Dinucleotide repeat polymorphism at the D20S27 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 Mfd25. Sequencing of Mfd25 provided the information necessary for polymerase chain reaction primer synthesis. The clone length was 190 bp, and the predicted length of the amplified fragment was 130 bp.

Primer sequences: TTTATGCGAGCGTATGGATA (CA strand); CACCACCATTGATCTGGAAG (GT strand).

Frequency: Estimated from 110 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.64.

Allele (bp)	Frequency	Allele (bp)	Frequency
138	0.11	132	0.35
136	0.15	128	0.01
134	0.38		

Chromosomal Localization: Assigned to chromosome 20 using DNA templates isolated from panels of somatic cell hybrids.

Mendelian Inheritance: Co-dominant segregation was observed in 40 two or three 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 Mfd25 was of the form (AC)₁₁. The sequence of Mfd25 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.

* To whom correspondence should be addressed

Dinucleotide repeat polymorphism at the D4S171 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 Mfd22. Sequencing of Mfd22 provided the information necessary for polymerase chain reaction primer synthesis. The clone length was 264 bp, and the predicted length of the amplified fragment was 150 bp.

Primer sequences: TGGGTAAAGAGTGAGGCTG (CA strand); GGTCCAGTAAGAGGACAGT (GT strand).

Frequency: Estimated from 96 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.67.

Allele (bp)	Frequency	Allele (bp)	Frequency
161	0.01	149	0.04
157	0.02	147	0.09
155	0.08	145	0.01
153	0.39	143	0.01
151	0.34		

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 and were the averages of the sizes of the GT-strand and CA-strand bands. The dinucleotide repeat sequence in Mfd22 was of the form (AC)₂₀AG(AGAC)₅AGA. The sequence of Mfd22 has been submitted to GenBank.

Acknowledgements: This work was supported by the Marshfield Clinic and NIH grant GM41773. S. Naylor provided DNA from a chromosome 4-specific somatic cell hybrid.

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

* To whom correspondence should be addressed