Loss of VPS13C Function in Autosomal-Recessive Parkinsonism Causes Mitochondrial Dysfunction and Increases PINK1/Parkin-Dependent Mitophagy

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Autosomal-recessive early-onset parkinsonism is clinically and genetically heterogeneous. The genetic causes of approximately 50% of autosomal-recessive early-onset forms of Parkinson disease (PD) remain to be elucidated. Homozygosity mapping and exome sequencing in 62 isolated individuals with early-onset parkinsonism and confirmed consanguinity followed by data mining in the exomes of 1,348 PD-affected individuals identified, in three isolated subjects, homozygous or compound heterozygous truncating mutations in vacuolar protein sorting 13C (VPS13C). VPS13C mutations are associated with a distinct form of early-onset parkinsonism characterized by rapid and severe disease progression and early cognitive decline; the pathological features were striking and reminiscent of diffuse Lewy body disease. In cell models, VPS13C partly localized to the outer membrane of mitochondria. Silencing of VPS13C was associated with lower mitochondrial membrane potential, mitochondrial fragmentation, increased respiration rates, exacerbated PINK1/Parkin-dependent mitophagy, and transcriptional upregulation of PARK2 in response to mitochondrial damage. This work suggests that loss of function of VPS13C is a cause of autosomal-recessive early-onset parkinsonism with a distinctive phenotype of rapid and severe progression.

Introduction

Parkinson disease (PD [MIM: 168600]) is a motor syndrome with variable combinations of akinesia, rigidity, and rest tremor responding to levodopa. It is caused by degeneration of the dopaminergic neurons in the substantia nigra pars compacta and is associated with Lewy bodies, intraneuronal inclusions enriched in α-synuclein. In recent years, our understanding of the pathophysiological mechanisms underlying molecular defects in familial forms of PD has greatly advanced. Three genes have been conclusively associated with autosomal-dominant (AD) forms of PD (SNCA [MIM: 163890], LRRK2 [MIM: 609007], and VPS35 [MIM: 601501]) and eight genes (PARK2 [MIM: 602544], PINK1 [MIM: 608309], DJ-1 [MIM: 602533], ATP13A2 [MIM: 610513], FBXO7 [MIM: 605648], PLA2G6 [MIM: 630604], SYNF [MIM: 604297], and DNAJC6 [MIM: 608375]) with early-onset (EO) autosomal-recessive (AR) forms.1 EO AR parkinsonism is clinically and genetically heterogeneous: mutations in PARK2, PINK1, and DJ-1 cause phenotypes similar to idiopathic PD with good and prolonged response to dopaminergic

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therapy. Other EO AR PD-associated genes cause more severe disease, a poor response to levodopa, and additional clinical signs, such as dystonia and cognitive impairment. Mutations in PARK2 and PINK1 are the most common cause of EO AR PD, accounting for ~50% and 4% of familial cases in Europe, respectively. A significant proportion of cases remain genetically unexplained.

EO AR PD is linked to mitochondrial dysfunction. The mitochondrial kinase PINK1 and the E3 ubiquitin-protein ligase Parkin cooperate in mitochondrial quality control. They promote the removal of dysfunctional mitochondria in a process termed mitophagy that might also involve FBXO7. In addition, they play a role in a vesicular trafficking pathway targeting damaged mitochondrial components to the lysosome. To identify additional PD-associated genes involved in AR EO parkinsonism, we performed homozygosity mapping and exome sequencing in consanguineous PD families and isolated individuals and used data mining in the exomes of 1,348 unrelated PD-affected individuals. Five truncating mutations in vacuolar protein sorting 13C (VPS13C [MIM: 608879]) were identified in three unrelated PD-affected isolated individuals. We provide evidence that depletion of VPS13C exacerbates mitochondrial vulnerability to stress.

Subjects and Methods

Participants

Gene Discovery Cohort

We selected nine PD-affected families (with two or more affected siblings) and 43 unrelated isolated individuals according to the following criteria: (1) diagnosed by neurologists according to the UK Parkinson’s Disease Society Brain Bank (PDSBB) clinical diagnostic criteria and onset ≤55 years in at least one affected family member; (2) with no mutations in known PD-associated genes; and (3) with confirmed consanguinity (inbreeding coefficient F ≠ 0 computed with the FEstim program†). Sixteen families or isolated subjects were European, 16 North African, 19 Turkish, and 1 Lebanese. A total of 66 PD-affected individuals (23 family members and 43 isolated subjects) and 39 unaffected relatives were included for the genome-wide screen study. 62 affected and 10 unaffected individuals were subsequently selected for whole-exome sequencing.

