Dinucleotide repeat polymorphism at the D4S174 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 Mfd59. Sequencing of Mfd59 provided the information necessary for polymerase chain reaction primer synthesis. The clone length was 318 bp, and the predicted length of the amplified fragment was 183 bp.

Primer Sequences: AAGAACCATGCGATACGACT (CA strand); CATTCCTAGATGGGTAAAGC (GT strand).

Frequency: Estimated from 120 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.86.

Allele(bp)	Frequency	Allele(bp)	Frequency
195	0.01	183	0.11
193	0.04	181	0.08
191	0.14	179	0.14
189	0.06	177	0.12
187	0.11	175	0.01
185	0.18		

Chromosomal Localization: Assigned to chromosome 4 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 Mfd59 was of the form $(AC)_{23}A$. The sequence of Mfd59 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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Dinucleotide repeat polymorphism at the D6S87 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 Mfd47. Sequencing of Mfd47 provided the information necessary for polymerase chain reaction primer synthesis. The clone length was >280 bp, and the predicted length of the amplified fragment was 148 bp.

Primer Sequences: ACAGAGTGAGACCGTGTAAC (CA strand); AGAGAAGCATCTCACTTAGT (GT strand).

Frequency: Estimated from 106 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.53.

Allele(bp)	Frequency	Allele(bp)	Frequency
155	0.01	143	0.01
153	0.02	141	0.33
149	0.04	139	0.02
147	0.53	137	0.01
145	0.03		

Chromosomal Localization: Assigned to chromosome 6 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 Mfd47 was of the form $(AC)_{17}A$. The sequence of Mfd47 has been submitted to GenBank.

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

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

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