ScrFI polymorphism in the 2nd intron of the HMGCR gene

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Source/Description: Oligonucleotide primers derived from the cDNA sequence of the human 3-hydroxy-3-methylglutaryl coenzyme A reductase gene (HMGCR) (1) were used to amplify the 2nd intron of the reductase gene.

PCR Primers:

HMG116 5'-TACTGGTAACAATAAGATCTGTGGT-3'
HMG117 5'-ATATTTTGATCCAAGTTGACGTAAA-3'

Polymorphism: ScrFI (CCNGG) identifies a two allele polymorphism with bands of either 165 bp or 120 and 45 bp (which comigrates with a nonpolymorphic band). In addition nonpolymorphic bands of approximately 430, 380, 90, 88, 68, 50, 45, and 42 bp are observed. The same polymorphism can also be detected using BstNI (CCA/TGG) where the polymorphic bands are the same but the nonpolymorphic bands are approximately 470, 430, 130, 68, 50, and 45 bp.

Frequency: Studied in 11 unrelated American Caucasian individuals (22 alleles).

A1 = 165 bp band Frequency A1 = 0.55
A2 = 120 bp band A2 = 0.45

Not Polymorphic For: The amplified fragment was not polymorphic for HpaII, BstUI, AluI, HaeIII, RsaI, Sau96I, HhaI, MboI, DdeI, HinfI or TaqI using a panel of 8 unrelated individuals.

Chromosomal Localization: The HMG CoA reductase locus has been assigned to 5q13.3–13.4 (2).

Mendelian Inheritance: Co-dominant segregation demonstrated in 1 family.

PCR Conditions: One microgram of genomic DNA, 100 pmol of each oligonucleotide primer and 20 μ Ci α -³²P-dCTP were amplified for 35 cycles with an annealing temperature of 68°C and a denaturing temperature of 95°C. The ³²P-labeled amplified fragments were gel purified and then ~15,000 cpm were digested with ScrFI for 2 hrs. The products were analyzed by electrophoresis on a 12% polyacrylamide gel followed by autoradiography.

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HgiAI polymorphism near the HMGCR promoter

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Source/Description: pHRed24 contains a 2.3 kb SphI fragment that spans the human 3-hydroxy-3-methylglutaryl coenzyme A reductase (HMGCR) promoter (1) cloned into the SphI site of pBR322.

Polymorphism: HgiAI identifies a two allele polymorphism with bands at either 3.1 or 3.3 kb, as well as a nonpolymorphic band at 2.2 kb.

Frequency: Studied in 17 American Caucasian individuals.

A1 = 3.1 kb Frequency A1 = 0.8
A2 = 3.3 kb A2 = 0.2

Not Polymorphic For: ApaI, ApaLI, Asp718, AvaII, BamHI, BglII, EcoRI, NcoI, NheI, PstI, PvuII, SacI, SpeI, StuI did not detect polymorphisms in 8 unrelated individuals.

Chromosomal Localization: The HMG CoA reductase locus has been assigned to 5q13.3–13.4 (2).

Mendelian Inheritance: Co-dominant segregation demonstrated in 2 families (see Figure).

Probe Availability: Available from the American Type Culture Collection (No. 59566).

Other Comments: Genomic DNA was digested with HgiAI (10 units/ μ g DNA) for 4 hrs and separated on a 1% agarose gel.

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