Dinucleotide repeat polymorphism at the D13S71 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 Mfd44. Sequencing of Mfd44 provided the information necessary for polymerase chain reaction primer synthesis. The clone length was >250 bp, and the predicted length of the amplified fragment was 75 bp.

Primer Sequences: GTATTTTGGTATGCTTGTGC (CA strand); CTATTTTGGGAATATATGTGCCT (GT strand).

Frequency: Estimated from 126 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.67.

Allele(bp)	Frequency	Allele(bp)	Frequency
79	0.05	73	0.26
77	0.25	67	0.06
75	0.38		

Chromosomal Localization: Assigned to chromosome 13 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 Mfd44 was of the form (CA)₁₇. The sequence of Mfd44 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 D14S34 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 Mfd42. Sequencing of Mfd42 provided the information necessary for polymerase chain reaction primer synthesis. The clone length was 179 bp, and the predicted length of the amplified fragment was 114 bp.

Primer Sequences: GGCCTCAAAGAATCCTACAG (CA strand); GACACGTAGTTGCTTATTAC (GT strand).

Frequency: Estimated from 112 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.59.

Allele(bp)	Frequency	Allele(bp)	Frequency
117	0.38	111	0.01
115	0.14	107	0.05
113	0.42		

Chromosomal Localization: Assigned to chromosome 14 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 Mfd42 was of the form (CA)₁₆T(AC)₃A. The sequence of Mfd42 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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