Dinucleotide repeat polymorphism at the D15S87 locus

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Source/Description: A human genomic *Sau3AI* fragment was cloned into mp19 and selected by hybridization to poly(dC-dA)·poly(dG-dT). The cloned fragment was designated Mfd49. Sequencing of Mfd49 provided the information necessary for polymerase chain reaction primer synthesis. The clone length was >240 bp, and the predicted length of the amplified fragment was 87 bp.

Primer Sequences: GATAAATGCCAAACATGTTGT (CA strand); TGCTCTCAGGATTCCTCCA (GT strand).

Frequency: Estimated from 120 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.85.

Allele(bp)	Frequency	Allele(bp)	Frequency
98	0.01	86	0.15
96	0.02	84	0.14
94	0.03	82	0.07
92	0.05	80	0.23
90	0.09	78	0.08
88	0.13		

Chromosomal Localization: Assigned to chromosome 15 using DNA templates isolated from panels of somatic cell hybrids.

Mendelian Inheritance: Co-dominant segregation was observed in 15 two 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. The most intense band for each allele on the denaturing polyacrylamide gels was used to obtain allele size. The dinucleotide repeat sequence in Mfd49 was of the form (CA)₂₂. The sequence of Mfd49 has been submitted to GenBank.

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

Dinucleotide repeat polymorphisms at the D17S250 and D17S261 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
D17S250	Mfd15	261 bp	162 bp	GGAAGAATCAAAATAGACAAT (CA strand) GCTGGCCATATATATTTAAACC (GT strand)
D17S261	Mfd41	>293 bp	159 bp	CAGGTTCTGTCATAGGACTA (CA strand) TTCTGGAACCTACTCTCTGA (GT strand)

Frequency: Mfd15: Estimated from 112 chromosomes of unrelated CEPH family parents (Caucasians). PIC = 0.81.

Allele (bp)	Frequency	Allele (bp)	Frequency
169	0.01	159	0.08
167	0.05	157	0.16
165	0.05	155	0.12
163	0.05	153	0.32
161	0.04	151	0.12

Mfd41: Estimated from 116 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.44.

Allele (bp)	Frequency	Allele (bp)	Frequency
171	0.01	161	0.10
165	0.01	159	0.71
163	0.04	157	0.13

Chromosomal Localization: Mfd15 was assigned to 17q11.2-q12 and Mfd41 assigned to 17p12-p11.1 using DNA templates isolated from panels of chromosomal and subchromosomal somatic cell hybrids (1–3).

Mendelian Inheritance: Co-dominant segregation of Mfd15 and Mfd41 was observed in 18 and 15 two or three generation families respectively.

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 Mfd15, and the sizes of the most intense bands for Mfd41. The dinucleotide repeat sequence in Mfd15 was of the form (AC)₂₅, and in Mfd41 of the form (AC)₁₇. The sequences of Mfd15 and Mfd41 have been submitted to GenBank.

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