Dinucleotide repeat polymorphism at the D10S89 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 Mfd28. Sequencing of Mfd28 provided the information necessary for polymerase chain reaction primer synthesis. The clone length was 229 bp, and the predicted length of the amplified fragment was 150 bp.

Primer Sequences: AACACTAGTGACATTATTTTCA (CA strand); AGCTAGGCCTGAAGGCTTCT (GT strand).

Frequency: Estimated from 120 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.71.

Allele(bp)	Frequency	Allele(bp)	Frequency
156	0.02	148	0.08
154	0.04	146	0.03
152	0.15	144	0.38
150	0.28	142	0.02

Chromosomal Localization: Assigned to chromosome 10 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 Mfd28 was of the form $(AC)_{10}AG(AC)_{21}A$. The sequence of Mfd28 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.

* To whom correspondence should be addressed

Dinucleotide repeat polymorphism at the D12S43 locus

James L.Weber*, Anne E.Kwitek, Paula E.May and Mihael Polymeropoulos[1]
Marshfield Medical Research Foundation, 510 North St. Joseph Avenue, Marshfield, WI 54449, and [1]National Institute of Mental Health, WAW Building, Room 119, 2700 Martin Luther King Avenue, Washington, DC 20032, USA

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 Mfd84. Sequencing of Mfd84 provided the information necessary for polymerase chain reaction primer synthesis. The clone length was >323 bp, and the predicted length of the amplified fragment was 111 bp.

Primer Sequences: AATGTCCTTGTACTTAGGAT (CA strand); CACTTAATATCTCAATGTATAC (GT strand).

Frequency: Estimated from 116 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.71.

Allele(bp)	Frequency	Allele(bp)	Frequency
113	0.04	105	0.33
109	0.26	103	0.03
107	0.09	99	0.25

Chromosomal Localization: Assigned to chromosome 12 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 Mfd84 was of the form $(AC)_5AT(AC)_2AGAT(AC)_2GG(AC)_{17}$. The sequence of Mfd84 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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