Dinucleotide repeat polymorphism at the D1S102 locus

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Source/Description: A human genomic *Sau3A* I fragment was cloned into mp19 and selected by hybridization to poly(dC-dA)·poly(dG-dT). The cloned fragment was designated Mfd52. Sequencing of Mfd52 provided the information necessary for polymerase chain reaction primer synthesis. The clone length was 365 bp, and the predicted length of the amplified fragment was 200 bp.

Primer sequences: AAATCAGACAAGTACAGGTG (CA strand); ATGAACTTGTCTGGGAGGA (GT strand).

Frequency: Estimated from 120 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.50.

Allele (bp)	Frequency	Allele (bp)	Frequency
204	0.01	190	0.60
202	0.03	186	0.26
200	0.10		

Chromosomal Localization: Assigned to chromosome 1 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 determine allele size. The dinucleotide repeat sequence in Mfd52 was of the form (AC)₁₈TTG(CA)₃. The sequence of Mfd52 has been submitted to GenBank.

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

Dinucleotide repeat polymorphism at the D1S103 locus

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Source/Description: A human genomic *Sau3A* I fragment was cloned into mp19 and selected by hybridization to poly(dC-dA)·poly(dG-dT). The cloned fragment was designated Mfd64. Sequencing of Mfd64 provided the information necessary for polymerase chain reaction primer synthesis. The clone length was >243 bp, and the predicted length of the amplified fragment was 85 bp.

Primer sequences: ACGAACATTCTACAAGTTAC (CA strand); TTTCAGAGAACTGACCTGT (GT strand).

Frequency: Estimated from 118 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.78.

Allele (bp)	Frequency	Allele (bp)	Frequency
102	0.01	90	0.38
100	0.03	88	0.08
98	0.05	86	0.17
96	0.03	84	0.04
94	0.11	82	0.03
92	0.06		

Chromosomal Localization: Assigned to chromosome 1 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 determine allele size. The dinucleotide repeat sequence in Mfd64 was of the form (AC)₁₅A. The sequence of Mfd64 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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