

Ataxia with Oculomotor Apraxia Type 2

[AOA2]

Maria-Céu Moreira, MS, PhD

Department of Pediatrics

Division of Genetics and Developmental Medicine

University of Washington School of Medicine

Seattle

mceu@u.washington.edu

Michel Koenig, MD, PhD

Institut de Génétique et de Biologie Moléculaire et Cellulaire

CNRS/INSERM/Université Louis-Pasteur

Strasbourg

mkoenig@igbmc.u-strasbg.fr

Initial Posting: November 15, 2004.

Last Update: March 5, 2007.

Summary

Disease characteristics. Ataxia with oculomotor apraxia type 2 (AOA2) is characterized by onset between age three and 30 years, cerebellar atrophy, axonal sensorimotor neuropathy, oculomotor apraxia, and elevated serum concentration of alpha-fetoprotein (AFP).

Diagnosis/testing. The diagnosis of AOA2 is based on clinical and biochemical findings, family history, and exclusion of the diagnosis of ataxia-telangiectasia and AOA1. AOA2 is associated with mutations in the gene *SETX*, which encodes the protein senataxin. Molecular genetic testing is available on a clinical basis.

Management. *Treatment of manifestations:* physical therapy for disabilities resulting from peripheral neuropathy; wheelchair for mobility as needed; educational support (e.g., computer with speech recognition and special keyboard for typing) to compensate for difficulties in reading (caused by oculomotor apraxia) and in writing (caused by upper-limb ataxia). *Surveillance:* routine follow-up with a neurologist.

Genetic counseling. AOA2 is inherited in an autosomal recessive manner. Each sib of an affected individual has a 25% chance of being affected, a 50% chance of being an asymptomatic carrier, and a 25% chance of being unaffected and not a carrier. No laboratories offering prenatal testing are listed in the GeneTests Laboratory Directory; however, such testing may be available through laboratories offering custom prenatal diagnosis.

Diagnosis

Clinical Diagnosis

Ataxia with oculomotor apraxia type 2 (AOA2) is suspected in individuals with the following findings [Moreira et al 2004]:

- Cerebellar ataxia
- Oculomotor apraxia (in <47% of individuals)

- Areflexia and later a peripheral axonal sensorimotor neuropathy (>90% of individuals)
- Onset between age three and 30 years
- Slow progression
- Absence of cardiac involvement, cancer predisposition, or immunodeficiency, and rare or absent telangiectasia
- Family history consistent with autosomal recessive inheritance

MRI. Marked cerebellar atrophy on MRI was detected in all individuals undergoing this examination [Moreira et al 2004, Duquette et al 2005, Asaka et al 2006, Criscuolo et al 2006, Fogel & Perlman 2006]. In the case described by Chen et al (2006), MRI at age 40 years showed mild cerebellar hemispheric and moderate vermian hypoplasia/atrophy.

EMG. Signs of axonal neuropathy are found in 90%-100% of individuals with AOA2 [Moreira et al 2004, Duquette et al 2005, Asaka et al 2006, Criscuolo et al 2006].

Testing

Laboratory findings that can be used to establish the diagnosis of AOA2 in a symptomatic individual include the following:

- **Serum alpha-fetoprotein (AFP) concentration** greater than 20 ng/mL (in >90% of affected individuals) [Moreira et al 2004, Duquette et al 2005, Asaka et al 2006, Chen et al 2006, Criscuolo et al 2006, Fogel & Perlman 2006]. Although normal laboratory values for serum AFP concentration are highly variable, the majority range between 0 and 20 ng/mL. Serum AFP concentration varies over time and is lower than that usually observed in ataxia-telangiectasia [Le Ber et al 2004].
- **Serum total cholesterol concentration** greater than 5.6 mmol/L (in ~50% of affected individuals) [Le Ber et al 2004]. Normal value: 3.5-5.8 mmol/L.
- **Serum creatine kinase (CK) concentration** is increased in some affected individuals and elevated immunoglobulin levels (IgG and A) have been found in several families [Watanabe et al 1998, Le Ber et al 2004].

