A biallelic DNA polymorphism of the human beta-2-adrenergic receptor detected by Ban I-Adrb-2

K.-U. Lentes, W.H. Berrettini², M.R. Hoehe¹, F.-Z. Chung and E.S. Gershon¹

Section of Receptor Biochemistry and Molecular Biology, Laboratory of Molecular and Cellular Neurobiology, NINCDS, NIH and ²Section of Clinical Genetics, NIMH, ADAMHA, Bethesda, MD 20892, USA

SOURCE/DESCRIPTION:

A 2.6 kb human genomic DNA fragment (Pvu II) of the beta-2-adrenergic receptor containing the whole coding region plus 1000 bp of the 5'-flanking and 400 bp of the 3'-untranslated region was isolated from the human genomic clone LCV-517 (20 kb insert) (1) and subcloned into the Sma I site of the expression vector pMSG (Pharmacia).

POLYMORPHISM:

Hybridization of human genomic DNA digested with Ban I identifies a two allele polymorphism with bands at 3.4 kb (A) and 3.7 kb (B).

FREQUENCY:

20 unrelated Caucasians (North America) were tested.

A allele: 0.75

B allele: 0.25

NOT POLYMORPHIC FOR:

Alu I, Apa I, Apa LI, Ava II, Bam HI, Ban II, Bcl I, Bgl I, Bgl II, Bsp 1286, Bst EII, Bst NI, Dde I, Dra I, Dra II, Eco RI, Eco RV, Fnu 4H, Fok I, Hae II, Hae III, Hgi AI, Hha I, Hinc II, Hind III, Hinf I, Hpa II, Hph I, Kpn I, Mbo I, Nae I, Nar I, Nci I, Pst I, Pvu II, Rsa I, Sac I, Sal I, Sau 3A, Sau 96, Sca I, Scr I, Sma I, Stu I, Sty I, Taq I, Xba I.

CHROMOSOMAL LOCALIZATION:

The human beta-2-adrenergic receptor gene has been assigned to chromosome 5q31-32 (2).

MENDELIAN INHERITANCE:

Codominant segregation in 3 families with 2 generations.

OTHER COMMENTS:

High stringency wash of the blots in 0.1XSSC/0.1%SDS at 65°C shows no significant background.

PROBE AVAILABILITY:

Available on request from K.-U. Lentes.

Present address: Institut für Humangenetik der Universität Bonn, Wilhelmstrasse 31, D-5300 Bonn 1, FRG.

REFERENCES:

- (1) F.-Z. Chung et al., 1987, FEBS Lett. 211, 200-206.
- (2) B.K. Kobilka et al., 1987, PNAS 84, 46-50.

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