Validation Cohort

Exome data were obtained from a series of 1,348 additional PD-affected individuals (99% unrelated, 99% of European ancestry, 60% males; mean age at onset 41.7 ± 11.0 years), including 249 French PD-affected probands (57% males, age at onset ≤40 years, 50 individuals with atypical forms of parkinsonism) recruited by the French network for the study of PD genetics (PDG) and 530 matched control subjects (95% of European ancestry, 65% males, mean age at examination: 45.1 ± 10.7 years) from the International Parkinson Disease Genomics Consortium (IPDGC).

100 Turkish control subjects without family history of PD (43% males; mean age at examination, 60.4 ± 13.9 years) served to check for the absence of the identified variant in family A, which originated from Turkey.

A flow diagram detailing the selection criteria of PD-affected individuals and control subjects and the different experimental steps of the study is provided (Figure S1).

Study Approval

Informed consent was obtained from all participants, and the genetic studies were approved by local ethics committees (INSERM, CCPRPB du Groupe Hospitalier Pitié-Salpêtrière, Paris, France).

Neuropathological Assessment

The autopsy of the affected individual II-1 in family B (Figure 1) was performed approximately 36 hr post mortem. Brain tissues were fixed for 6 weeks in 10% buffered formalin, extensively sampled, and processed as previously described. Immunohistochemistry was performed by a Ventana Benchmark automate. We used hematoxylin-eosin staining for histopathology. For immunohistochemistry, the antibodies used were: anti-Tau (in-house AD2, 1 ng/mL), anti-β-amyloid (4G8, 1:1,000, Sigma), anti-α-synuclein (LB509, 1:500, Abcam), anti-ubiquitin (1:1,000, Dako), anti-TDP-43 (1:500, Protein Tech), and anti-glial fibrillary acid protein (GFAP, 1:20,000, Dako). The degree of neuronal loss and the frequency of α-synuclein-immunoreactive and other inclusions were determined semiquantitatively by visual inspection, in comparison to brains of three age-matched controls (two males and one female) from the Lille Neurobank collection.

Molecular Studies

Whole-Genome Homozygosity Linkage Mapping

Genome-wide screens were performed on all available affected (n = 66) and unaffected (n = 39) individuals from the gene discovery cohort using the Illumina HumanCytoSNP-12 v2.1 DNA Analysis BeadChip microarrays that contain ~300,000 SNPs and ~1,300 markers of common copy-number variations (CNVs). Homozygosity tracks (>2 Mb) were visualized with the Homozygosity Detector module and CNV with the Illumina cnvPartition module. The inbreeding coefficients F were computed with the FEstim program. Samples from individuals with confirmed consanguinity (F ≠ 0) were subjected to exome sequencing.

Whole-Exome Sequencing

Exons from 62 affected (19 relatives and 43 isolated individuals) and 10 unaffected family members from the gene discovery cohort and all the 1,348 affected and 530 control individuals from the validation cohort were captured using different exome enrichment kits from fragmented genomic DNA and sequenced as indicated in Table S1. 10-fold mean sequencing depth was achieved in 96.4% and 88.8% of baited regions in PD-affected individuals and control subjects, respectively, and 30-fold mean sequencing depth was achieved across ~75% of targeted regions.

Human reference sequence UCSC hg19 was used for sequence alignment and variant calling with the Burrows-Wheeler Aligner and the Genome Analysis Toolkit. PCR duplicates were removed prior to variant calling using Picard software. Variants were annotated with ANNOVAR software (exomes from validation cohort) or SpnEff and SpnSift programs (exomes from gene discovery cohort). Data were analyzed with Ingenuity Variant Analysis (IVA) TM software from Ingenuity System. Effects on mRNA splicing by putative splice variants (±5 base pairs around splice junctions according to IVA threshold) were analyzed with Splice Site Finder, MaxEntScan, NNSplice, Genesplicer, and Human Splicing Finder, all included in Alamut v.3 software. The human VPS13C protein and its closest homologs were aligned with Alamut v.3 software, computed by Ensembl, and aligned with MUSCLE.
An in-house pipeline crossed the output data from IVA and Homozygosity Mapping to filter and identify the variants of interest (Figure S2). These variants were visualized with the Broad Institute Integrative Genomics Viewer (IGV) and verified by bidirectional Sanger sequencing using primers designed with Primer3 (Table S2) on an ABI 3730 automated sequencer (Life Technologies). Sanger sequencing confirmed the absence of mutations in origin-matched controls and determined the genetic status of unaffected relatives. Mutation nomenclature follows Human Genome Variation Society (HGVS) recommendations: the longest \( VPS13C \) transcript 2A cDNA nucleotides (''c.'') are numbered from the adenine of the first ATG translation initiation codon as nucleotide +1 (reference sequence GenBank: NM_020821.2).

