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U-Fiber Leukoencephalopathy Due to a Novel Mutation in the *TACO1* Gene

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Translational activator of cytochrome c oxidase I (TACO1) is a mitochondrial translation factor involved in mitochondria-encoded cytochrome c oxidase subunit I (MT-CO1) synthesis.[1,2] Loss-of-function mutations in the *TACO1* gene cause respiratory chain complex IV deficiency. Clinically heterogeneous human diseases are due to cytochrome c oxidase (COX) deficiency, ranging from Leigh syndrome to myopathy, deafness, or ataxia. Recently, 2 different TACO1 mutations have been identified in 3 families with late-onset Leigh syndrome and a leukoencephalopathy involving predominantly basal ganglia and cystic changes.[3,4] Here, we report a subject carrying a novel homozygous truncating mutation in the *TACO1* gene and presenting an adult-onset slowly progressive spastic paraparesis with cognitive impairment and a subcortical U-fiber leukoencephalopathy.

Case Presentation

The proband is a 50-year-old Italian woman with a 20-year history of slowly progressive spastic gait and mild cognitive impairment. No family history and no clear consanguinity have been reported. She has a daughter, now 24-years-old, healthy. Neurologic examination showed diffuse signs of upper motor neuron involvement and an impairment of executive functions in a context of low cognitive ability setting. Neither involuntary movements nor cerebellar dysfunction signs were present. Optical coherence tomography highlighted a significant bilateral temporal retinal nerve fiber layer thickness reduction. Brain MRI showed a white matter disease with an extensive symmetrical involvement of U-fibers (figure 1A). Laboratory panels (including creatine kinase and lactic acid) and EMG were unremarkable. In a 10-year follow-up, we observed a spastic gait worsening leading to the necessary use of 2 sticks, and a cognitive impairment progression in terms of perseveration and reduced speed in information processing. MRI follow-up displayed a brain atrophy increase.

Genetics and Functional Studies

Whole-exome sequencing was performed on the proband, her healthy sister, and daughter after written informed consent. Two variants in *TACO1* and mitochondrial distribution and morphology regulator 1 (*MSTO1*) were identified in the proband: a novel homozygous truncating change c.676G>T (p.Glu226Ter) in *TACO1* and c.833A>G (p.Tyr278Cys) (rs143029385) in *MSTO1* (freq. 0.04% in ExAC). None of the variants segregated in the sister, whereas the daughter is a carrier of the *TACO1* change (figure 1B). Based on this, we speculated that *TACO1* variant might be the disease-causing mutation. Functional studies demonstrated that the newly identified *TACO1* mutation is highly pathogenic. Indeed, sodium dodecyl sulfate–

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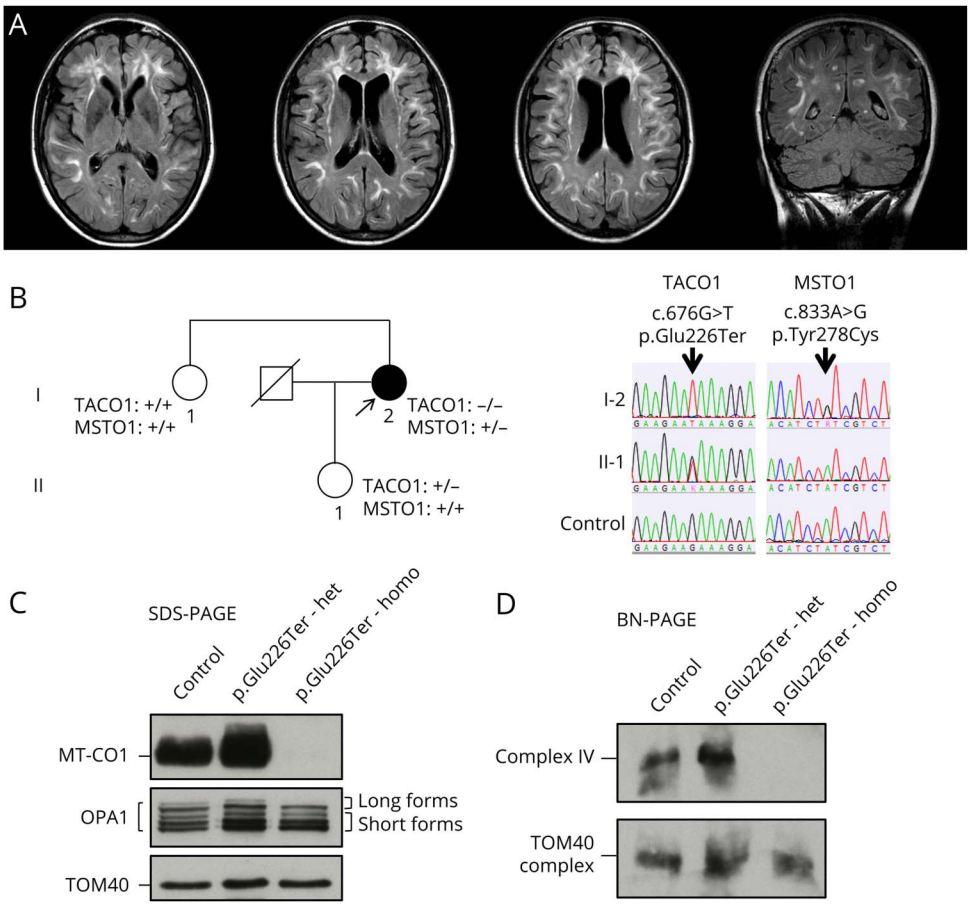
Figure 1 Brain MRI, the Result of Sequence Analysis, SDS-PAGE, and BN-PAGE



