Dinucleotide repeat polymorphism at the D19S75 locus

James L.Weber*, Clarisse Kappel,
Paula E.May and Anne E.Kwitek
Marshfield Medical Research Foundation, 510
North St. Joseph Avenue, Marshfield, WI 54449,
USA

Source/Description: A human genomic *Sau3AI* fragment from a large insert human chromosome 19-specific phage library (LL19NL01) was cloned into mp18 and selected by hybridization to poly(dC-dA)·poly(dG-dT). The cloned fragment was designated Mfd13. Sequencing of Mfd13 provided the information necessary for polymerase chain reaction primer synthesis. The clone length was 242 bp, and the predicted length of the amplified fragment was 143 bp.

Primer Sequences: ATTAATCCATCTAAAAGCGAA (CA strand); TTCCCTTTGCTCCCCAAACG (GT strand).

Frequency: Estimated from 100 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.61.

Allele(bp)	Frequency	Allele(bp)	Frequency
152	0.01	144	0.12
150	0.11	142	0.02
148	0.56	136	0.05
146	0.13		

Chromosomal Localization: Assigned to chromosome 19 using DNA templates isolated from panels of somatic cell hybrids.

Mendelian Inheritance: Co-dominant segregation was observed in 14 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 and were the averages of the sizes of the GT-strand and CA-strand bands. The dinucleotide repeat sequence in Mfd13 was of the form (CA)₄CGCG (CA)₁₉C. The sequence of Mfd13 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 polymorphism at the D22S156 locus

James L.Weber* and Paula E.May
Marshfield Medical Research Foundation, 510
North St. Joseph Avenue, Marshfield, WI 54449,
USA

Source/Description: A human genomic *AluI* fragment was cloned into mp10 and selected by hybridization to poly(dC-dA)·poly(dG-dT). The cloned fragment was designated Mfd33. Sequencing of Mfd33 provided the information necessary for polymerase chain reaction primer synthesis. The clone length was 115 bp, and the predicted length of the amplified fragment was 106 bp.

Primer Sequences: AGCCTGGGAGTCAGAGTGA (CA strand); AGCTCCAAATCCAAAGACGT (GT strand).

Frequency: Estimated from 116 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.64.

Allele(bp)	Frequency	Allele(bp)	Frequency
110	0.01	102	0.24
108	0.04	98	0.01
106	0.27	96	0.01
104	0.42		

Chromosomal Localization: Assigned to chromosome 22 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 and were the averages of the sizes of the GT-strand and CA-strand bands. The dinucleotide repeat sequence in Mfd33 was of the form (AC)₁₄AT(AC)₁₃. The sequence of Mfd33 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.

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