Dinucleotide repeat polymorphisms at the DXS453, DXS454 and DXS458 loci

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Source/Description: Human genomic DNA fragments were cloned into m13 and selected by hybridization to poly(dC-dA)·poly(dG-dT). Sequencing of the clones provided the information necessary for polymerase chain reaction primer synthesis.

Locus	Clone <u>Designation</u>	Clone <u>Length</u>	Predicted Len of Amplified <u>Fragment</u>		
DXS453	Mfd66	>235 bp	170 bp		CA strand) GT strand)
DXS454	Mfd72	387 bp	145 bp		CA strand) GT strand)
DXS458	Mfd79	300 bp	186 bp	GATAAAACTGCATAGAAATGCG CAACTGGGATATTGACATTG	(CA strand) (GT strand)

Frequency: Mfd66: Estimated from 87 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.63.

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Allele (bp)	Frequency	Allele (bp)	Frequency				
170	0.21	164	0.01				
168	0.48	160	0.12				
166	0.18						
Mfd72: Estimated from 73 chromosomes of unrelated CEPH							
family grandparents (Caucasians). PIC = 0.59 .							
		Allele (bp)					
152	0.07	146	0.49				
148	0.16	144	0.27				
Mfd79: Estimated from 103 chromosomes of unrelated CEPH							
family grandparents (Caucasians). PIC = 0.62 .							
Allele (bp)		Allele (bp)	Frequency				
190	0.05	182	0.08				
188	0.52	180	0.13				
186	0.20	178	0.01				
184	0.01						

Chromosomal Localization: Mfd66 was provisionally assigned to Xp11.23-q21.1, and Mfd72 and Mfd79 were both provisionally asigned to Xq21.1-q23 using DNA templates isolated from panels of chromosomal and subchromosomal somatic cell hybrids (1, 2).

Mendelian Inheritance: Co-cominant segregation of Mfd66, Mfd72, and Mfd79 were observed in 15, 14 and 1 two generation families respectively.

Other Comments: Conditions for the amplification reactions were as described (3) except that samples were processed through 27 temperature cycles consisting of 1 min at 94°, 2 min at 55° and 2 min at 72°. Sizes of the alleles were determined by comparison to mp8 DNA sequencing ladders. The most intense band on the autoradiographs for each allele was used to obtain allele sizes. The dinucleotide repeat sequence in Mfd66 was of the form $(AC)_{22}$, in Mfd72 $(AC)_{17}G(GA)_8$ and in Mfd79 $(AC)_{15}A$. All three sequences have been submitted to GenBank.

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