(A) Brain MRIs showing multifocal confluent T2/FLAIR hyperintense lesions involving the supratentorial bihemispheric subcortical white matter, mainly located at the cortical-juxtacortical junction involving the U-fibers. Periventricular white matter is involved bilaterally, and the body of the corpus callosum showed few focal lesions. Hyperintense T2/FLAIR putaminal rim could be detected on both sides, involving the external capsule bilaterally. The cortex is preserved. After contrast injection, no area of enhancement could be picked up (not shown). Frontal subcortical lesions were partially necrotic on T1-weighted images. No focal lesions were detected at the level of the basal ganglia, as well as the brainstem and cerebellum. There is evidence of a mild brain atrophy, with a moderate ventricular system enlargement and prominent sulci at the vertex. MR spectroscopy did not show any abnormal findings (data not shown). (B) Family pedigree of the patient. Black and white symbols indicate the proband and healthy family members, respectively. Electropherograms of wild-type and mutated sequences are shown below. (C) SDS-PAGE and WB analysis of MT-CO1 and OPA1 normalized on translocase of outer mitochondrial membrane 40 (TOM40). (D) BN-PAGE and WB analysis of assembled COX (200 kDa) normalized on TOM complex (400 kDa). BN-PAGE = blue native polyacrylamide gel electrophoresis; COX = cytochrome c oxidase; FLAIR = fluid-attenuated inversion recovery; MSTO1 = mitochondrial distribution and morphology regulator 1; MT-CO1 = mitochondria-encoded cytochrome c oxidase subunit I; OPA1 = optic atrophy gene 1; SDS-PAGE = sodium dodecyl sulfate–polyacrylamide gel electrophoresis; TACO1 = translational activator of cytochrome c oxidase I; WB = Western blot.

polyacrylamide gel electrophoresis showed a striking reduction of MT-CO1 in patient fibroblasts compared with the heterozygous daughter and a healthy control (figure 1C). Destabilized MT-CO1 resulted in a fully compromised assembly of COX, as assessed by blue native polyacrylamide gel electrophoresis on isolated mitochondria from proband and control fibroblasts (figure 1D). To determine whether COX dysfunction could cause fragmentation of the mitochondrial network in the proband, we assayed mitochondrial morphology by live imaging microscopy in primary fibroblasts (supplemental data, links.lww.com/NXG/A400). Despite a mild reduction of optic atrophy gene 1 long forms, which are the active mediators of mitochondrial fusion (figure 1C), the proband displayed a mitochondrial network morphology comparable to controls, with the highest percentage of cells showing fused and interconnected organelles (figures e-1 and e-2, links.lww.com/NXG/A397). This finding also demonstrates that the heterozygous *MSTO1* variant identified is likely not pathogenic, as it does not affect mitochondrial morphology.

Discussion

We reported a novel mutation in the *TACO1* gene causing a striking reduction in the MT-CO1 synthesis and compromised COX assembly in fibroblasts. Complex IV, the last enzyme of the mitochondrial respiratory chain, catalyzes electrons transfer to the final acceptor O2 for adenosine triphosphate synthesis.[5] Three of the 14 COX subunits are encoded by mitochondrial DNA (mtDNA), and their synthesis is regulated by different nuclear genes like *TACO1*.[2] To date, this is the third *TACO1* homozygous mutation reported. In the first and second one,[3,4] a juvenile-onset Leigh-like disease was described with wide symptom variability also within the same family. We expanded the clinical

and neuroradiologic spectrum associated with *TACO1* mutations, reporting a non-Turkish woman with a novel clinical and neuroradiologic phenotype. Subcortical arcuate U-fibers are among the slowest and latest myelinating fibers, with a reduced rate of myelin turnover; therefore, they are generally spared in other inherited leukodystrophies,[6] except for Alexander and Canavan disease. In mitochondrial disorders, white matter involvement is a common feature. Usually, lesions caused by mtDNA point mutation predominantly affect deep gray matter with minor peripheral white matter involvement, whereas diffuse necrotic or cystic changes associated with brain atrophy are frequently observed in patients with Leigh disease due to mutation in nuclear genes encoding for complex I or IV and assembly factor. Late-onset and slow progressing neurologic manifestations make the described case an uncommon variant of COX deficiency spectrum disorder[7] and are apparently in contrast with functional data showing a markedly reduced COX activity in fibroblasts. This discrepancy highlights the complex protein interactions involved in COX synthesis and assembly, which are probably tissue and development specific.

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Disclosure

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