Dinucleotide repeat polymorphism at the D9S43 locus

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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 Mfd14. Sequencing of Mfd14 provided the information necessary for polymerase chain reaction primer synthesis. The clone length was 175 bp, and the predicted length of the amplified fragment was 93 bp.

Primer Sequences: TTCTGATATCAAAACCTGGC (CA strand); AAGGATATTGTCCTGAGGA (GT strand).

Frequency: Estimated from 106 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.74.

Allele(bp)	Frequency	Allele(bp)	Frequency
102	0.01	92	0.19
100	0.01	90	0.05
98	0.21	86	0.01
96	0.33	80	0.02
94	0.18		

Chromosomal Localization: Assigned to chromosome 9 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 Mfd14 was of the form (AC)₂₃A. The sequence of Mfd14 has been submitted to GenBank.

Acknowledgements: This work was supported by the Marshfield Clinic and NIH grant GM41773.

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

Dinucleotide repeat polymorphism at the D2S71 locus

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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 Mfd19. Sequencing of Mfd19 provided the information necessary for polymerase chain reaction primer synthesis. The clone length was 200 bp, and the predicted length of the amplified fragment was 147 bp.

Primer sequences: GCTTGTTACATTGTTGCTTC (CA strand); TCTAACCCTTTGGCCATTG (GT strand).

Frequency: Estimated from 102 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.57.

Allele (bp)	Frequency	Allele (bp)	Frequency
154	0.01	144	0.02
152	0.61	142	0.01
150	0.04	140	0.06
148	0.09	138	0.15
146	0.02		

Chromosomal Localization: Assigned to chromosome 2 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 Mfd19 was of the form (AC)₈AG(AC)₃AG(AC)₂₄TCA(CT)₇. The sequence of Mfd19 has been submitted to GenBank.

Acknowledgements: This work was supported by the Marshfield Clinic and NIH grant GM41773.

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

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