Detection of CD2 polymorphism on chromosome 1 with EcoRI

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Source/Description: A 1.5 kb cDNA, clone 254 (1) coding for the translated region of CD2 cloned in pUC9 at the EcoRI site.

Polymorphism: EcoRI (BRL) identified a two allele polymorphism with two bands at 25 kb and 17 kb (A1) or one band at 42 kb (A2) (see Figure).

Frequency: Studied in 63 unrelated North Americans
25 kb, 17 kb allele (A1) 0.95
42 kb allele (A2) 0.05

Not Polymorphic For: PstI, BamHI, HindIII, SstI tested on a panel of 10 unrelated individuals.

Chromosomal Localisation: Assigned to Chromosome 1 by *in situ* hybridization (2).

Mendelian Inheritance: Co-dominant segregation shown in two informative families, 4 offspring, 2 heterozygous offspring 25 kb, 17 kb/42 kb, 1 homozygous offspring 42 kb/42 kb and 1 homozygous offspring 25, 17 kb/25, 17 kb.

Probe Availability: Contact M. Crumpton, Imperial Cancer Research Fund, London, UK.

Other Comments: Detection facilitated with low percentage Agarose gels (0.6–0.8%), and acid depurination prior to transfer.

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References: 1) Sewell, W.A. *et al.*, *Proc. Natl. Acad. Sci. USA* (1986) **83**, 8718. 2) Brown, M.H. *et al.*, *Human Genetics* (1987) **76**, 191–195.

Southern blot of genomic DNA digested with EcoRI and hybridized with ³²P CD2 cDNA probe (A). Lanes 1–5, unrelated individuals (B). Lane 1 and 2 mother and daughter positive for the 42 kb allele.

Dinucleotide repeat polymorphism at the D18S35 locus

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Source/Description: A human genomic *AluI* fragment was cloned into mp10 and selected by hybridization to poly(dC-dA)·(dG-dT). The cloned fragment was designated Mfd32. Sequencing of Mfd32 provided the information necessary for polymerase chain reaction primer synthesis. The clone length was 143 bp, and the predicted length of the amplified fragment was 104 bp.

Primer Sequences: AGCTAGATTTTACTTCTCTG (CA strand); CTGGTTGTACATGCCTGAC (GT strand).

Frequency: Estimated from 106 chromosomes of unrelated CEPH family grandparents (Caucasians). PIC = 0.65.

Allele (bp)	Frequency	Allele (bp)	Frequency
124	0.04	108	0.09
122	0.26	106	0.13
118	0.02	104	0.45

Chromosomal Localization: Assigned to chromosome 18 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 1 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 Mfd32 was of the form (AC)₁₂A. The sequence of Mfd32 has been submitted to GenBank.

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Reference: 1) Weber, J.L. and May, P.E. (1989) *Am. J. Hum. Genet.* **44**, 388–396.

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