Parkinsonism in GTP cyclohydrolase 1 mutation carriers

Ilaria Guella,1 Holly E. Sherman,1 Silke Appel-Cresswell,2 Alex Rajput,3 Ali H. Rajput3 and Matthew J. Farrer1

1 Djavad Mowafaghian Centre for Brain Health, Department of Medical Genetics, University of British Columbia, Vancouver, BC, Canada
2 Pacific Parkinson’s Research Centre, Department of Medicine (Neurology), University of British Columbia Vancouver, BC, Canada
3 Division of Neurology, University of Saskatchewan and Saskatoon Health Region, Saskatoon, SK, Canada

Correspondence to: Ilaria Guella, PhD, Djavad Mowafaghian Centre for Brain Health, University of British Columbia, Vancouver, BC, Canada, V6T 1Z3
E-mail: iguella@can.ubc.ca

Sir,

We read with great interest the article by Mencacci and colleagues (2014) reporting a significantly higher frequency of GTP cyclohydrolase 1 (GCH1) variants in patients with Parkinson’s disease compared to controls. Whole-exome sequencing of a large case-control cohort showed that rare GCH1 coding variants are associated with a 7-fold increased risk of Parkinson’s disease.

Heterozygous loss-of-function mutations in GCH1, a crucial enzyme for dopamine production in nigrostriatal neurons (Kaufman, 1959; Nagatsu et al., 1964), are the most common cause of DOPA-responsive dystonia (DRD) (Ichinose et al., 1994). DRD is a rare hereditary disease characterized by childhood-onset, generalized dystonia and a dramatic long-lasting response to levodopa (Segawa et al., 1976). The disease may also manifest in adulthood with parkinsonism as the sole or dominant clinical feature (Hjermind et al., 2006; Momma et al., 2009). GCH1 mutations have been shown to segregate in pedigrees with multiple individuals affected by isolated parkinsonism, a phenotype that is likely due to nigrostriatal degeneration (Kikuchi et al., 2004; Hjermind et al., 2006; Eggers et al., 2012; Mencacci et al., 2014). Herein, we report GCH1 variability in patients with Parkinson’s disease (n = 361, 68.7% male, mean age 69.9 ± 12.8 years; mean age at onset 58.3 ± 12.9 years), atypical parkinsonism (n = 167, male 61.7%, mean age 77.5 ± 12.2 years; mean age at onset 66.3 ± 11.2 years, including diagnostic categories of dementia with Lewy bodies, progressive supranuclear palsy and multiple system atrophy) and control subjects (n = 290, 59% male; mean age 73.3 ± 11.2 years).

Sequencing of GCH1 coding regions, performed on the SOLiD 5500xl platform (Life Technologies), identified four rare heterozygous non-synonymous coding substitutions including: (i) a novel missense variation (p.A99D); (ii) the known DRD pathogenic mutation (p.K224R); and (iii) two benign variants (p.P23L and p.P69L) (Jarman et al., 1997; Mencacci et al., 2014). The p.A99D mutation was identified in a male patient with typical late-onset Parkinson’s disease (age at onset 61 years) with an extensive family history of dementia and parkinsonism. This amino acid position is highly conserved, and substitution of a hydrophobic non-polar (alanine) to a negatively charged (glutamic acid) amino acid is likely to perturb the amphipathic alpha-helical structure of this domain. The mutation has not been reported in the publically available Exome Variant Server data set (http://evs.gs.washington.edu/EVS/), which suggests it is unlikely to be a benign, albeit rare, variant. The p.K224R mutation, previously described in pedigrees with dominantly inherited DRD (Leuzzi et al., 2002), was detected in two unrelated Canadian patients. One had asymmetrical tremor onset parkinsonism (age at onset 82 years) and good levodopa response. She died at 90 years and brain pathology showed...
Moreover the presence of GCH1 targets. Overall, the frequency of GCH1 pathogenic mutations in patients is 0.57% (3/528), whereas only two benign variants were identified in one control subject, consistent with the recently published results (frequency in patients with Parkinson’s disease 0.75% versus controls 0.1%) (Mencacci et al., 2014) and may concur with a mega meta-analysis of genome-wide association data which have highlighted GCH1 as a low-risk susceptibility locus for Parkinson’s disease (Nalls et al., 2014). Taken together these data suggest that GCH1 genetic variability should be considered as a risk factor for parkinsonism.

Past studies investigating the role of GCH1 variability in early-onset Parkinson’s disease have reported negative results (Hertz et al., 2006; Cobb et al., 2009), although they were performed in relatively small cohorts insufficiently powered to assess the contribution of rare variants. To confirm pathogenicity, segregation analysis of putative GCH1 mutations within extended pedigrees is warranted; whether GCH1 parkinsonism is more penetrant in females, as for DRD (Furukawa et al., 1998) may also be qualified. Moreover the presence of GCH1 copy number variants may be as frequent and should be assessed (Wider et al., 2008). Additional autopsy studies may address whether post-mortem tauopathy is an incidental finding, merely concurrent, or a consequence of GCH1 mutations. Insight into the pathogenic mechanism may help elucidate the role of dopamine metabolism in nigrostriatal degeneration and parkinsonism, and to develop new therapeutic targets.

Funding

Canada Excellence Research Chairs program (M.J.F.), the Cundill Foundation (M.J.F), Leading Edge Endowment. Funds provided by the Province of British Columbia, LifeLabs, and Genome BC which support the Dr Donald Rix BC Leadership Chair (M.J.F), as well as the Pacific Parkinson’s Research Institute (S.A.C.).

References


