR typing of human telogen hairs -a new approach"

- Hellmann, *et al.* (2001) *Int. J. Legal Med.* 114(4-5): 269-273
- Primer pairs with annealing positions close to the repeat units of the STR loci FES/FPS, TPOX, and TH01 were used for amplification.
- Shed telogen hairs could be typed!

Future Plans Testing and characterization of more markers. Population Databasing. Testing on degraded materials. Information will be posted on STRBase website and published as these loci are characterized We would welcome collaborations with those wishing to

test some of these new miniSTR systems