Neuropathology. Nerve biopsy confirms axonal neuropathy.

Molecular Genetic Testing

GeneReviews designates a molecular genetic test as clinically available only if the test is listed in the GeneTests Laboratory Directory by either a US CLIA-licensed laboratory or a non-US clinical laboratory. GeneTests does not verify laboratory-submitted information or warrant any aspect of a laboratory's licensure or performance. Clinicians must communicate directly with the laboratories to verify information.—ED.

Molecular Genetic Testing—Gene. *SETX* is the only gene currently known to be associated with AOA2 [Moreira et al 2004].

Clinical uses

- Confirmatory diagnostic testing
- Carrier testing
- Prenatal diagnosis

Clinical testing

- **Sequence analysis.** Direct sequencing of the *SETX* coding sequence, intronic flanking sequences, and a part of 5' and 3' UTRs identified mutations in families from Algeria, Canada, Cape Verde, France, Italy, Japan, Pakistan, Portugal, Spain, Tunisia, Turkey, United Kingdom, United State, and Vietnam [Moreira et al 2004, Duquette et al 2005, Asaka et al 2006, Criscuolo et al 2006, Fogel & Perlman 2006]. Mutation detection rates have not yet been reported.

Table 1 summarizes molecular genetic testing for this disorder.

Table 1. Molecular Genetic Testing Used in Ataxia with Oculomotor Apraxia Type 2

Test Method	Mutations Detected	Mutation Detection Frequency ¹	Test Availability
Sequence analysis	<i>SETX</i> sequence alterations	Unknown	Clinical Testing

1. Proportion of affected individuals with a mutation(s) as classified by gene/locus, phenotype, population group, and/or test method

Interpretation of test results. For issues to consider in interpretation of sequence analysis results, click here.

Testing Strategy

When the clinical findings are characteristic of AOA2, sequence analysis of the *SETX* full coding sequence, intronic flanking sequences, and a part of 5' and 3' UTRs is performed.

Genetically Related (Allelic) Disorders

Juvenile amyotrophic lateral sclerosis (ALS4) (also known as distal hereditary motor neuropathy with pyramidal features, or dHMN) is associated with three different missense mutations (T3I, L389S, and R2136H) in *SETX* [Chen et al 2004]. ALS4 is a rare autosomal dominant form of amyotrophic lateral sclerosis (ALS) characterized by severe distal muscle weakness and atrophy, normal sensation, and pyramidal signs associated with degeneration of motor neurons in the brain and spinal cord. Individuals affected with ALS4 usually have onset before age 25 years, a slow rate of progression, sparing of bulbar and respiratory muscles, and a normal life span [Chance et al 1998, Rabin et al 1999, De Jonghe et al 2002, Chen et al 2004].

An autosomal dominant form of ataxia appears to be associated with two *SETX* missense mutations (N603D-Q653K) shared in *cis* configuration by a mother and daughter [Bassuk et al 2007]. Both had cerebellar ataxia with atrophy of the cerebellum, dysarthria, oculomotor defects (saccadic pursuits and gaze-evoked nystagmus), and tremor. The mother had onset of cerebellar ataxia at age 13 years, the daughter at age three years. Mental status, reflexes, sensation, muscle tone, and levels of alpha-fetoprotein and serum creatine kinase were within normal range.

Clinical Description

Natural History

Ataxia is the first sign of ataxia with oculomotor apraxia type 2 (AOA2) and is the major cause of disability early in the disease course. Later, peripheral sensorimotor neuropathy, particularly of the lower limbs, plays a significant role in disease progression.

Findings by Le Ber et al (2004), Moreira et al (2004), Duquette et al (2005), Asaka et al (2006), Chen et al (2006), Criscuolo et al (2006), Fogel & Perlman (2006) showed the following:

Cerebellar ataxia. All affected individuals, after initial normal development, show cerebellar ataxia, with slowly progressive gait imbalance [Watanabe et al 1998, Nemeth et al 2000]. The first symptoms are recognized between age ten and 23 years (mean 15.0 years). In a recent study of ten affected individuals from Italy, age at onset ranged between three and 30 years (mean 20.3 years) [Criscuolo et al 2006].

