The GTP Cyclohydrolase I Gene in Russian Families With Dopa-Responsive Dystonia

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Objective: To search for mutations in the GTP cyclohydrolase I (GCH-I) gene in a set of Russian families with dopa-responsive dystonia (DRD).

Design: Six large families with 54 affected family members and 2 patients with sporadic DRD were examined. Mutation screening was performed using single-strand conformation polymorphism analysis followed by direct sequencing of the presumably mutated exons; in patients whose results showed a normal pattern on single-strand conformation polymorphism analysis, the entire coding region of the GCH-I gene was sequenced.

Results: Three new heterozygote point mutations located within exons 1, 2, and 4 of the GCH-I gene were identified in 3 families with autosomal-dominant inheritance. All these mutations are predicted to cause amino acid changes in the highly conserved regions of the gene. In patients from 3 other families and in both patients with sporadic DRD, no alterations in the translated portion of the GCH-I gene were observed.

Conclusions: Mutations in the coding region of the GCH-I gene account for a significant fraction (up to half) of the patients with a typical clinical picture of DRD. None of the mutations in the GCH-I gene described so far were detected more than once, which precludes the possibility of creating simple DNA testing procedures for routine clinical practice.

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PATIENTS AND METHODS

We examined 6 large, multigenerational families (comprising 54 affected members) and 2 patients with sporadic DRD. The main criterion for inclusion was a marked and sustained response to low doses of levodopa. Such a response was observed in all the familial cases examined, as well as in 1 patient with a negative family history; in 1 sporadic case, levodopa treatment caused only a moderate improvement. Thirty-seven patients, including 35 familial cases, were examined by 2 of us (E.D.M. and L.A.I.-S.), and their clinical features are reported elsewhere. Segregation analysis in the familial cases (Figure 1) suggested autosomal-dominant inheritance with reduced penetrance in all the pedigrees, except family DRD-6, for which a mode of transmission could not be determined with certainty (see the “Comment” section).

Blood samples were obtained with informed consent from 16 individuals, and genomic DNA was extracted by standard procedures. Our strategy of mutation screening was based on single-strand conformation polymorphism (SSCP) analysis, followed by direct sequencing of the presumably mutated exons. Six exons of the GCH-I gene, including splicing junctions, were amplified using a polymerase chain reaction. Primer sequences used for amplification of exon 1 were as follows: 5′ portion of the exon, 5′-GGCCACGGGCGAGGATTAGGCCGACG-3′ and 5′-GGGAGGTTCAGCTCGTTATCCTC-3′; and 3′ portion of the exon, 5′-CCCGGGGACGGCGGAGTACG-3′ and 5′-CCCCCGGGGACCGCTTACGC-3′. For exons 2 through 6, primers were used as reported elsewhere.15

For SSCP analysis, the GCH-I gene exons were amplified in a 5-µL volume containing 50 ng of DNA, 50 mmol of potassium chloride, 10 mmol of Tris-hydrochloride (pH 8.4), 1.5 mmol of magnesium chloride, 250 µmol of each deoxynucleotidetriphosphate, 8 pmol of each primer (1 primer being biotinylated), and 2.5 U of AmpliTaq polymerase. A temperature profile was the same as for SSCP analysis, except that annealing temperature was 52°C and 30 cycles were performed. Polymerase chain reaction products were purified and concentrated with SURE-02 (Takara, Osaka, Japan) and sequenced directly with the same primers as for amplification. Sequencing was performed using an automated ALF DNA Sequencer II (Pharmacia, Uppsala, Sweden), an AutoRead Sequencing Kit (Pharmacia) and streptavidin-coated beads for producing single-stranded DNA (Dynal, Oslo, Norway), or conventional autoradiography and a Sequenase Version 2.0 Kit (U.S.B., Cleveland, Ohio). Sequences were confirmed on identical and complementary strands.

RESULTS

Three new heterozygote mutations identified in our families are shown in the Table. The presence of these mutations was presumed on the basis of altered bands on SSCP analysis and was confirmed by direct sequencing of the corresponding exons in one affected member from each family (not shown). In family DRD-4, a T→A transition in exon 1 of the gene resulted in a methionine-to-lysine substitution at residue 102. This mutation destroys a restriction site for the enzyme NlaIII, and restriction analysis confirmed that all the affected family members are heterozygous carriers of the mutation (Figure 2). In family DRD-1, an abnormally migrating band on SSCP analysis of exon 2 was found in 2 affected persons and 1 obligate carrier (Figure 1); sequencing of
the exon revealed a T→G transversion resulting in a cysteine-to-tryptophan change at residue 141. In family DRD-2, an altered SSCP band of exon 4 in 2 affected persons (Figure 1) suggested the existence of a disease-causing change, and direct sequencing of the sample revealed a G→C transversion that is predicted to cause a serine-to-threonine change at residue 176.

All these sequence alterations are located within highly conserved regions of the gene\textsuperscript{25} and are likely to disturb activity of the GCH-I. Moreover, because their presence was confirmed by either SSCP or restriction analysis in several patients in each family (including an obligate carrier in family DRD-1), this may serve as additional evidence for the pathogenic role of the mutations identified.

In patients from 3 families, and in both patients with sporadic DRD, no abnormally migrating bands were observed on SSCP analysis; direct sequencing of the entire coding region and splicing junctions of the GCH-I gene in these patients revealed no variations compared with the control sequence.
Our results confirm that heterozygous mutations of the GCH-I gene are associated with autosomal–dominantly inherited DRD. We identified 3 new point mutations distributed throughout the coding region of the GCH-I gene, all being missense mutations resulting in protein amino acid sequence alterations. Several previous groups also observed disease-causing changes in GCH-I exons 1, 2, and 4, including transitions within highly conserved regions of the gene.12-16 None of the mutations of the GCH-I gene reported in these Russian families with DRD or described so far in other series of molecularly studied DRD cases12,13,19 were detected more than once. We agree with Bandmann et al16 that these findings may preclude the possibility of creating simple DNA testing procedures in families with DRD for routine clinical practice.

We found no mutations in the translated portion of the GCH-I gene in 3 families with typical autosomal-dominant DRD or in 2 patients with sporadic DRD. These data are in agreement with those of other groups.12,16 There are several possible explanations for these findings. First, some sequence alterations within the noncoding region of the gene may account for the disease phenotype in these patients. Second, because the number of available DNA samples from affected members of families DRD-3 and DRD-5 was limited and did not allow us to confirm linkage to chromosome 14q, we cannot exclude a causative role of another, as yet unidentified, gene(s) in autosomal-dominant DRD. Further data collection with detailed clinical, molecular genetic, and biochemical studies will help characterize involvement of different genes in the pathogenesis of DRD.

Our experience shows that in the case of the normal pattern on SSCP analysis, the possibility of identifying mutations of the GCH-I gene through sequencing of the entire coding region seems unlikely. We conclude that the strategy used in the present study for the purpose of mutation screening is the most appropriate in families with autosomal-dominant 14q-linked DRD and in sporadic cases with the presumed clinical diagnosis of DRD.

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REFERENCES