

Research article

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Assessing the molecular genetics of attention networks

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HD. Based on 7 cases (4 die) and 4 family-based (9 die), hereditary hemochromatosis is a genetically determined haemochromatosis with a significant clinical

~~On significant end e e b e ed f. DATC COMTin~~

Conclusions

Modeling of the genetic architecture of the candidate gene has affected aminergic signaling. The association between the global mean of efficiency of specific anatomical channels and the efficiency of the AT1 receptor gene is a significant finding.

Methods

Subjects

Subjects were recruited from the vicinity of the Yick Hospital in the age range 25-35 years. They were recruited from the vicinity of Peking University and the adjacent area. The subjects were all of Chinese descent. Paid and unpaid subjects were recruited from Peking University and the adjacent area. Subjects with a history of chronic alcohol and/or smoking were excluded. A total of 220 adult subjects, age 18-50 years old were included in the study. All subjects were of normal intelligence. While making reference to the study, 2 subjects were excluded.

Behavioral data

The AT1 receptor gene was described [1]. Briefly, a 1000 bp fragment of the human gene was amplified by PCR. Simultaneously, a 500 bp fragment of the human gene was amplified by PCR. The amplified DNA was digested with EcoRI and HindIII. The digested DNA was ligated into the pUC19 vector. The recombinant plasmid was transformed into E. coli cells. The plasmid was extracted and sequenced. The sequence was compared with the AT1 receptor gene sequence. The AT1 receptor gene was found to be identical to the human gene.

The subjects were asked to identify the direction of the central line by being asked to identify the left and right directions. The subjects were asked to identify the direction of the 100 m scale. The subjects were asked to identify the direction of the 100 m scale. The subjects were asked to identify the direction of the 100 m scale. The subjects were asked to identify the direction of the 100 m scale.

a d d d n a d e c i b e d i n [89], e e e d f c a d: 5 -GTT-
 GTCTGTCTTTTCTCATTGTTTCCATTG-3 R e e e 5 -
 CAAGGAGCAGGCACCGTGAGC-3 i m e f c g e n c
 i n g f h e D R D C C T c h a n g e a C i i c n -521 a d e
 c i b e d i n [3], f c a d: 5 -
 CCGGGCCTGAGCACCAGAGGCTGCT-3 a n d R e e e 5 -
 GCATCGACGCCAGCGCCATCCTACC-3 e e e d f c
 l c e d b d i g e i c n i h F I f c g e n c i n g f h e D A T 1
 4 0 b - e e a (V T R) C m C h i m i n h e 3 n a n l a e d
 e g i c n a d e c i b e d i n [90], f c a d: 5 -TGTGGTGTAG-
 GGAACGGCCTGAG-3 R e e e 5 -CTTCCTGGAGGT-
 CACCGCTCAAGG-3 i m e e e e d f c g e n c i n g
 f h e C O M T V a l C M e c h a n g e a C i i c n 108 a d e
 c i b e d i n [91], f c a d: 5 -ACTGTGGCTACTCAGCT-
 GTG-3 a n d R e e e 5 -CCTTTTCCAGGTCTGACAA-3
 i m e e e e d f c l c e d b e i c i c n d i g e i c n i h
 l a i l f c g e n c i n g f h e M A O A 30 - b e e a i n C
 m C a d e c i b e d (55 T [(GT)5.9I5.9(IJT)*.3(g)-12.8(e)4 6cT)5.9I5ee 108 a3(-)dCeec c (-)-6(-)-5.8(8(e)6:9)6.eCG @ 8