Neuropathy. Ninety percent to 100% of the individuals with AOA2 have sensorimotor neuropathy (i.e., absent or diminished tendon reflexes and sensorimotor deficit).

Oculomotor apraxia. Oculomotor apraxia is present in about 50% of individuals. It is characterized by a dissociation of eye-head movements in the "head-free" condition, in which the head reaches the lateral target before the eyes. In the Italian cohort, this feature was present in only 20% of individuals [Criscuolo et al 2006]. Saccadic pursuit and gaze-evoked nystagmus have also been observed in several individuals [Nemeth et al 2000].

Movement disorders. Dystonic posture of the hands, choreic movements, and head or postural tremor are observed in about 20% of individuals [Nemeth et al 2000, Le Ber et al 2004]. The severity of the movement disorders persists in individuals with AOA2 in contrast to the movement disorder in individuals with AOA1, in which chorea tends to disappear with time [Le Ber et al 2003, Le Ber et al 2004]. In the Italian study, extrapyramidal symptoms (including choreiform head movements, truncal dystonia, and head tremor) were reported in 20% of individuals; however, they rapidly disappeared as the disease progressed [Criscuolo et al 2006]. In the French-Canadian group of individuals tremor was an inconsistent feature present in 57% [Duquette et al 2005].

Intellect. Mild cognitive impairment is present in some individuals [Le Ber et al 2004], but none have had severe mental retardation or dementia, even after long disease duration [Le Ber et al 2004]. In the Criscuolo et al (2006) study, three out of ten persons presented with mild mental impairment with onset around age 50 years.

Other. Deep sensory loss, extensor plantar reflexes, swallowing difficulties, and sphincter disturbances are observed in some individuals [Le Ber et al 2004]. No signs of extraneurologic involvement, other than early-onset menopause [Le Ber et al 2004, Criscuolo et al 2006], are evident.

Neuropathology. Chronic axonal neuropathy with preferential loss of large myelinated fibers and to a lesser degree small myelinated fibers is detected in sural nerve biopsies [Duquette et al 2005, Criscuolo et al 2006].

Postmortem brain examination in a 79-year-old Italian who died of heart failure revealed reduction in the overall size of the brain, including atrophy of the cerebellar folia and marked widening of the sulci [Criscuolo et al 2006]. Cerebellar atrophy was most evident at the level of the vermis and the anterior lobe. The brain stem and spinal cord were slightly reduced in size without other anomalies. The substantia nigra appeared normally pigmented. Atheromatous plaques were present in all the arteries of the circle of Willis. Histologic examination showed normal cortical neurons (both in number and shape), marked loss of Purkinje cells in the cerebellar cortex, and mild fibrous gliosis that was more severe in the vermis than in the hemispheres. No inclusions or torpedos were found. The neurons of the dentate nuclei were slightly reduced in number. Chromatolysis of the oculomotor and raphe nuclei was observed in the brain stem. The inferior and accessory olives appeared relatively spared. In the spinal cord severe demyelination of the gracilis and cuneatus funiculi and degeneration of Clarke's columns with gliosis were observed.

Life span. In individuals studied to date, disease duration ranged between age two and 53 years, corresponding to the maximum age of last examination (79 years).

Genotype-Phenotype Correlations

No obvious genotype-phenotype correlations have been established.

Nomenclature

AOA2 was first known as "ataxia with later onset and high level of alpha-fetoprotein."

Prevalence

The prevalence of L1976R and E65K mutations was studied by genotyping 154 samples from the Gaspésie region, including 82 French-Canadian and 72 Anglo-Norman control samples [Duquette et al 2005]. In this study, five individuals (3 of Anglo-Norman and 2 of French-Canadian backgrounds) were carriers of the L1976R common French-Canadian mutation and none was a carrier of the rarer E65K mutation. According to these results, the carrier rate for the L1976R mutation is estimated to be 3.5% (1:28) for Quebecois of Anglo-Norman origin and 2.1% (1:47) for the French-Canadian population of Gaspésie. No individuals homozygous for the mutations L1976R and E65K were identified.