**Splicing Defect Analysis by RT-PCR**

Keratinocytes from affected individual V-2 in family A or peripheral blood lymphocytes from affected individual II-1 in family C (Figure 1) were used for splicing defects analyses. Hair follicles were plucked under sterile conditions and cultured in flasks coated with MG (1:10, Corning). Keratinocytes were grown on 20 mg/mL collagen IV (Sigma-Aldrich)-coated dishes containing EpiLife medium with the HKGS supplement (Life Technologies). Total RNA extraction was carried out with the RNeasy Kit (QIAGEN), according to the manufacturer's manual. RNA (250 ng) was reverse transcribed into cDNA using iScript reverse transcription supermix (Bio-Rad). Primers are listed in Table S2. RT-PCR products were Sanger sequenced.
directly or after sub-cloning into the pJET1.2/blunt vector (Thermo Scientific).

Studies in Mammalian Cells

Mammalian Expression Vectors, siRNAs, Cell Culture, and Transfection

COS-7 and HEK293T cells were grown in Dulbecco's Modified Eagle Medium + Glutamax (Life Technologies) supplemented with 10% goat serum (Life Technologies) and 1% penicillin-streptomycin (Life Technologies). Cells were plated, at 80% confluence, on glass coverslips (Thermo Scientific) in 24-well cell plates for immunofluorescence, 6-well plates for qPCR, 10-cm Petri dishes for subcellular fractionation by differential centrifugation and for the mitochondrion isolation kit, or 75-cm² flasks for continuous sucrose gradient and Percoll gradient purification. Cells were co-transfected with siRNAs (15 to 30 nM) and expression vectors using Lipofectamine 2000 (Life Technologies), in an antibiotic-free medium, according to the manufacturer's instructions. The siRNA used were: Hs_VPS13C_5 and Hs_VPS13C_6 (siVPS13C, QIAGEN); PINK1 stealth siRNAs (siPINK1, Invitrogen); and AllStars negative control siRNA (siControl, QIAGEN). Their efficacy was controlled by quantitative real-time RT-PCR (Figure S5). The expression vectors were: pcDNA3-HA-PARK2, pcDNA3-HA-PINK1, pcDNA3-HA,17 and pEGFP-C1 (Life Technologies). Where indicated, the cells were incubated with 10 μM CCCP (Sigma).

Subcellular Fractionation, Trypsin Digestion Assay, and Western Blot Analyses

For sucrose density gradient, confluent HEK293T cells from five 75-cm² flasks were harvested and disrupted with a Dounce homogenizer (80 manual strokes) in 10 mM Tris-HCl buffer (pH 7.6) containing 10% w/v sucrose, 10 mM ethylenediaminetetraacetic acid (EDTA), 0.5 mM dithiothreitol (DTT), supplemented with protease and phosphatase inhibitors (0.2 mM sodium orthovanadate, 4 mg/mL sodium fluoride, 5.4 mg/mL β-glycerophosphate, and Complete cocktail 1X – 11836145001, Roche). After three centrifugations at 600 × g for 5 min to remove cell debris, the cell lysate was layered on a 20%–60% linear sucrose gradient in 0.1 mM EDTA, 0.5 mM DTT, 0.1% BSA, and protease and phosphatase inhibitors and the crude mitochondrial fraction was acquired with an Olympus FV-1000 confocal microscope (36× oil objective). The mitochondrial parameters: basal oxygen consumption (expressed in pmol of O₂/s/mg of total protein), maximal respiratory capacity (maximal uncoupled respiration – non-mitochondrial respiration), reserve respiratory capacity (= maximal uncoupled respiration – basal respiration), and non-mitochondrial respiration (rotenone/antimycin A-inhibited respiration). Cells were then lysed to quantify the protein content using the Bradford reagent, which was used to normalize the oxygen consumption data. The results were expressed in pmol of O₂/s/mg of total protein.

Immunostaining, ΔΨmt, Respiration, Mitochondrial Morphology, and Parkin-Dependent Mitophagy

Immunocytochemical stainings were performed as described previously with the antibodies and dilution conditions indicated in Table S3. Changes in ΔΨmt were evaluated with the potential-dye tetramethylrhodamine methyl ester (TMRM) as described.19 Mitochondrial morphology was analyzed on COS-7 cells immunostained for the Beta subunit of the mitochondrial processing peptidase (PMPCB) using an image-processing algorithm and two descriptive parameters to assess mitochondrial length and branching: aspect ratio, calculated as the ratio between major and minor axes of each mitochondrial object, representing its length; and form factor, calculated as perimeter²/(4π × area), representing a combined evaluation of the length and degree of branching. The protein content of these fractions was determined with Bio-Rad protein assay (Bio-Rad, 500-0006), based on the Bradford method. Samples were boiled in protein sample buffer, resolved by SDS-PAGE, transferred onto a nitrocellulose membrane (Protran, Whatman), and analyzed by Western blotting with selected primary and secondary antibodies (Table S3). Membranes were incubated with enhanced chemiluminescence substrate (Pierce); chemiluminescent and fluorescent signals were revealed on film (ECL, Amersham Hyperfilm) or captured with Odyssey Imaging (Li-COR) systems and quantified with ImageJ software (NIH). Total or cytoplasmic fractions were normalized to α-tubulin, mitochondrial fractions to PMPCB. Three to six independent fractionation experiments were quantified.

