Dinucleotide repeat polymorphisms at the D7S435 and D7S440 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
D7S435	Mfd20	282 bp	132 bp	TTAAAATGTTGAAGGCATCTTC (CA strand) TTTGAGTAGGTGGCATCTCA (GT strand)
D7S440	Mfd50	317 bp	175 bp	ACATTCCTAAGACTTCCCAAT (CA strand) AGAGCATGCACCCCTGAATTG (GT strand)

Frequency: Mfd20: Estimated from 112 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.53.

Allele (bp)	Frequency	Allele (bp)	Frequency
134	0.01	126	0.57
132	0.27	122	0.03
128	0.12		

Mfd50: Estimated from 112 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.70.

Allele (bp)	Frequency	Allele (bp)	Frequency
191	0.02	181	0.02
189	0.13	179	0.04
187	0.23	177	0.04
185	0.04	175	0.44
183	0.03	169	0.01

Chromosomal Localization: Mfd20 and Mfd50 were assigned to chromosome 7 by using DNA templates isolated from panels of somatic cell hybrids.

Mendelian Inheritance: Co-dominant segregation of Mfd20 and Mfd50 was observed in 18 and 15 two or three generation families respectively.

Other Comments: Conditions for the amplification reactions were as described in the references 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 Mfd20, and the sizes of the most intense bands for Mfd50. The dinucleotide repeat sequence in Mfd20 was of the form (AC)₁₇, and in Mfd50 of the form (CA)₁₉. Sequences of both clones have been submitted to GenBank.

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Reference: 1) Weber, J.L. and May, P.E. (1989) *Am. J. Hum. Genet.* **44**, 388–396.

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