Differential Diagnosis

For current information on availability of genetic testing for disorders included in this section, see GeneTests Laboratory Directory. —ED.

Childhood. The diagnosis of ataxia with oculomotor apraxia type 2 (AOA2) can be difficult to establish in young children because all features of the disease are not present or apparent. AOA2 in childhood needs to be distinguished from the following disorders:

- AOA1 is a progressive cerebellar ataxia characterized by childhood onset (age 2-15 years [Moreira et al 2004]), followed by oculomotor apraxia, which is usually noticed a few years after the onset of ataxia, and progressing to external ophthalmoplegia. The majority of individuals with AOA1 have generalized areflexia followed by a peripheral neuropathy and quadriplegia with loss of ambulation about seven to ten years after onset [Tachi et al 2000, Barbot et al 2001, Le Ber et al 2003, Tranchant et al 2003]. Cognitive impairment in different degrees is observed in individuals of different ethnic origins, while in others, intellect remains normal [Tachi et al 2000; Moreira, Barbot, Tachi, Kozuka, Mendonca et al 2001; Shimazaki et al 2002; Le Ber et al 2003; Sekijima et al 2003]. After a long disease duration (>15 years), low serum concentration of albumin and high serum concentration of total cholesterol are observed [Tachi et al 2000; Moreira, Barbot, Tachi, Kozuka, Uchida et al 2001]. AOA1 is caused by mutations in *APTX*, the gene encoding aprataxin [Date et al 2001; Moreira, Barbot, Tachi, Kozuka, Uchida et al 2001].
- When oculomotor apraxia and/or high serum concentrations of alpha-fetoprotein are present, ataxia-telangiectasia (caused by mutations in *ATM*) and ataxia-telangiectasia-like disorder (caused by mutations in *MRE11A*) should also be considered.

Adolescence

- Friedreich ataxia (FRDA) can be excluded on clinical grounds, as oculomotor apraxia is not observed in FRDA and cerebellar atrophy is not observed on MRI in FRDA early in the disease course. Molecular genetic testing of the gene *FRDA* can detect mutations in virtually 100% of affected individuals.

- Ataxia with vitamin E deficiency (AVED) and Q10 deficiency [Musumeci et al 2001] should be considered because they are treatable.

Adulthood. In simplex cases (i.e., a single occurrence in a family), the possibility of spinocerebellar ataxia type 2 (SCA2) (a dominant form of ataxia which also associates cerebellar ataxia with slow eye movements) can be excluded by molecular genetic testing of the *SCA2* gene [Pulst et al 1996].

Management

Evaluations Following Initial Diagnosis

To establish the extent of disease in an individual diagnosed with oculomotor apraxia type 2 (AOA2):

- Assessment of cognitive function
- Examination of cranial nerve function
- Neurologic examination including assessment of gait and limb ataxia, coordination, tone, strength, reflexes, and sensory perception
- Oculomotor examination

Treatment of Manifestations

Physical therapy may be helpful, particularly for disabilities resulting from peripheral neuropathy.

A wheelchair is usually necessary for mobility by age 30 years.

Educational support (such as use of a computer with speech recognition and special keyboard for typing) should be provided to compensate for difficulties in reading (caused by oculomotor apraxia) and in writing (caused by upper-limb ataxia).

Prevention of Secondary Complications

A low-cholesterol diet is advised.

Surveillance

Routine visits to the attending neurologist are indicated.

Therapies Under Investigation

Search ClinicalTrials.gov for access to information on clinical studies for a wide range of diseases and conditions. Note: There may not be clinical trials for this disorder.

Other

Genetics clinics are a source of information for individuals and families regarding the natural history, treatment, mode of inheritance, and genetic risks to other family members as well as information about available consumer-oriented resources. See the GeneTests Clinic Directory.

Support groups have been established for individuals and families to provide information, support, and contact with other affected individuals. The Resources section (below) may include disease-specific and/or umbrella support organizations.