Analysis of Mitochondrial Respiration

Cellular oxygen consumption was measured via high-resolution respirometry (OROBOROS Oxygraph-2k) in a temperature-regulated chamber at 37°C. Oxygen consumption was measured in intact COS-7 cells at a density of 2.5 × 10⁶ cells in 2 mL of respiration assay medium (1× DMEM, GlutaMAX, GIBCO) containing 4.5 g/L D-glucose and 4 mM L-glutamine, by sequential additions of 1 μg/mL oligomycin, 2.5 μM CCCP, and 5 μM rotenone/10 μM antimycin A. We determined the following mitochondrial parameters: basal oxygen consumption (= basal cellular respiration – non-mitochondrial respiration), proton leak (= oligomycin-inhibited respiration – non-mitochondrial respiration), maximal respiratory capacity (= maximal uncoupled respiration – non-mitochondrial respiration), reserve respiratory capacity (= maximal uncoupled respiration – basal respiration), and non-mitochondrial respiration (rotenone/antimycin A-inhibited respiration). Cells were then lysed to quantify the protein content using the Bradford reagent, which was used to normalize the oxygen consumption data. The results were expressed in pmol of O₂/s/mg of total protein.

Quantitative Real-Time RT-PCR

To demonstrate the efficiency of the siRNA-mediated silencing of endogenous VPS13C in HEK293T cells, total RNA was isolated from cells transfected with control or VPS13C or PINK1 siRNA using the RNeasy plus Mini Kit (QIAGEN) and QIAshredder (QIAGEN). RNA from each sample (500 ng) was reverse transcribed into cDNA using iScript reverse transcription supermix (Bio-Rad). Real-time PCR was performed with the LightCycler 480 System (Roche Applied Science) and SsoAdvanced Universal SYBR Green Supermix (Bio-Rad). Results were analyzed with LightCycler 480 sw 1.5 quantification Software (Roche Applied Science). Beta-actin (ACTB) was used as the reference gene for normalization. Primers are listed in Table S2.
Statistical Analysis
Statistical significance was established at \( p < 0.05 \) and determined with an unpaired t test in Figures 4A (Aspect Ratio) and S6A; matched t test in Figures 4C, SB, and SD; Mann-Whitney-Wilcoxon test in Figure 4A (Form Factor); one-way ANOVA in Figures 6 and S5; or two-way ANOVA in Figures 4B, SE, and SF.

Results

Truncating Mutations in VPS13C Cause AR Parkinsonism

Genome-wide screens in an initial series of 66 affected and 39 unaffected subjects using DNA microarrays identified a mean of 16.3 regions of homozygosity \( \geq 2 \) Mb on the 22 autosomes of each consanguineous individual (gene discovery cohort). No rare deleterious large genomic rearrangements were detected. Exomes were subsequently sequenced in the 62 affected individuals with confirmed consanguinity (inbreeding coefficient \( F \neq 0 \)) and 10 unaffected family members to identify homozygous variants which: (1) in priority, would disrupt the protein function (frameshifts, stop codons, or splicing variants); (2) were rare (minor allele frequency [MAF] \(< 1\% \)) in dbSNP137, the National Heart Lung and Blood Institute (NHBLI), Exome Sequencing Project (ESP) database, and the 1000 Genomes Project; (3) were shared by affected siblings when available; (4) were heterozygous in parents and/or heterozygous or wild-type in unaffected siblings when available; (5) fell within homozygous intervals; and (6) were absent in the homozygous state from DNA of 530 controls. We identified rare or undescribed homozygous truncating variants within 32 genes, each found in a single affected individual with consanguinity that fulfilled all these prioritization criteria (Table S4). We screened these candidate genes for additional homozygous or compound heterozygous mutations in a validation cohort. VPS13C (also known as KIAA1421; GenBank: NM_020821.2) on chr15q22 was mutated in a consanguineous Turkish family (also known as KIAA1421; GenBank: NM_020821.2) on chr15q22 was mutated in a consanguineous Turkish family, including 14 present in at least one of the 530 European control subjects (Table S5). No additional homozygous or compound heterozygous variants were found in the 31 other candidate genes.

