

DNA haplotype analysis of CAG repeat in Taiwanese Huntington's disease patients

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摘要

Abstract

We studied the expanded CAG repeat and adjacent CCG repeat in 53 Huntington's disease (HD) patients and 172 unrelated normal subjects matched to the patients for ethnic origin. The range of the CAG repeat varied from 38 to 109 in the HD patients and from 10 to 29 in the control group. A significant negative correlation was found between the age at onset and the CAG expansion, with no significant influence of the adjacent CCG repeat on the age at onset by multiple regression analysis. Allelic association using CCG repeat and 2 flanking dinucleotide repeat markers within 150 kb of the HD gene revealed linkage disequilibrium for 2 of 3 markers. Haplotype analysis of 24 HD families using these markers identified 3 major haplotypes underlying 87.5% of HD chromosomes. The data suggested frequent haplotypes in the Taiwanese population on which one or more mutational events leading to the disease occurred