Glucocerebrosidase Gene Mutations

A Risk Factor for Lewy Body Disorders

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Background: Mutations in the glucocerebrosidase (GBA) gene have been reported to modify risk for Parkinson disease (PD) and dementia with Lewy bodies (DLB). However, these findings have not been consistently replicated, and most studies have had substantial methodological shortcomings.

Objective: To better assess the role of GBA variants in altering risk for Lewy body disorders.

Design: Case-control study.

Setting: Four movement disorder clinics in the Seattle, Washington, area.

Participants: Seven hundred twenty-one patients with PD, 554 healthy control subjects, and 57 patients with DLB.

Main Outcome Measures: Disease status and presence or absence of the 2 most common GBA mutations (N370S and L444P).

Results: We observed a significantly higher heterozygote frequency for the 2 mutations in patients with PD (2.9%; P = .001) and those with DLB (3.5%; P = .045) compared with control subjects (0.4%).

Conclusion: Our findings suggest that GBA mutations exert a large effect on susceptibility for Lewy body disorders at the individual level but are associated with a modest (approximately 3%) population-attributable risk in individuals of European ancestry.

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Although these case-control data are intriguing, interpretation has been difficult and several criticisms have been raised. Most of the studies had adequate power to detect only large effects at the expected allele frequencies, 2 failed to include an independent control group, and in some race/ethnicity was incompletely characterized. The number of mutations assessed varied greatly, from only the 2 most common (N370S and L444P) to comprehensive screenings of the entire coding region. Finally, mutation frequencies in patients have varied several-fold among studies, even within individuals of similar ancestry. With these issues in mind, we sought to further assess the role of GBA in Lewy body disorders by examining the frequency of the N370S and L444P mutations in a large PD case-control sample of European origin and in a cohort of patients with DLB.

STUDY PARTICIPANTS

The study population included 721 patients with PD, 554 control subjects, and 57 pa-
patients with DLB. The PD group was primarily composed of a cohort of patients (n = 706) consecutively recruited at 4 movement disorder clinics in the Seattle, Washington, area. All patients with PD met clinical diagnostic criteria for PD as determined by a movement disorder specialist, and neuro-pathological confirmation was available for 1 patient. Control subjects had no history of parkinsonism or dementia (by structured interview) and were either spouses of patients with PD (n = 310) or volunteers from the local community (n = 244). Only patients with PD and control subjects of European origin were included in the study.

The DLB group was composed of 3 living patients who met revised clinical diagnostic criteria for probable DLB and patients with dementia who met pathologic criteria for high-(n = 21) or intermediate- (n = 33) likelihood DLB. Patients with Lewy-related pathology confined to the amygdala were excluded from the study. Only patients with DLB of self-defined white ancestry were included in the analysis. Insufficient information was available to differentiate between patients with DLB of European vs Middle Eastern–North African origin (eg, Ashkenazi Jews).

All study participants had previously been screened for pathogenic LRRK2 mutations, and those who carried 1 or more of these variants were excluded from the study. The institutional review boards at each participating site approved the study, and all participants gave informed consent.

### GENOTYPING AND DATA ANALYSIS

We genotyped N370S by TaqMan Assay (Applied Biosystems, Foster City, California) using primers 5′-GCTTATCTTCTTTTGTGTGC-3′ (forward) and 5′-GGGTTCAGGGCAAGGTT-3′ (reverse) and probes 5′-VIC-TACCCTAGAacCCTCCTG-3′ and 5′-6FAM-TACCCTAGGcCCTCCT-3′. The L444P mutation was genotyped by sequencing a polymerase chain reaction template that spanned the 3′ half of exon 9 and the full length of exon 10 using primers 5′-CAAATTTGGGTGTCAACTTT-3′ (forward) and 5′-TAGGGAGCAGGGAGAG-3′ (reverse). L444P occurs either as an individual mutation or in cis with other variants (eg, A456P and V460V) as a recombinant allele formed by recombination between GBA and a nearby pseudogene.

Genotype frequencies in patients and control subjects were compared by means of the Fisher exact test. Population-attributable risk was calculated using the following equation:

\[ P(OR−1)/1 + P(OR−1) \]

where \( P \) is the prevalence of mutation carriers among control subjects and OR is the odds ratio for disease (PD or DLB).

### RESULTS

Twenty-one of the 721 patients with PD (2.9%), 2 of the 57 patients with DLB (3.5%), and 2 of the 554 control subjects (0.4%) were heterozygous for GBA mutations N370S or L444P (Table 1). A significantly higher frequency of mutation carriers was found in the PD sample compared with the control group (odds ratio, 8.3; 95% confidence interval, 2.0-73.1; \( P < .001 \)). A marginally significant overrepresentation of mutation carriers was observed among patients with DLB (odds ratio, 10.0; 95% confidence interval, 0.7-139.8; \( P = .045 \)).

