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Characterization and Performance of New Mini-STR Loci for Typing Degraded DNA

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21st Congress of the International Society for Forensic Genetics
 Portugal - Ponta Delgada, Azores
 14 September 2005

A miniSTR is a reduced size STR amplicon that enables higher recovery of information from degraded DNA samples

Testing must be performed to show allele concordance between primer sets

Conventional STR test (COfiler™ kit)

MiniSTR assay (using Butler et al. 2003 primers)

Butler, J.M. (2005) *Forensic DNA Typing, 2nd Edition*, Figure 7.2, ©Elsevier Science/Academic Press

Why Go Beyond the CODIS Loci?

(1) Large Allele Ranges (e.g. FGA)

(2) "Unclean" Flanking Sequences

Locus	Distance 3' end from Repeat	Comment
D7S820	F 4	
	R 65	polyA stretch just 3' of repeat
D18S51	F 5	
	R 33	partial repeat just 3' to repeat

Butler, J.M., Shen, Y., McCord, B.R. (2003) *JFS* 48(8): 1054-1064

Initial Testing Results with Potential miniSTR Loci

Under investigation currently

Coble and Butler (2005) *J. Forensic Sci.* 50(1): 43-53

Miniplex "NC01"

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

Coble and Butler (2005) Characterization of new miniSTR loci to aid analysis of degraded DNA *J. Forensic Sci.* 50(1): 43-53

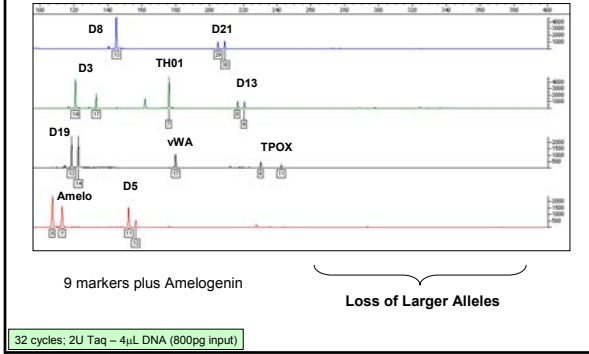
MiniSTR performance on degraded DNA samples

Blood Stain – 2 Weeks

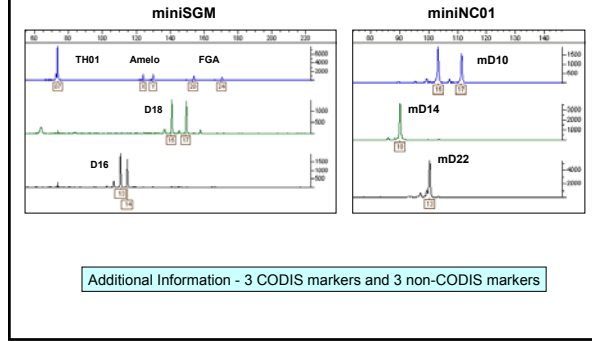
Allelic drop out at D16 and FGA
 Failure at D18

EDNAP/ENFSI Degraded DNA Study – Fall 2004
 Dixon et al., manuscript submitted

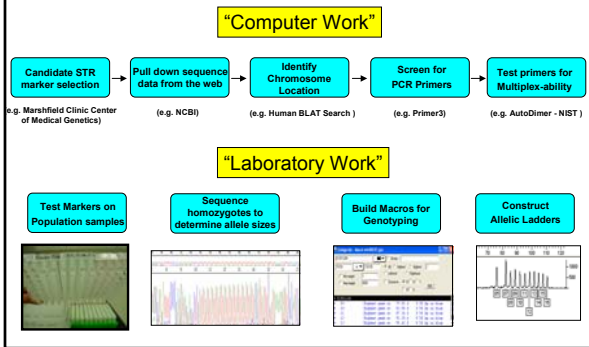
Previous Work with Shed Hairs –
AAFS Talk Feb. 2005



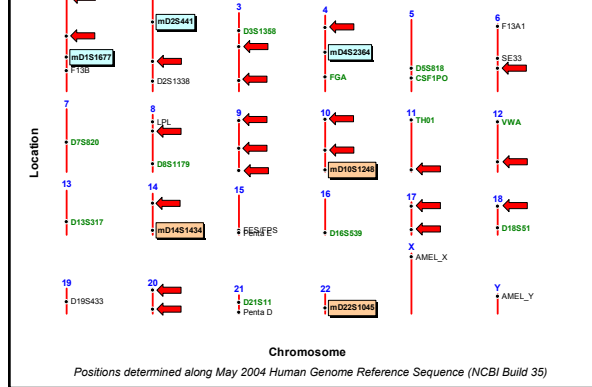
Previous Work with Shed Hairs –
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Characterization of New miniSTR Loci



STR Loci Positions
(including CODIS 13 STRs)



10 New Non-CODIS MiniSTRs

We are in the process of developing 27 loci

Candidate Marker	Repeat Type	Obs. Allele Range	Allele Size Range (bp)	Observed Heterozygosity		
				Caucasian (n = 262)	African Am. (n = 260)	Hispanic (n = 140)
D3S3053	Tetra	8 - 14	84 - 108	0.724	0.713	0.814
D6S474	Tetra	11 - 18	107 - 135	0.802	0.765	0.679
D20S482	Tetra	9 - 19	86 - 126	0.689	0.673	0.729
D1Sa	Tetra	7 - 13	81 - 105	0.632	0.673	0.727
D1Sb	Tri	10 - 16	81 - 99	0.737	0.783	0.693
D2Sa	Tetra	6 - 14	127 - 161	0.801	0.740	0.734
D3Sa	Tetra	12 - 19	111 - 139	0.723	0.752	0.829
D4Sa	Tetra	7 - 13	85 - 109	0.709	0.752	0.691
D9Sa	Tetra	9 - 17	93 - 125	0.742	0.753	0.686
D12Sa	Tri	10 - 20	76 - 106	0.842	0.788	0.879

NC03

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

NC03 Allelic Ladders