The affected individual V-2 in family A harbored a homozygous splice-site mutation c.8445+2T>G, intron 61 in VPS13C confirmed by Sanger sequencing; eight unaffected relatives, including the mother, had heterozygous c.8445+2T>G mutations or wild-type sequences (Figures 1A and S3A). Affected individuals in families B and C were compound heterozygotes (Figures 1A, S3B, and S3C); the affected individual II-1 in family B with c.[806_807insCAGA];[9568G>T], p.[Arg269Serfs*14];[Glu3190*] variants; the affected individual II-1 in family C with c.[4165G>C];[4777delC], p.[Gly1389Arg];[Gln1593Lysfs*7] variants. Direct sequencing of VPS13C in the three unaffected siblings (II-2, II-3, and II-4) in family B and the unaffected mother (I-1) in family C showed that they all carried heterozygous mutations or wild-type alleles (Figures 1A and S3), indicating that all variations were located on different alleles. The five VPS13C variants were absent from dbSNP137, 1000 Genomes Project, EVS (Table S6A), Exome Aggregation Consortium (ExAC) databases (Table S6B), and our European control exomes, except for the missense p.Gly1389Arg variant found on one control chromosome. In addition, the c.8445+2T>G mutation was absent from 200 Turkish control chromosomes. No disruptive bi-allelic variants were found in our 530 control subjects; one disruptive homozygous variant (rs199602573) was found in the EVS database and ExAC populations (1/6,246 and 2/61,547, respectively), indicating that VPS13C homozygous disruptive variants are extremely rare in non-PD-affected populations (Tables S6 and S7).

The c.4165G>C and c.8445+2T>G mutations were predicted in silico to modify donor splice sites, one base upstream and two bases downstream, respectively, of splice junctions (Figure S4A). Reverse-transcription PCR analysis of potential splicing defects confirmed the predictions (Figure S4B). RNA from the homozygous individual of family A showed at least three shorter transcripts, lacking up to 231 nucleotides at the end of the exon 61. In the subject with the heterozygous variant, shorter transcripts were barely visible, probably due to a high instability of these aberrant RNAs. In family C, the longer transcript was found in the subject with the heterozygous variant, containing 14 additional nucleotides from intron 37.

VPS13C contains 86 exons spanning a 208-kb genomic region and has two main transcript variants, 1A (GenBank: NM_017684.4) and 2A (GenBank: NM_020821.2) (Figure 1B). Although the transcript 1A, lacking exons 6 and 7 and encoding a 3,710-amino acid protein, is expressed in most tissues, including brain and peripheral blood cells, the longest transcript 2A encodes a brain-specific 3,753-amino acid protein. Two additional isoforms with uncharacterized expression pattern are reported in Ensembl (GenBank: NM_018080.3 and NM_001018088.2) and lack the last four exons. All the isoforms contain the splice site variants found in families A and C. VPS13C contains a chorein domain at its N terminus, a DUF1162 domain which is located in the DUF1162 domain of unknown function, and a putative autophagy-related domain (Figure 1B). Except for the c.8445+2T>G variant, which is located in the DUF1162 domain, none of the variants were found in the predicted domains.

Clinical and Pathological Characteristics of Affected Individuals Harboring VPS13C Mutations

The three affected individuals harboring VPS13C mutations had early disease onset (25 to <46 years) and typical parkinsonism (akineto-rigid syndrome, rest tremor, good...
levodopa response). Disease progression, however, was particularly severe, with early cognitive decline, loss of response to treatment, axial symptoms, and dysautonomia. Affected subjects were bedridden within 15 years of clinical onset. Pyramidal signs and motor deficits were observed in two affected individuals. Brain MRI was normal early in the disease, and then bilateral atrophy was observed in the frontal, parietal, and temporal lobes (Table 1). Post-mortem examination of the brain of the affected individual II-1 in family B, who died at age 49 of aspiration pneumonia, showed mild frontal atrophy, including the primary motor area (Figures 2A–2C). The pathology resembled diffuse Lewy body disease. Alpha-synuclein and ubiquitin positive-Lewy bodies were observed in the brainstem, limbic system, hippocampus, and all cortical associative areas, including the parieto-occipital region (Figures 2D–2F, Table S8). Tau-immunoreactive neurofibrillary tangles and neurites were seen in the brainstem, hippocampus, and primary motor cortex (Figure 2G, Table S8). There were no glial-, α-synuclein-, Aβ-, or TDP-43-immunoreactive inclusions.

**Loss of VPS13C Function Affects Mitochondrial Morphology, Transmembrane Potential, and Respiration**

To investigate the function of VPS13C, we explored its subcellular distribution in human HEK293T by sucrose gradient fractionation (Figure 3A). VPS13C was enriched in the low-density fractions 1 and 2 containing the early endosomal marker EEA1 and most of the cytosolic protein Parkin. VPS13C was also found in higher-density fractions containing membrane and soluble markers of the Golgi apparatus (GOLGA2), the ER (Calnexin, BiP), and mitochondria (TOMM70, PMPCB, PINK1). Here, it was most abundant in fractions 8–10, containing the greatest proportion of TOMM70 and PMPCB. The mitochondrial localization of VPS13C was confirmed in mitochondrion-enriched fractions and pure mitochondria from HEK293T and COS-7 cells (Figures 3B and 3C). Limited trypsin digestion of mitochondrion-enriched fractions caused concomitant loss of VPS13C and the outer mitochondrial membrane receptor TOMM70 under conditions preserving the outer mitochondrial membrane channel TOMM40 and mitochondrial matrix enzyme PMPCB, indicating that VPS13C is located on the mitochondrial surface (Figure 3C).