Genetic Counseling

Genetic counseling is the process of providing individuals and families with information on the nature, inheritance, and implications of genetic disorders to help them make informed medical and personal decisions. The following section deals with genetic risk assessment and the use of family history and genetic testing to clarify genetic status for family members. This section is not meant to address all personal, cultural, or ethical issues that individuals may face or to substitute for consultation with a genetics professional. To find a genetics or prenatal diagnosis clinic, see the GeneTests Clinic Directory.

Mode of Inheritance

Ataxia with oculomotor apraxia type 2 (AOA2) is inherited in an autosomal recessive manner.

Risk to Family Members

Parents of a proband

- The parents of an affected child are obligate heterozygotes and therefore carry one mutant allele.
- Heterozygotes (carriers) are asymptomatic.

Sibs of a proband

- At conception, each sib of an affected individual has a 25% chance of being affected, a 50% chance of being an asymptomatic carrier, and a 25% chance of being unaffected and not a carrier.
- Once an at-risk sib is known to be unaffected, the risk of his/her being a carrier is 2/3.
- Heterozygotes (carriers) are asymptomatic.

Offspring of a proband. No individuals with AOA2 have been known to reproduce.

Other family members of a proband. Each sib of the proband's parents is at a 50% risk of being a carrier.

Carrier Detection

Carrier testing for at-risk family members is available on a clinical basis once the mutations have been identified in the proband.

Related Genetic Counseling Issues

Family planning. The optimal time for determination of genetic risk and clarification of carrier status is before pregnancy.

DNA banking. DNA banking is the storage of DNA (typically extracted from white blood cells) for possible future use. Because it is likely that testing methodology and our understanding of genes, mutations, and diseases will improve in the future, consideration should be given to banking DNA of affected individuals. DNA banking is particularly relevant in situations in which the sensitivity of currently available testing is less than 100%. See DNA Banking for a list of laboratories offering this service.

Prenatal Testing

Prenatal diagnosis for pregnancies at increased risk is possible by analysis of DNA extracted from fetal cells obtained by amniocentesis usually performed at about 15-18 weeks' gestation or chorionic villus sampling (CVS) at about ten to 12 weeks' gestation. Both disease-causing

alleles of an affected family member must be identified or linkage established in the family before prenatal testing can be performed.

Note: Gestational age is expressed as menstrual weeks calculated either from the first day of the last normal menstrual period or by ultrasound measurements.

Preimplantation genetic diagnosis (PGD) may be available for families in which the disease-causing mutations have been identified in an affected family member. For laboratories offering PGD, see **Testing**.

Molecular Genetics

Information in the Molecular Genetics tables is current as of initial posting or most recent update. —ED.

Table A. Molecular Genetics of Ataxia with Oculomotor Apraxia Type 2

Gene Symbol	Chromosomal Locus	Protein Name
<i>SETX</i>	9q34	Probable helicase senataxin

Data are compiled from the following standard references: Gene symbol from HUGO; chromosomal locus, locus name, critical region, complementation group from OMIM; protein name from Swiss-Prot.

Table B. OMIM Entries for Ataxia with Oculomotor Apraxia Type 2

606002	SPINOCEREBELLAR ATAXIA, AUTOSOMAL RECESSIVE 1; SCAR1
608465	SENATAXIN

Table C. Genomic Databases for Ataxia with Oculomotor Apraxia Type 2

Gene Symbol	Entrez Gene	HGMD	GeneCards	GenAtlas
<i>SETX</i>	23064 (MIM No. 608465)	SETX	<i>SETX</i>	SETX

For a description of the genomic databases listed, click [here](#).

Normal allelic variants: *SETX* is composed of 24 coding and two non-coding exons. To date, eight different polymorphisms have been identified, all located in exon 8: 3147C>T, 3455G>T, 3576T>G, 3754G>A, 4156G>A [Moreira et al 2004], 4755T>G, 2975A>G, and 4755T>G [Fogel & Perlman 2006].

Pathologic allelic variants: To date, 27 mutations have been found in 32 families from 14 countries (Table 2, pdf). Also see Genomic Databases table.

