Dinucleotide repeat polymorphism at the CRP locus

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Source/Description: A (dC-dA)_n·(dG-dT)_n sequence was found within an intron of the human C-reactive protein gene by computer search of GenBank (Accession number M11880). Polymerase chain reaction primers were selected from the sequence to give an amplified fragment with predicted length of 131 bp. The pair of primers was designated Mfd57.

Primer Sequences: GATCTATCCCCTCACTTACG (CA strand); TATGAACAGAACAGTGGAGC (GT strand).

Frequency: Estimated from 114 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.53.

Allele(bp)	Frequency	Allele(bp)	Frequency
145	0.01	133	0.02
141	0.32	131	0.55
139	0.04	129	0.01
137	0.01	127	0.03
135	0.01		

Chromosomal Localization: Floyd-Smith *et al.* (1) mapped CRP to 1q21-q23. Assignment to chromosome 1 was confirmed by 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 (2) 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 at CRP was of the form (CA)₁₅C.

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

References: 1) Floyd-Smith,G., Whitehead,A.S., Colten,H.R. and Francke,U. (1986) Immunogenetics **24**, 171–176. 2) Weber,J.L. and May,P.E. (1989) *Am. J. Hum. Genet.* **44**, 388–396.

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Dinucleotide repeat polymorphism at the D3S196 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 Mfd17. Sequencing of Mfd17 provided the information necessary for polymerase chain reaction primer synthesis. The clone length was 180 bp, and the predicted length of the amplified fragment was 94 bp.

Primer Sequences: ACTCTTTGTTGAATTCCCAT (CA strand); TTTCCACTGGGGAACATGGT (GT strand).

Frequency: Estimated from 104 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.68.

Allele(bp)	Frequency	Allele(bp)	Frequency
98	0.06	90	0.04
96	0.16	88	0.37
94	0.32	86	0.02
92	0.03		

Chromosomal Localization: Assigned to chromosome 3 using DNA templates isolated from panels of somatic cell hybrids.

Mendelian Inheritance: Co-dominant segregation of Mfd17 was observed in 43 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 Mfd17 was of the form (AC)₂₃. The sequence of Mfd17 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 3-specific somatic cell hybrid.

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

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