We then investigated the impact of loss of VPS13C function on mitochondrial morphology, transmembrane potential, and respiration, reported to be affected in models of PARK1 or PARK2 deficiency.24,25 The siRNA-mediated silencing of VPS13C in COS-7 cells reduced VPS13C mRNA levels to no more than 25% of the control condition (Figure S6) and was associated with perinuclear redistribution of mitochondria and mitochondrial

### Table 1. Clinical Characteristics of Affected Individuals Harboring VPS13C Mutations

<table>
<thead>
<tr>
<th></th>
<th>V-2 from Family A</th>
<th>II-1 from Family B</th>
<th>II-1 from Family C</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Origin</strong></td>
<td>Turkish</td>
<td>French</td>
<td>French</td>
</tr>
<tr>
<td><strong>Consanguinity</strong></td>
<td>yes</td>
<td>no</td>
<td>no</td>
</tr>
<tr>
<td><strong>Gender</strong></td>
<td>female</td>
<td>male</td>
<td>female</td>
</tr>
<tr>
<td><strong>Age at onset (years)</strong></td>
<td>&lt;46</td>
<td>33</td>
<td>25</td>
</tr>
<tr>
<td><strong>Symptoms at onset</strong></td>
<td>depression; asymmetric akineto rigid syndrome; no dystonia</td>
<td>asymmetric akineto rigid syndrome and rest tremor; limb dystonia</td>
<td>asymmetric akineto rigid syndrome; limb dystonia</td>
</tr>
<tr>
<td><strong>Response to levodopa</strong></td>
<td>yes, partial</td>
<td>yes, at early stage</td>
<td>yes, at early stage (evaluated at 75% initially)</td>
</tr>
<tr>
<td><strong>Complications with treatment</strong></td>
<td>no motor fluctuation nor dyskinesia</td>
<td>fluctuation and dyskinesia, ICD, somnolence</td>
<td>no motor fluctuation nor dyskinesia</td>
</tr>
<tr>
<td><strong>Evolution</strong></td>
<td>severe with early cognitive decline with spatial disorientation (MMSE 21), slurred speech and hallucinations at the age of 51; axial symptoms (postural instability, FOG, and falls) and dysautonomia with urinary incontinence at the age of 54; bedridden, unable to speak, apathetic, confused, cachexic with dysphagia at the age of 58</td>
<td>severe with early cognitive decline (MMSE 18 at the age of 40); axial symptoms (FOG at the age of 35, falls at the age of 39); dysautonomia (at the age of 35); bedridden at the age of 43, death at the age of 49 of aspiration pneumonia</td>
<td>severe with early cognitive decline, slurred speech before the age of 39; severe axial symptoms at early stage; bedridden at the age of 31; gastrostomia at the age of 37. Subject’s father died at 52 of a pancreatic cancer</td>
</tr>
<tr>
<td><strong>Atypical symptoms associated</strong></td>
<td>brisk tendon reflexes on the lower limbs but no pyramidal syndrome</td>
<td>motor neuron signs with pyramidal syndrome and limb atrophy at late stage</td>
<td>motor neuron signs with spastic tetraplegia</td>
</tr>
<tr>
<td><strong>Cerebral MRI</strong></td>
<td>asymmetric atrophy in frontal, parietal, and temporal areas at the expense of the left side</td>
<td>normal (performed at early stage)</td>
<td>normal (performed at early stage)</td>
</tr>
</tbody>
</table>

Abbreviations are as follows: ICD, impulse control disorder; MMSE, mini-mental state examination; FOG, freezing of gait.
fragmentation, as confirmed by quantitative image analysis (Figure 4A). Evaluation of the mitochondrial transmembrane potential (ΔΨmt) with the potentiometric dye tetramethylrhodamine methyl ester (TMRM) revealed a significant decrease in the mean fluorescence intensity of mitochondria in cells depleted of VPS13C (Figure 4B). The ΔΨmt decrease was accompanied by an increase in maximal respiration rates and respiratory reserve, as assessed by high-resolution respirometry in intact cells (Figure 4C). Similar results were obtained in HEK293T cells (data not shown).