Normal gene product: *SETX* encodes the newly identified and ubiquitously expressed 2,677 amino-acid protein, probable helicase senataxin. Senataxin is composed of four regions: an N-terminal region that shares homologies with the fungal Sen1p proteins; a second region that is not conserved; a third region that contains a classic seven-motif domain found in the superfamily 1 of helicases; and a C-terminal region that is not conserved [Moreira et al 2004].

Saccharomyces cerevisiae Sen1p is involved in splicing and termination of tRNA and small nuclear and nucleolar RNAs, and has RNA helicase activity encoded by its C-terminal domain [Ursic et al 1997, Rasmussen & Culbertson 1998, Kim et al 1999]. The first reported *Schizosaccharomyces pombe* Sen1p encoded by chromosome 1 (*S. pombe* has two *Sen1* genes) has both RNA and DNA helicase activities [Kim et al 1999]. The helicase domain of senataxin and the Sen1p proteins share significant similarity with two other members of the DExxQ-box family of helicases [Moreira et al 2004]: RENT1/Upf1, involved in nonsense-mediated RNA

decay [Wang et al 2001] and IGHMBP2, defective in spinal muscular atrophy with respiratory distress (SMARD1) [Grohmann et al 2001] and in mouse neuromuscular degeneration [Cox et al 1998]. SMARD1 is a human disease characterized by dysfunction and progressive loss of alpha-motor neurons in the anterior horn of the spinal cord, leading to neurogenic muscular atrophy with subsequent symmetric muscle weakness of the trunk and limbs [Grohmann et al 2001]. Life-threatening respiratory distress with clinical and radiologic evidence of unilateral or bilateral paralysis of the diaphragm is the most important presenting symptom of this disease.

Upf1 proteins have RNA helicase activity, but IGHMBP2 was initially identified as a DNA-binding protein with transcriptional transactivating properties. It is therefore possible that, like *S. pombe* Sen1p-1, senataxin has both RNA and DNA helicase activities and that senataxin acts in a DNA repair pathway, like several other proteins mutated in autosomal recessive cerebellar ataxias, for example, ataxia-telangiectasia [Shiloh 2003], ataxia with oculomotor apraxia type 1 [Moreira, Barbot, Tachi, Kozuka, Uchida et al 2001], ataxia-telangiectasia-like disorder [Stewart et al 1999], and spinocerebellar ataxia with peripheral neuropathy 1 [Takashima et al 2002]. The results also suggest that senataxin might be a nuclear RNA helicase with a role in the splicing machinery and that the molecular pathology of AOA2 may share features with spinal muscular atrophy and spinal muscular atrophy with respiratory distress.

The first data on senataxin characterization and localization showed that in murine brain, senataxin concentrates in several regions (including cerebellum, hippocampus, and olfactory bulb) with a general neuronal expression profile, colocalizing with NeuN (a protein present in neuronal nuclei). In cultured cells, *SETX* was found to be cytoplasmically diffuse, but in the nucleus, senataxin was punctuated, colocalizing with fibrillarin, a marker of the nucleolus. In differentiated non-cycling cells, nuclear senataxin was not restricted to the nucleolus but was diffuse within the nucleoplasm, suggesting cell cycle-dependent localization [Chen et al 2006].

Abnormal gene product: An important part of the missense mutations so far reported cluster within the N-terminus and helicase domains. Flag tagging at the N-terminus caused protein mislocation to the nucleoplasm and failure to export to the cytoplasm, suggesting that the N-terminus may be essential for correct senataxin localization [Chen et al 2006].

Resources

GeneReviews provides information about selected national organizations and resources for the benefit of the reader. GeneReviews is not responsible for information provided by other organizations. Information that appears in the Resources section of a GeneReview is current as of initial posting or most recent update of the GeneReview. Search GeneTests for this

*disorder and select **Resources** for the most up-to-date Resources information.*—ED.

euro-ataxia (European Federation of Hereditary Ataxias)

