Cerebellar Ataxia With Progressive Improvement

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Background: Nonprogressive cerebellar ataxies are characterized by a persistent, nonprogressive ataxia associated with cognitive impairment. Cerebellar hypoplasia on imaging is variable but is not predictive of the degree of ataxia or cognitive impairment.

Objective: To describe a family with a nonprogressive cerebellar ataxia associated with cognitive and motor impairments that improve with age.

Design: Genetic study in a family with nonprogressive cerebellar ataxia. Clinical and imaging features are also described.

Setting: Community hospital.

Patients: Both parents and 3 children from an affected family.

Main Outcome Measures: Clinical features, magnetic resonance imaging findings, and genetic findings.

Results: A genome-wide single nucleotide polymorphism screen did not show clear linkage to known spinocerebellar ataxia loci, in particular spinocerebellar ataxia type 15. Repeat spinocerebellar ataxia loci expansions were excluded. Magnetic resonance images of all affected individuals demonstrated cerebellar vermian abnormalities.

Conclusions: These findings suggest that nonprogressive cerebellar ataxia is genetically heterogeneous and, when associated with gradual improvement in cognition and motor skills, likely represents a separate, distinct clinical entity.

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The 35-year-old father (I:1 in Figure 1) had normal findings on neurologic examination and brain imaging. The family history is notable only for a maternal uncle with mental retardation and seizures.

**MOLECULAR STUDIES**

This study was reviewed and approved by the Children’s Hospital, Boston, institutional review board, and informed consent was obtained from the participants. Genomic DNA was extracted from peripheral whole blood lymphocytes using standard techniques (Qiagen, Valencia, Calif). Repeat expansions at SCA1, SCA2, SCA3, SCA7, SCA8, SCA10, SCA12, SCA17, and dentatorubral-pallidoluysian atrophy (DRPLA) loci were investigated by polymerase chain reaction using commercial laboratories. For a genome-wide screen, single nucleotide polymorphism analyses were performed on the affected individuals using the 10K Array Xba 142 2.0 set (Translational Genomics Research Institute, Phoenix, Ariz) according to the manufacturer’s instructions. The DNA chip data were analyzed using DNA-Chip Analyzer software. Additional linkage studies were performed using microsatellite markers (Applied Biosystems, Foster City, Calif) that localize to chromosome arm 3pter. The SCA15 locus (D3S1270, D3S1297, D3S3630, D3S3706, D3S1304, and D3S3728). Statistical calculation of single-point logarithm-of-odds scores was performed using the Allegro or DNA-Chip Analyzer program, assuming θ = 0, an autosomal dominant mode of inheritance, and a disease frequency of 1:10,000; given the early onset of disease, penetrance was set at 1.00.

**RESULTS**

No repeat expansions at the SCA1, SCA2, SCA3, SCA7, SCA8, SCA10, SCA12, SCA17, and DRPLA were detected by polymerase chain reaction. Negative logarithm-of-odds scores were obtained by a single nucleotide polymorphism genome-wide screen for SCA1, SCA4, SCA6, SCA7, SCA8, SCA10, SCA12, SCA13, SCA14, SCA16, SCA19, SCA22, SCA24, and DRPLA. Analysis of microsatellite markers for chromosome arm 3p excluded this region as a potential locus. The pedigree size was too small to definitively identify a gene locus.

**COMMENT**

No clear clinical and radiographic criteria have been established for NPCA. Families with NPCA uniformly show mild-to-moderate early-onset nonprogressive ataxia and delayed motor milestones. However, cognitive impairments and learning problems are only demonstrable in approximately half of the affected individuals. Other clinical findings, such as dysarthria, nystagmus, dysmetria, and brisk tendon reflexes, are not consistent in members of the same family. Moreover, the radiographic finding of cerebellar hypoplasia is variable, and the degree of cerebellar dysgenesis does not correspond to the level of cognitive or motor impairment. Boys have been reported to be more affected in another previous study.
Figure 2. Magnetic resonance images (MRIs) of the brain of affected individuals. Insets represent axial MRIs at the level of the cerebellum and brainstem that show the uniform finding of vermian atrophy in all affected individuals. The scales are in centimeters. A, Sagittal T1-weighted MRI of the mother (I:2) demonstrates cerebellar vermian atrophy, a mega cisterna magna, and callosal thinning. B, Axial T2-weighted MRI of the oldest affected son (II:1) shows subcortical heterotopia (arrows) along the lateral ventricles. C, Sagittal T1-weighted MRI of the same individual is also notable for inferior vermian hypogenesis, a mega cisterna magna, and callosal thinning. D, Sagittal T1-weighted MRI of the middle child (II:2) is remarkable for a cerebellar vermian hypoplasia, decreased white matter volume, and a mega cisterna magna. E, Axial T2-weighted MRI of the youngest child, a girl (II:3), demonstrates mild ventriculomegaly (asterisks). F, Sagittal T1-weighted MRI of the same individual reveals hypoplasia of the cerebellar vermis, a mega cisterna magna, and dysgenesis of the posterior aspect of the corpus callosum.
Three previously described families with NPCA have been found to have cerebellar hypoplasia, delayed cognitive and motor development, and progressive improvement of coordination and ataxia with increasing age.\textsuperscript{5,5,11} Exclusion of known SCA gene expansions or linkage to known SCA loci has not been performed in these families. The present study describes a fourth family with these same characteristics. Taken in this context, the forms of NPCA can be classified into at least 2 subtypes—disorders that show improvement of coordination and ataxia with increasing age (possibly due to maturation of the cerebellar system) and disorders that show only no progressive worsening of clinical deficits.

These forms represent a group of genetically heterogeneous disorders. No identified repeat expansions in or clear linkage to the known SCA regions and exclusion of the SCA10 and SCA15 loci in the current family with NPCA (that improves with age) suggest a possible new genetic basis for this disorder. The possible patterns of transmission are autosomal dominant, mitochondrial, and X-linked dominant. In addition, the findings in this family further support the idea that many adults previously labeled with cerebral palsy in childhood have imaging findings of brain malformations, with associated genetic implications.

Further classification of the different forms of congenital NPCA are necessary to identify causative genes. Consistent radiographic findings (vs variable findings) of cerebellar vermian abnormalities in any given pedigree may represent one basis for distinguishing the different disorders. Clinical recognition of improving cognitive and motor deficits vs nonprogressive cognitive and motor deficits may serve as a secondary basis for classification.

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Additional Information: Because the boys initially appeared more severely affected (suggesting at that time an X-linked mode of transmission), the OPHN1 gene was sequenced and found to be normal by Laurent Villard, PhD, at the University of Marseilles, France.

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REFERENCES