Mutations in GNAL  
A Novel Cause of Craniocervical Dystonia

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In two independent studies, exome sequencing of the GNAL gene (RefSeq NM_001142339) was used recently to study GNAL mutations as a cause of autosomal dominant primary torsion dystonia in patients of European and African American ancestry. The GNAL gene is located on the short arm of chromosome 18p11, and the absence of GNAL may contribute to dystonia in patients with the 18p deletion syndrome. Onset among mutation carriers occurred mainly in the neck (82%) at a mean age of onset at 31.3 (range, 7-54) years. On examination, almost all patients had cervical dystonia (93%), but cranial (57%) and speech involvement (44%) were also quite common.1

The GNAL gene encodes the stimulatory α subunit, Gαolf, that links G protein-coupled receptors to downstream effector molecules and functions as a heterotrimer composed of α, β, and γ subunits. The Gαolf subunit is expressed prominently in the brain, especially in the striatum, where it may couple dopamine D1 receptors and adenosine A2A receptors to the activation of adenylyl cyclase type 5. In fact, efficiency of heterotrimer formation or coupling to D1 receptors was previously shown to be impaired in GNAL mutation carriers using a bioluminescence energy transfer (BRET) assay.1 The Gαolf subunit is also involved in odorant signal transduction.2 Notably, Gnal-null mice are anosmic,3 raising the possibility that mutations in GNAL may also cause hyposmia in humans.2 Because Gαolf plays a role in dopamine signal transduction, mutations in GNAL potentially increase susceptibility to movement disorders induced by dopamine antagonists. Differential methylation of CpG islands in the vicinity of exon 1 also exists, suggestive of genomic imprinting of the GNAL gene.7 We screened for GNAL mutations in a multiethnic sample with different dystonia phenotypes and other clinical phenotypes linked to the putative function of the gene.

Methods

The study was approved by the respective institutional review boards, and all patients gave written informed consent. Patients were recruited from movement disorder clinics in Germany, Serbia, and Japan. The sample populations (Table) consisted of patients with different dystonia phenotypes, including cervical, segmental, and generalized dystonia; patients with...
idioPAThIC PD with low scores (~15th percentile) on the University of Pennsylvania Smell Identification Test; and patients with tardive dyskinesias or acute dystonic reactions to dopamine receptor-blocking agents. The diagnoses were based on accepted clinical criteria. A detailed neurological assessment was performed on mutation carriers, including a videotaped neurological examination and assessment of dystonia severity (Burke-Fahn-Marsden Dystonia Rating Scale) and cognition (Montreal Cognitive Assessment). Olfaction was assessed using either the Brief Smell Identification Test (BSIT; Sensonics, Inc) or by intravenous administration of thiamine propyldisulfide (Alinamin) as previously described. The GAG sensor (Sensonics, Inc) or by intravenous administration of thiamine propyldisulfide (Alinamin) as previously described.10 The GAG deletion in TOR1A (RefSeq NM_000113) and mutations in THAP1 (RefSeq NM_018105) had previously been excluded in the German and Serbian patients with dystonia.11

We extracted DNA from blood samples using standard methods. Sanger sequencing was performed for all 12 exons of GNAL and exon-intron junctions (Supplement [eTable 1]). When a potentially pathogenic variant was identified, we screened for this variant in an ethnically matched control sample. Quantitative polymerase chain reaction of exon 9 was performed on a commercially available system (LightCycler 480; Roche Diagnostics) using an asymmetrical cyanine dye (SYBR Green; Life Technologies) to test for whole gene deletions/duplications (Supplement [eTable 2]) and were absent in the exome //genetics.bwh.harvard.edu/pph2, and SIFT [http://sift.jcvi.org] (Supplement [eTable 2]) and were absent in the exome variant server database (http://evs.gs.washington.edu/ EVS) and in ethnically matched (538 German or 192 Japanese) control chromosomes. Furthermore, the BRET assay found that both variants disturbed Gαolf function markedly, with increased basal BRET ratios (R0) and a severely attenuated signal after application of dopamine (Rmax − R0) reflecting impairments in Gαolf − Gβγ heterotrimer formation and functional coupling to D2 receptors. The variant was absent in the German controls and predicted to be damaging using three different software tools (Mutation Taster [http://www.mutationtaster.org], PolyPhen-2 [http://genetics.bwh.harvard.edu/pph2], and SIFT [http://sift.jcvi.org]) (Supplement [eTable 2]) and were absent in the exome variant server database (http://evs.gs.washington.edu/EVS) and in ethnically matched (538 German or 192 Japanese) control chromosomes. Furthermore, the BRET assay found that both variants disturbed Gαolf function markedly, with increased basal BRET ratios (R0) and a severely attenuated signal after application of dopamine (Rmax − R0) reflecting impairments in Gαolf − Gβγ heterotrimer formation and functional coupling to D2 receptors, respectively (Figure 2). A p.Ala311Thr variant was found in a German patient with sporadic dystonia con- founded by the diagnosis of relapsing-remitting multiple sclerosis. The variant was absent in the German controls and predicted to be pathogenic on Mutation Taster and SIFT but was benign on PolyPhen-2 and indistinguishable from the wild type on the BRET assay. A p.Try92 Ala variant was detected in a patient of Filipino descent with cervical dystonia who was recruited from Germany; however, this variant was also present in 19 of 570 Filipino control chromosomes. In addition,
we found the novel synonymous variants p.Ile222Ile and p.Cys352Cys in a German patient and a Japanese patient, respectively, and nonsynonymous variants in 2 German controls (p.Ala303Thr and p.Ile272Phe) and 1 Japanese control (p.Met373Ile).

