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Dinucleotide repeat polymorphisms at the D16S260, D16S261, D16S265, D16S266, and D16S267 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
D16S260	Mfd12	318 bp	234 bp	GGTTGAGATGCTGACATGC (CA strand) CAGGGTGGCTGTTATAATG (GT strand)
D16S265	Mfd23	178 bp	100 bp	CCAGACATGGCAGTCTCTA (CA strand) AGTCCTCTGTGCACTTTGT (GT strand)
D16S261	Mfd24	>185 bp	89 bp	AAGCTTGTATCTTTCTCAGG (CA strand) ATCTACCTTGGCTGTCATTG (GT strand)
D16S266	Mfd62	202 bp	101 bp	AGCTTTACAGATGAGACCAG (CA strand) CAGCCAATTTCTTGAGTCCG (GT strand)
D16S267	Mfd65	220 bp	153 bp	GCAAACCACAATGGAATGCA (CA strand) CTTTACTTCCTTTGCCTCAG (GT strand)

Frequency: Mfd12: Estimated from 152 chromosomes of unrelated CEPH family parents (Caucasians). PIC = 0.43.

Allele (bp)	Frequency	Allele (bp)	Frequency
240	0.01	236	0.58
238	0.04	234	0.37

Mfd23: Estimated from 104 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.75.

Allele (bp)	Frequency	Allele (bp)	Frequency
117	0.01	105	0.01
115	0.01	103	0.18
113	0.03	101	0.05
111	0.05	99	0.07
109	0.11	95	0.01
107	0.07	89	0.41

Mfd24: Estimated from 122 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.66.

Allele (bp)	Frequency	Allele (bp)	Frequency
100	0.01	94	0.40
98	0.07	92	0.25
96	0.25	88	0.02

Mfd62: Estimated from 118 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.54.

Allele (bp)	Frequency	Allele (bp)	Frequency
104	0.02	98	0.08
102	0.06	96	0.57
100	0.26	94	0.01

Mfd65: Estimated from 120 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.45.

Allele (bp)	Frequency	Allele (bp)	Frequency
170	0.01	166	0.21
168	0.12	154	0.67

Chromosomal Localization: All five markers were assigned to 16 using DNA templates isolated from panels of somatic cell hybrids.

Mendelian Inheritance: Segregation of Mfd12 was not tested. Co-dominant segregation of Mfd23–Mfd65 was observed in 15–18 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 Mfd12, Mfd23 and Mfd24, and the sizes of the most intense bands for Mfd62 and Mfd65. The dinucleotide repeat sequence in Mfd12 was of the form $(AC)_{11}$ $AT(AC)_8A$, in Mfd23 $(AC)_{20}$, in Mfd24 $(AC)_7AGAG(AC)_{14}A$, in Mfd62 $(AC)_{21}$, and in Mfd65 $(CA)_{14}C$. Sequences of the five 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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