MUTATION IN PNKP PRESENTING INITIALLY AS AXONAL CHARCOT-MARIE-TOOTH DISEASE

PNKP (polynucleotide kinase 3'-phosphatase, OMIM #605610) product is involved in the repair of strand breaks and base damage in the DNA molecule mainly caused by radical oxygen species. Delterious variants affecting this gene have been previously associated with microcephaly, epilepsy, and developmental delay.1 According to a previous report, homozygous loss-of-function substitution in PNKP was associated with cerebellar atrophy, neuropathy, microcephaly, epilepsy, and intellectual disability.2 Recently, whole-exome sequencing (WES) performed in a cohort of Portuguese families with ataxia with oculomotor apraxia (AOA) disclosed pathogenic variants in PNKP in 11 individuals. Other clinical features in that study included neuropathy, dystonia, cognitive impairment, decreased vibration sense, pyramidal signs, mild elevation in α-fetoprotein, and low levels of albumin. This condition was named AOA type 4 (OMIM #616267), as the phenotype of AOA has been previously associated with 3 other genes: APTX, SETX, and PK3R5.3 Altogether, these reports demonstrate the great phenotypic diversity associated with PNKP mutations. In this article, we further enlarge this variability by demonstrating that early-onset axonal sensory-motor neuropathy (or axonal Charcot-Marie-Tooth (CMT) disease) followed years later by ataxia without oculomotor apraxia can be caused by deleterious variants in PNKP. Full consent was obtained from the patient and his parents for this publication. This study was approved by institutional ethics committees.

Case description. A 17-year-old boy presented with early onset of nonprogressive gait abnormalities and feet deformities observed since the first years of life. After the age of 9 years, his gait deteriorated. The combination of pes cavus, hammertoes, and absent deep tendon reflexes together with the nerve conduction velocity test and EMG disclosing sensory-motor axonal neuropathy prompted the diagnosis of axonal CMT disease; no ataxia was observed. Parents were nonconsanguineous and family history was unremarkable. Molecular analysis for axonal CMT genes, including MFN2, GDAP1, MPZ, NEFL, and GJB1, was negative. During the last 5 years, steppage gait, mild ataxia, and slurred speech were observed, and pes cavus and hammertoes became prominent (figure 1, A–C); he never had oculomotor apraxia. Brain MRI depicted mild cerebellar atrophy (figure 1, D and E). Other recessive ataxias were excluded.

WES was performed with the exome capture kit Nextera Sure Select (Agilent Technologies, Santa Clara, CA) and the sequencing platform Illumina HiSeq2500 (Illumina, San Diego, CA). Sequence alignment and variant call coverage of target bases with more than 10 reads was 96.4%. A homozygous variant (c.1221_1223delCAC [p.Thr408del]) that was previously reported in compound heterozygosity in a patient with AOA4 was detected, and his parents were heterozygous for this variant.

Functional analysis. PNKP-mutated cells (CMT01SP) were more sensitive to both chemicals than wild-type cells (normal human fibroblasts), as observed on a viability (2,3-bis-(2-methoxy-4-nitro-5-sulfophenyl)-2H-tetrazolium-5-carboxanilide) assay (figure e-1, A and B at Neurology.org/ng) and by the higher frequency of sub-G1 cells (normal human fibroblasts), as observed on a DNA damage marker.

To evaluate how the PNKP mutation affects the DNA repair capacity of these cells, we detected the levels of phosphorylation of histone H2AX (γH2AX)—widely used as a DNA damage marker—after treatment with H2O2 and doxorubicin.4 As clearly seen in figure e-1, F–H, after 24 hours, the PNKP-mutated cells showed a much larger population of γH2AX-positive cells than the control cells, and this persisted even after 72 hours, indicating that the patient’s cells were unable to efficiently repair DNA lesions caused by H2O2 and doxorubicin. Taken together, those results strongly indicate that the (c.1221_1223delCAC [p.Thr408del]) PNKP mutation has a substantial functional effect on protein activity, impairing DNA repair capacity on both base excision repair (BER) and non-homologous end joining (NHEJ) pathways.
Discussion. Recessive CMT, also known as CMT4, represents less than 10% of CMT cases. At least 22 genes are associated with CMT4, which can be axonal or demyelinating. Because clinical manifestations of CMT are usually not gene specific, molecular diagnosis is not a straightforward task and many patients remain without a genetic background. Next-generation sequencing will help to increase the number of genes associated with these disorders.

This report expands the phenotypic variability associated with mutations in PNKP, which spans from a more severe presentation of microcephaly, epilepsy, and mental retardation at one end of the spectrum to a milder, CMT-like phenotype with ataxia but no oculomotor apraxia, epilepsy, or cognitive impairment, as seen in our patient, at the other side of the spectrum. In addition, it demonstrates that even with a milder phenotype, as occurred in our patient, DNA repair capacity is impaired on both BER and NHEJ pathways.

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