Boherboy Dunlavin

Co Wicklow

Ireland

Phone: +353 45 401218

Fax: +353 45 401371

Email: mary.kearneyl@euro-ataxia.org

www.euro-ataxia.org

International Network of Ataxia Friends (INTERNAF)

www.internaf.org

National Ataxia Foundation
 2600 Fernbrook Lane Suite 119
 Minneapolis MN 55447
Phone: 763-553-0020
Fax: 763-553-0167
Email: naf@ataxia.org
 www.ataxia.org

WE MOVE (Worldwide Education and Awareness for Movement Disorders)
 204 West 84th Street
 New York NY 10024
Phone: 800-437-MOV2 (800-437-6683)
Fax: 212-875-8389
Email: wemove@wemove.org
 www.wemove.org

References

Medical Genetic Searches: A specialized PubMed search designed for clinicians that is located on the PubMed Clinical Queries page. [PubMed](#)

Published Statements and Policies Regarding Genetic Testing

No specific guidelines regarding genetic testing for this disorder have been developed.

Literature Cited

- Asaka T, Yokoji H, Ito J, Yamaguchi K, Matsushima A. Autosomal recessive ataxia with peripheral neuropathy and elevated AFP: novel mutations in SETX. *Neurology*. 2006;66:1580–1. [PubMed: 16717225]
- Barbot C, Coutinho P, Choro R, Ferreira C, Barros J, Fineza I, Dias K, Monteiro J, Guimaraes A, Mendonca P, do Ceu Moreira M, Sequeiros J. Recessive ataxia with ocular apraxia: review of 22 Portuguese patients. *Arch Neurol*. 2001;58:201–5. [PubMed: 11176957]
- Bassuk AG, Chen YZ, Batish SD, Nagan N, Opal P, Chance PF, Bennett CL. In cis autosomal dominant mutation of Senataxin associated with tremor/ataxia syndrome. *Neurogenetics*. 2007;8:45–49. [PubMed: 17096168]
- Chance PF, Rabin BA, Ryan SG, Ding Y, Scavina M, Crain B, Griffin JW, Cornblath DR. Linkage of the gene for an autosomal dominant form of juvenile amyotrophic lateral sclerosis to chromosome 9q34. *Am J Hum Genet*. 1998;62:633–40. [PubMed: 9497266]
- Chen YZ, Bennett CL, Huynh HM, Blair IP, Puls I, Irobi J, Dierick I, Abel A, Kennerson ML, Rabin BA, Nicholson GA, Auer-Grumbach M, Wagner K, De Jonghe P, Griffin JW, Fischbeck KH, Timmerman V, Cornblath DR, Chance PF. DNA/RNA helicase gene mutations in a form of juvenile amyotrophic lateral sclerosis (ALS4). *Am J Hum Genet*. 2004;74:1128–35. [PubMed: 15106121]
- Chen YZ, Hashemi SH, Anderson SK, Huang Y, Moreira MC, Lynch DR, Glass IA, Chance PF, Bennett CL. Senataxin, the yeast Sen1p orthologue: characterization of a unique protein in which recessive mutations cause ataxia and dominant mutations cause motor neuron disease. *Neurobiol Dis*. 2006;23:97–108. [PubMed: 16644229]
- Cox GA, Mahaffey CL, Frankel WN. Identification of the mouse neuromuscular degeneration gene and mapping of a second site suppressor allele. *Neuron*. 1998;21:1327–37. [PubMed: 9883726]
- Criscuolo C, Chessa L, Di Giandomenico S, Mancini P, Sacca F, Grieco GS, Piane M, Barbieri F, De Michele G, Banfi S, Pierelli F, Rizzuto N, Santorelli FM, Galloisi L, Filla A, Casali C. Ataxia with oculomotor apraxia type 2: a clinical, pathologic, and genetic study. *Neurology*. 2006;66:1207–10. [PubMed: 16636238]
- Date H, Onodera O, Tanaka H, Iwabuchi K, Uekawa K, Igarashi S, Koike R, Hiroi T, Yuasa T, Awaya Y, Sakai T, Takahashi T, Nagatomo H, Sekijima Y, Kawachi I, Takiyama Y, Nishizawa M, Fukuhara