Sequencing of complementary DNA revealed comparable levels of mutant and wild-type messenger RNA (ie, equal expression of both alleles) in peripheral blood leukocytes from the two patients with likely pathogenic mutations (p.Gly213Ser and p.Ala353Thr). Both mutation carriers had onset of dystonia in the cervical region. No pathogenic mutations were identified in patients with PD and hyposmia, tardive dyskinesias, or acute dystonic reactions. No patients were found to have exon 9 deletions or duplications. A follow-up clinical evaluation was performed on mutation carriers. No other family members were available for clinical or genetic assessment.

Report of Cases

The carrier of the p.Gly213Ser mutation was a man in his 50s (individual L4486) who had onset of cervical dystonia at 40 years of age. On examination he had severe retrocollis, laterocollis to the left, torticollis to the right, head tremor, left shoulder elevation, oromandibular dystonia, and blepharospasm (Video). The family history was negative for cervical dystonia, and results of assessment of olfaction (ie, sense of smell on the Brief Smell Identification Test) and cognition (29 of 30 on the Montreal Cognitive Assessment) were normal.

The Japanese patient carrying the p.Ala353Thr variant was a woman in her 50s with isolated cervical dystonia and an age at onset of 44 years. No evidence of hyposmia (normal latency and duration for the thiamine propyldisulfide test) or cog-
Nitive dysfunction (30 of 30 on the Montreal Cognitive Assessment) was found. Her father, who died in a motor vehicle crash at age 73 years, was also affected by cervical dystonia, with onset in the fifth decade of life after a traumatic head injury.

Discussion

Mutations in GNAL have been identified in families of European and African American descent with multi-incident dystonia.\(^1\)\(^2\) In this screening study, we detected likely pathogenic GNAL mutations in a German and a Japanese patient. The predominant phenotype appears to be dystonia, with onset in the neck and progression to other sites, particularly the cranial region. The family history in both GNAL mutation carriers was difficult to confirm given that no family members were available for assessment, and the father of the Japanese patient developed cervical dystonia after a head injury.

Putatively pathogenic mutations in GNAL were found in approximately 1% of patients with cervical dystonia in this sample. Most of the patients in this sample had sporadic cervical dystonia (82.1% without a known family history vs 17.9% with a known family history). This result extends the original study that found GNAL mutations in 19% of multiplex families with primary torsion dystonia.\(^1\) The GNAL gene is now one of several implicated as a cause of primary torsion dystonia, including TOR1A (DYT1), THAP1 (DYT6), and more recently CIZ1,\(^13\) ANO3,\(^13\) and TUBB4.\(^14\) Of these genes, THAP1, CIZ1, ANO3, TUBB4, and GNAL are considered to have prominent cranio-cervical involvement, although the pathophysiological basis for this anatomical predilection is not clear. In the present study, neither carrier of confirmed mutations had evidence of hyposmia, so olfactory dysfunction may not be a useful biomarker for GNAL mutations. Moreover, no mutations were found in patients with PD and hyposmia, tardive dyskinesias, or acute dystonic reactions, so these phenotypes are less likely to be linked to mutations in GNAL.

Although GNAL has been suggested to be an imprinted gene, we demonstrated equal expression of mutant and wild-type alleles in peripheral blood leukocytes. This finding argues against allele-specific expression dependent on the parental origin of the allele. Furthermore, the BRET assay might serve as a valuable tool to support the pathogenicity of detected variants in the GNAL gene. Although dopamine receptor pathways are clearly implicated in the etiology of dystonia, potential Gαolf interactions with adenosine receptors might also be affected, or mutations could influence other unknown binding partners or activities. Therefore, if a variant exhibits wild-type behavior on the BRET assay, a dystonia-causing mutation is not necessarily excluded. Also of note, the ethically matched control populations in this study were relatively small.

Figure 2. Functional Effects of GNAL Mutations in a Cell-Based Bioluminescence Energy Transfer (BRET) Assay

We have identified likely pathogenic GNAL mutations in patients of German and Japanese descent with cranio-cervical dystonia. Further studies of the pathophysiological mechanisms underlying GNAL mutations are now required.
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Author Contributions: Dr Klein had full access to all the data in the study and takes responsibility for the integrity of the data and the accuracy of the data analysis.

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