The clinical characteristics of the 21 patients with PD heterozygous for GBA mutations are given in Table 2. Most of these patients had late-onset disease (14 of 21) and reported no family history of PD (17 of 21). Five of the patients had developed substantial cognitive impairment more than 1 year after onset of parkinsonism. No significant difference was found in mean age at onset, disease duration, or sex distribution between patients with PD with and without mutations (Table 3).

The 2 patients with DLB who carried GBA mutations both had diffuse neocortical Lewy-related pathology. One carried a recombinant allele (Rec 1) that contained L444P and had a high level of concomitant Alzheimer-type pathology (Braak stage V, Consortium to Establish a Registry for Alzheimer's Disease plaque score C; intermediate-likelihood DLB). The other was heterozygous for N370S and had a low degree of Alzheimer pathology (Braak stage II, Consortium to Establish a Registry for Alzheimer's Disease plaque score A; high-likelihood DLB).

In sequencing the region flanking L444P, we identified 2 novel variants (H422T and T410T) and several intronic polymorphisms of unknown functional significance. However, we did not detect any other mutations that have been reported as pathogenic for Gaucher disease.

Our data suggest that GBA mutations might represent a significant risk factor for Lewy body disorders. However, although the effect sizes observed in our case-control sample were large (odds ratios in the 8-10 range), the frequency of mutation carriers among both the PD and DLB groups was low (Table 1). Thus, we estimate that the population-attributable risk for GBA mutations in Lewy body disorders is only approximately 3% in individuals of European ancestry (Table 1).

Most patients with PD heterozygous for GBA mutations in our cohort had sporadic, late-onset disease that was responsive to levodopa, consistent with previously published data (Table 2). This finding is in contrast to some parkinsonian patients with Gaucher disease in whom parkinsonism was of early onset and refractory to treatment.

Our work has 3 major strengths compared with previously published studies on GBA mutations in PD populations of primarily European origin. First, our study had a large sample size. A frequent observation among genetic association analyses is the initial report of a large effect in a small sample followed by more powerful studies that typi-

### COMMENT
GBA mutations have been previously mentioned, the first study reported a mutation frequency of 14% among 57 patients with PD and 0% among 44 control samples derived from US brain banks. The 5 subsequent studies have observed effects of marginal or no significance, but 4 of these have included a PD cohort of fewer than 100 patients and were thus underpowered. Our study addressed this issue by using a PD cohort that exceeded the combined sample size of patients with PD across all 6 studies and suggests a potentially bona fide but more modest effect than originally reported.

Second, our study limited the sample to individuals of European ancestry. The N370 mutation has a much higher prevalence among Ashkenazi Jews than in individuals of European origin. Thus, spurious associations might arise if cases and control subjects are drawn differentially from these populations. We collected detailed information on ancestry from patients with PD and control subjects at the time of enrollment and were thus able to account for this important confounder. In contrast, such data were largely lacking in previous studies.

Third, we included a matched control group. Some studies have failed to include a control group and have instead relied on previous estimates of GBA mutation frequencies derived indirectly from epidemiologic studies on Gaucher disease. Another derived control subjects from brain banks with minimal data available on ancestry. These approaches are subject to substantial bias and confounding. We used a control group screened for parkinsonism and matched closely for age, ancestry, and area of residence.

Our study also had several limitations. Although more than 200 pathogenic GBA mutations have been reported, we genotyped only the 2 most common ones, N370S and N370G.
which together account for approximately 70% of the disease alleles in white patients with Gaucher disease (excluding Ashkenazi Jews; International Collaborative Gaucher Group Gaucher Registry, unpublished data, September 2006). Thus, we might have underestimated the true mutation frequency. The sample size of the DBL group was small, and there was insufficient information to separate individuals of European ancestry from those of other white populations. Thus, findings from our analysis of the DBL group must be interpreted with caution, but these data suggest that the remarkably high mutation frequency (23%) observed in a previous DBL sample (n = 35) might be an overestimate. 

Common variants in many genes have been nominated as risk factors for PD in populations of European origin, but arguably all but 2 (SNCA and MAPT) have later failed validation. This phenomenon has engendered a healthy skepticism in evaluating newly nominated susceptibility genes, and GBA is no exception. Given the large burden of proof incumbent on candidate gene studies, our findings should not be considered definitive replication but indicate that the role of GBA in Lewy body disorders merits intensive study. This will require large-scale collaborative efforts and well-designed studies on thousands of individuals.

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