Dinucleotide repeat polymorphisms at the D8S85, D8S87, and D8S88 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 Designation	Clone Length	Predicted Length of Amplified Fragment		Primer Sequences
			Length	Fragment	
D8S85	Mfd18	203 bp	80 bp		AGCTATCATCACCCCTATAAAAT (CA strand) AGTTTAACCATGTCTCTCCCG (GT strand)
D8S87	Mfd39	266 bp	150 bp		GGGTGGTTGTAAATTAAAC (CA strand) TGTCAAATACTTAAGCACAG (GT strand)
D8S88	Mfd45	>285 bp	87 bp		TCCAGCAGAGAAAGGGTTAT (CA strand) GGCAAAGAGAACTCATCAGA (GT strand)

Frequency: Mfd18: Estimated from 116 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.69.

Allele (bp)	Frequency	Allele (bp)	Frequency
84	0.01	76	0.22
82	0.36	74	0.22
80	0.19		

Mfd39: Estimated from 96 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.65.

Allele (bp)	Frequency	Allele (bp)	Frequency
157	0.02	149	0.14
155	0.18	147	0.04
153	0.06	145	0.05
151	0.51		

Mfd45: Estimated from 120 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.82.

Allele (bp)	Frequency	Allele (bp)	Frequency
100	0.02	88	0.15
98	0.04	86	0.25
96	0.10	84	0.12
92	0.04	82	0.03
90	0.21	76	0.03

Chromosomal Localization: The three markers were assigned to chromosome 8 using DNA templates isolated from panels of somatic cell hybrids.

Mendelian Inheritance: Co-dominant segregation of Mfd18, Mfd39, and Mfd45 were observed in 15–19 two or three generation families.

Other Comments: Conditions for the amplification reactions were as described in the reference 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 and were the averages of the sizes of the GT-strand and CA-strand bands for Mfd18 and Mfd39, and the sizes of the most intense bands for Mfd45. The dinucleotide repeat sequence in Mfd18 was of the form (AC)₁₈, in Mfd39 (TC)₁₂TGTT(TC)₁₂(AC)₁₃. A(AC)₆, and in Mfd45 (CA)₂₀C. Sequences of all three clones have been submitted to GenBank.

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Reference: Weber, J.L. and May, P.E. (1989) *Am. J. Hum. Genet.* **44**, 388–396.

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