**Loss of VPS13C Function Exacerbates PINK1/Parkin-Dependent Responses to Mitochondrial Depolarization**

We further investigated the relationship between VPS13C and PINK1 and PARK2, both at the transcript and protein levels, with respect to their well-characterized response to mitochondrial damage. PINK1 accumulates on mitochondria and recruits Parkin to initiate mitophagy in response to mitochondrial dysfunction. Mitochondrial depolarization, triggered by the protonophore CCCP, partially redistributed VPS13C from mitochondria to the cytoplasm without significantly changing VPS13C transcript levels (Figures 5A, SB, and SF, left); under these conditions, PINK1 accumulated on mitochondria, as expected. VPS13C silencing did not affect PINK1 levels under basal conditions, but it exacerbated CCCP-induced mitochondrial accumulation of PINK1 without impacting PINK1 mRNA abundance (Figures 5C, SD, and SF, middle). Moreover, VPS13C silencing enhanced mitochondrial translocation of Parkin triggered by CCCP (Figures 5C and 5E). It also upregulated Parkin protein abundance in the cytosol without affecting PARK2 transcript levels at 3 hr of CCCP treatment (Figures 5E and 5F, right). PARK2 expression increases in response to mitochondrial damage caused by mitochondrial toxins, including CCCP.26,27 Here, PARK2 transcript levels tended to be higher at 48 hr of CCCP treatment (Figure 5F, right). This response was significantly enhanced after silencing of VPS13C or PINK1, suggesting greater mitochondrial damage. PINK1 silencing was also associated with downregulation of VPS13C transcript levels under basal conditions (Figure 5F, left), an effect that was reversed by PINK1 overproduction (Figure 5S), indicating the existence of multiple regulatory loops between VPS13C, PARK2, and PINK1. Consistent with the above described effects on PINK1 and Parkin, VPS13C silencing exacerbated PINK1/Parkin-mediated mitophagy triggered by CCCP in COS-7 cells, a model that we previously validated for the study of this process (Figures 6 and S6).17,19

**Discussion**

This study establishes VPS13C mutations as a monogenic cause of EO AR parkinsonism. Homozygous or compound
heterozygous truncating mutations in three PD-affected individuals, absent from or present in the heterozygous state in available unaffected family members and in a very large number of control subjects, strongly support the pathogenicity of VPS13C in EO parkinsonism. We identified three affected individuals harboring VPS13C mutations and could not perform co-segregation analyses, due to the lack of additional affected relatives in the corresponding families. However, the affected individuals shared a specific, rare, and extremely distinctive phenotype consisting of EO parkinsonism with very rapid progression and dementia, which argues strongly for the pathogenicity of VPS13C mutations. The initial phenotype, EO parkinsonism and a good response to levodopa treatment, is similar to that of PD-affected individuals with PARK2, PINK1, or DJ-1 mutations. However, the affected individuals rapidly became bedridden because of the worsening of motor dysfunction and loss of response to treatment. Dysautonomia and pyramidal signs were observed in two affected individuals, also distinguishing the phenotype from the classical, slowly progressive EO PD. The presence of numerous α-synuclein and ubiquitin-positive-Lewy bodies in the brainstem, limbic system, and many cortical areas was reminiscent of diffuse Lewy body disease, consistent with a motor phenotype associated with dementia. α-synuclein Lewy bodies are absent in most PD-affected individuals with PARK2 mutations, but were observed in the single autopsy case subject with PINK1 mutations reported. Tau-immunoreactive neurofibrillary tangles and neurites were also observed in case subjects with PARK2 mutations. These features define VPS13C-associated EO parkinsonism as a clinical, pathological, and genetic entity belonging to the group of synucleinopathies. In addition, our study also provides 31 potential candidate genes harboring disruptive homozygous mutations in a single PD-affected individual. However, genetic replication and functional validation are still needed to confirm their relevance to PD.

Alterations in other members of the VPS13 family cause AR neurodegenerative disorders: VPS13A (MIM: 605978) (CHAC [MIM: 200150]) is mutated in chorea-acanthocytosis characterized by progressive neurodegeneration and red cell acanthocytosis, and VPS13B (MIM: 607817) (COH1 [MIM: 216550]) is mutated in Cohen syndrome characterized by psychomotor retardation, microencephaly, and eye abnormalities. VPS13A, VPS13B, and VPS13C are also mutated in gastric and colorectal cancers with unstable microsatellites.

