Dinucleotide repeat polymorphism at the 3′ end of the LDL receptor gene

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Source/Description: A polymorphic dinucleotide tandem repeat (dTùdA) is located in exon 18 of the LDL receptor gene (at nucleotide 4780) (1). Two oligonucleotides homologous to the sequences flanking the tandem repeat (GZ-7 and GZ-8) were used to amplify the region and generate a fragment of the predicted size of 106 bp.

Primer Sequences:
GZ-7 = CACTTTGTATATTGGTTGAAACTGT
GZ-8 = CACTGAACAAATACAGCAACCAGGG

Frequency: Estimated in 27 unrelated Caucasian American individuals:

Allele (nt)	Number of (TA) Repeats	Frequency
112	10	0.20
108	8	0.10
106	7	0.70

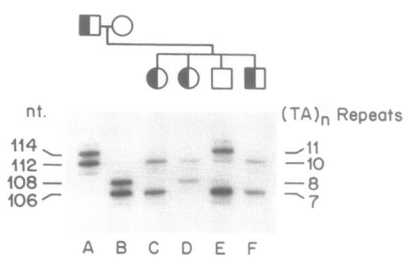
The heterozygosity index was 48.5%.

Mendelian Inheritance: Co-dominant segregation was observed in two families with a total of seven informative meiosis.

Chromosomal Localization: The LDL receptor gene has been assigned to chromosome 19p13.1-p13.3. (2).

Other Comments: The PCR reaction was performed on genomic DNA as previously described (3) with the following modifications: 1) the DNA was denatured at 96°C for 1 min, 2) annealing and extension was performed at 68°C for 3 min, and 3) the number of cycles was 20. PCR products were fractionated on an 8% denaturing polyacrylamide gel and the size of the alleles was determined by comparison with end-labeled MspI digested pBR322 DNA. The analysis of a Puerto Rican family with familial hypercholesterolemia showed an additional allele of 114 nt (11 repeats) not seen in any Caucasian American individuals.

References: 1) Yamamoto,T. *et al.* (1984) *Cell* **39**, 27–38. 2)Lindgren,N.V. *et al.* (1985) *Proc. Natl. Acad. Sci. USA* **82**, 8567–8571. 3) Saiki,R.K. *et al.* (1988) *Science* **230**, 487–491.



PvuII and XhoI/EcoRV polymorphisms adjacent to the α A-crystallin (CRYA1) gene on human chromosome 21

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Source/Description: An 1800 bp KpnI/HindIII single copy genomic DNA insert in bacteriophage M13 mp19 was used as a hybridization probe. This clone (pαA-T2) contains a fragment of the human α A-crystallin gene, that includes exons 1 and 2 and a portion of intron 2 (1).

Polymorphisms: After PvuII digestion the pαA-T2 probe reveals a VNTR polymorphism with at least 4 alleles between 7.8 kb and 10.5 kb. A constant fragment of 1.5 kb is also observed. A double digest with XhoI/EcoRV reveals a second DNA polymorphic system with allelic fragments of A1: 5.2 and 14.0 kb, A2: 16.5 and 21.0 kb and A3: 17.0 kb.

Frequency: The observed heterozygosity of the PvuII VNTR polymorphism in the 40 CEPH families is 34%. The frequency of the alleles of the XhoI/EcoRV polymorphism in 183 CEPH chromosomes studied is A1: 13 (7.1%); A2: 169 (92.3%); A3: 1 (0.5%), with PIC value of 0.12.

Not Polymorphic For: BglII, EcoRI, HincII, HindIII, KpnI, PstI, SstI, StuI, TaqI and XbaI (5 unrelated individuals tested).

Chromosomal Localization: The CRYA1 gene maps on 21q22.3 (2).

Mendelian Inheritance: Demonstrated in 40 CEPH families.

Probe Availability: Contact C.J.Jaworski.

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References: 1) Jaworski,C.J. and Piatigorsky,J. (1989) *Nature* **337**, 752–754. 2) Hawkins,J.W. *et al.* (1987) *Hum. Genet.* **76**, 375–380.