A NotI RFLP in the human alpha2-C4 adrenergic receptor locus (ADRA2RL2) detected by PFGE

W.-T. Hsieh*, J.L. Barrick, M.R. Hoehe and E.S. Gershon
Clinical Neurogenetics Branch, Bldg 10/Rm 3N218, NIMH, ADAMHA, Bethesda, MD 20892, USA

Source/Description: Probe pADRA2RL2 (1) containing 1270 bp coding sequence and 240 bp of the 3' flanking region of the human alpha2-C4 adrenergic receptor encoding the putative alpha2B-AR (2).

Polymorphism: A two-allele polymorphism with fragments of 800 kb (B1) and 400 kb (B2) is revealed after hybridization with NotI digested human genomic DNA.

Not Polymorphic For: MluI and NruI.

Frequency: 26 unrelated Caucasians were studied.
B1 allele: 0.37
B2 allele: 0.63

Chromosomal Location: The alpha2-C4 adrenergic receptor has been mapped to the short arm of chromosome 4 just proximal to Huntington's disease gene marker G8 (4p16.3) (M.R. Hoehe et al., in preparation).

Mendelian Inheritance: Co-dominant segregation in 3 families.

Other Comments: The digests were run on a 1% agarose gel in TBE at 330 V using a Pulsaphor (Pharmacia/LKB) with a pulse time of 100 s or 40 s for 40 hours. The probe also hybridizes to an MluI fragment larger than 1,000 kb, and to two NruI fragments of 750 and 450 kb. This polymorphism is independent of the Bsu36I polymorphism reported earlier (1).

Probe Availability: Generously provided on request from Drs. J.W. Regan and R.J. Lefkowitz. Howard Hughes Medical Institute at Duke University Medical Center, Department of Medicine, Biochemistry, and Physiology, Durham, NC 27710.


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Sequence polymorphism in the human alpha-2-macroglobulin (A2M) gene

W. Poller, J.-P. Faber1 and K. Oiiek1
Medizinische Universitätsklinik, Klinikum Bergmannsheil, Ruhr – Universität Bochum, Gösingstrasse 14, D-4630 Bochum, FRG and 1 Institut für Klinische Biochemie der Universität, Sigmund-Freud-Strasse 25, D-5300 Bonn, FRG

Description: The thiolester site of the human alpha-2-macroglobulin (A2M) is essential for the function of A2M as a proteinase inhibitor (1, 2). This site, which is encoded for by exon 24 of the A2M gene, was amplified by polymerase chain reaction (PCR) using the primer 5'-CTGAAAGATTTCCTCCTGGAAAC-3' and 5'-GGTTTTCCTGCCATATCGCTC-3'. PCRs were performed in 100 µl volumes containing 0.5 µg genomic DNA, 25 pmols of each primer, 200 µM of each dNTP in 50 mM KCl, 10 mM Tris-HCl, 3.0 mM MgCl2, 0.01% (w/v) gelatin and 2.5 U Taq polymerase. 30 cycles of amplification were conducted, each consisting of 1 min at 94°C, 1 min at 58°C, 30 sec at 72°C. Sequencing of the 0.8 kb amplification product with the primer 5'-AGGCTCTGCCATGCAA-3' according to the method of Wong et al. (3) showed a sequence polymorphism of the gene.

Polymorphism: A point mutation near the thiol ester site changing codon 1000 from GTC to ATC with a corresponding amino acid exchange Val1000 to Ile1000 creates a new Sau3A restriction site (Fig. 1).

Frequency: Frequencies of the two alleles among 30 unrelated Caucasians:

GTC (Val1000), Sau3A-: 0.30
ATC (Ile1000), Sau3A+: 0.70

Chromosomal Localization: 12 pl3.3–pl2.3

Mendelian Inheritance: Co-dominant segregation shown in one informative family.


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