VPS13C belongs to a family of large VPS13 proteins (VPS13A–D) similar to yeast Vps13p. Like yeast Vps, mammalian vacuolar sorting proteins are crucial for vesicular transport. Initial studies linked yeast VPS13 orthologs to the delivery of proteins to the vacuole, the mammalian lysosome equivalent. Mutations in VPS35, encoding a core component of the retromer complex regulating endosomal protein sorting, are implicated in AD late-onset PD. VPS35 is also involved in protein trafficking from mitochondria to peroxisomes through mitochondria-derived vesicles. PINK1 and Parkin play a role in this transport route, which delivers damaged mitochondrial cargo directly to lysosomes in response to mitochondrial stress. However, the machinery regulating cargo selection and sorting into vesicles remains to be identified. VPS13C might be involved in this process. Such a mechanism would be consistent with its mitochondrial localization and the observed relocation to the cytosol in response to mitochondrial damage.
Several other observations in mammalian cells suggest that, like PINK1 and Parkin, VPS13C plays a role in mitochondrial maintenance. VPS13C depletion led to reduction of DJ_mit and mitochondrial fragmentation in cell lines. Moreover, it enhanced maximal respiration rates, suggesting compensatory adaptation aimed at preserving DJ_mit levels. In neuronal cells, which produce ATP mainly through mitochondrial oxidative phosphorylation and are unable to switch to glycolysis under acute mitochondrial stress, such changes might in the long term exacerbate generation of reactive oxygen species and trigger irreversible mitochondrial damage.38,39 VPS13C depletion also upregulated PINK1/Parkin-dependent mitophagy, and, similarly to PINK1 depletion, it enhanced the previously reported transcriptional upregulation of Parkin in response to toxin-induced mitochondrial dysfunction. Overall, these data suggest that loss of VPS13C function increases mitochondrial vulnerability to stress and thereby activates PINK1/Parkin-dependent mitochondrial quality control pathways. Based on the inverse relationship between VPS13C and PINK1 protein levels on the mitochondrial surface, we cannot exclude that VPS13C also acts as a negative regulator of PINK1.

Mitochondrial function is ensured by a series of interconnected finely orchestrated pathways, activated in response to different degrees of mitochondrial dysfunction.40 Excessive mitophagy has been associated with α-synuclein-independent neurodegeneration.41 Further work is required...
to clarify the role of VPS13C in mitochondrial maintenance and dissect its possible relation to PINK1/Parkin-dependent pathways.

Enrichment of VPS13C in cell fractions containing the early endosomal marker EEA1 suggests broader roles for VPS13C in vesicular trafficking. A more general involvement in endosomal-lysosomal trafficking, possibly counteracting α-synuclein pathology as recently reported for VPS35,42 might explain the diffuse α-synuclein pathology and rapid progression to dementia in individuals with VPS13C.
mutations. Such a mechanism would potentially represent a unifying link with cellular pathways involved in AD PD.

In summary, we describe truncating mutations in VPS13C associated with EO parkinsonism with rapid progression and widely distributed Lewy bodies. A meta-analysis of PD genome-wide association studies recently identified a susceptibility allele ~250 kb from VPS13C but not associated with either CpG methylation or mRNA expression, suggesting that VPS13C can either cause a monogenic form of EO parkinsonism or confer genetic susceptibility to PD. Although we are confident that our work strongly implicates VPS13C mutations in PD, further genetic studies in other populations are needed to confirm their pathogenicity. The development of animal models in which VPS13C is stably inactivated will help dissect the mechanisms by which loss of VPS13C function affects the survival of dopaminergic neurons.

Accession Numbers

The accession numbers for the variations in VPS13C reported in this paper are ClinVar: SCV000262816, SCV000262817, SCV000262818, SCV000262819, and SCV000262820.

Figure 6. Loss of VPS13C Function Exacerbates PINK1/Parkin-Dependent Mitophagy

(A) Immunofluorescence staining of a representative experiment illustrating PINK1/Parkin-dependent mitophagy in COS-7 cells overproducing Parkin and silenced for VPS13C or PINK1 (20 nM siRNA) after CCCP treatment (10 μM for 48 hr): red, Parkin; green, mitochondrial matrix marker PMPCB. Open arrows indicate loss of mitochondrial networks; white arrows show preserved networks. Scale bars represent 10 μm.

(B) Quantification of mitophagy in the conditions described in (A), expressed as the proportion of COS-7 cells without PMPCB (black bars) or TOMM20 (gray bars) staining; the siVPS13C treatment increased and siPINK1 decreased the proportion. In the absence of exogenous Parkin (−Parkin; cells overproducing the control protein EGFP) or CCCP (not shown), all the cells harbored normal mitochondrial PMPCB staining, whether or not VPS13C was silenced (means ± SEM; *p < 0.05, **p < 0.01 of 3 independent experiments; 100 cells scored per condition).

(C) Proportion of COS-7 cells without PMPCB staining after transfection with half-doses (10 nM) of each siRNA and 48 hr of CCCP treatment. The mitophagy-promoting effect of VPS13C depletion was ablated by concomitant silencing of PINK1 (means ± SEM; *p < 0.05 of 3 independent experiments; 100 cells scored per condition).

Supplemental Data

Supplemental Data include six figures and eight tables and can be found with this article online at http://dx.doi.org/10.1016/j.ajhg.2016.01.014.

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Web Resources

The URLs for data presented herein are as follows:

1000 Genomes, http://browser.1000genomes.org
ExAC Browser, http://exac.broadinstitute.org/
MUSCLE, http://www.ebi.ac.uk/Tools/msa/muscle/
Primer3, http://www.bioinformatics.nl/cgi-bin/primer3plus/primer3plus.cgi
UCSC Genome Browser, http://genome.ucsc.edu

References