N, Saito K, Sugano S, Tsuji S. Early-onset ataxia with ocular motor apraxia and hypoalbuminemia is caused by mutations in a new HIT superfamily gene. *Nat Genet.* 2001;29:184–8. [PubMed: [11586299](#)]

De Jonghe P, Auer-Grumbach M, Irobi J, Wagner K, Plecko B, Kennerson M, Zhu D, De Vriendt E, Van Gerwen V, Nicholson G, Hartung HP, Timmerman V. Autosomal dominant juvenile amyotrophic lateral sclerosis and distal hereditary motor neuropathy with pyramidal tract signs: synonyms for the same disorder? *Brain.* 2002;125:1320–5. [PubMed: [12023320](#)]

Duquette A, Roddier K, McNabb-Baltar J, Gosselin I, St-Denis A, Dicaire MJ, Loisel L, Labuda D, Marchand L, Mathieu J, Bouchard JP, Brais B. Mutations in senataxin responsible for Quebec cluster of ataxia with neuropathy. *Ann Neurol.* 2005;57:408–14. [PubMed: [15732101](#)]

Fogel BL, Perlman S. Novel mutations in the senataxin DNA/RNA helicase domain in ataxia with oculomotor apraxia 2. *Neurology.* 2006;67:2083–4. [PubMed: [17159128](#)]

Grohmann K, Schuelke M, Diers A, Hoffmann K, Lucke B, Adams C, Bertini E, Leonhardt-Horti H, Muntoni F, Ouvrier R, Pfeufer A, Rossi R, Van Maldergem L, Wilmshurst JM, Wienker TF, Sendtner M, Rudnik-Schoneborn S, Zerres K, Hubner C. Mutations in the gene encoding immunoglobulin mu-binding protein 2 cause spinal muscular atrophy with respiratory distress type 1. *Nat Genet.* 2001;29:75–7. [PubMed: [11528396](#)]

Kim HD, Choe J, Seo YS. The sen1(+) gene of *Schizosaccharomyces pombe*, a homologue of budding yeast SEN1, encodes an RNA and DNA helicase. *Biochemistry.* 1999;38:14697–710. [PubMed: [10545196](#)]

Le Ber I, Bouslam N, Rivaud-Pechoux S, Guimaraes J, Benomar A, Chamayou C, Goizet C, Moreira MC, Klur S, Yahyaoui M, Agid Y, Koenig M, Stevanin G, Brice A, Durr A. Frequency and phenotypic spectrum of ataxia with oculomotor apraxia 2: a clinical and genetic study in 18 patients. *Brain.* 2004;127:759–67. [PubMed: [14736755](#)]

Le Ber I, Moreira MC, Rivaud-Pechoux S, Chamayou C, Ochsner F, Kuntzer T, Tardieu M, Said G, Habert MO, Demarquay G, Tannier C, Beis JM, Brice A, Koenig M, Durr A. Cerebellar ataxia with oculomotor apraxia type 1: clinical and genetic studies. *Brain.* 2003;126:2761–72. [PubMed: [14506070](#)]

Moreira MC, Barbot C, Tachi N, Kozuka N, Mendonca P, Barros J, Coutinho P, Sequeiros J, Koenig M. Homozygosity mapping of Portuguese and Japanese forms of ataxia-oculomotor apraxia to 9p13, and evidence for genetic heterogeneity. *Am J Hum Genet.* 2001;68:501–8. [PubMed: [11170899](#)]

Moreira MC, Barbot C, Tachi N, Kozuka N, Uchida E, Gibson T, Mendonca P, Costa M, Barros J, Yanagisawa T, Watanabe M, Ikeda Y, Aoki M, Nagata T, Coutinho P, Sequeiros J, Koenig M. The gene mutated in ataxia-ocular apraxia 1 encodes the new HIT/Zn-finger protein aprataxin. *Nat Genet.* 2001;29:189–93. [PubMed: [11586300](#)]

Moreira MC, Klur S, Watanabe M, Nemeth AH, Le Ber I, Moniz JC, Tranchant C, Aubourg P, Tazir M, Schols L, Pandolfo M, Schulz JB, Pouget J, Calvas P, Shizuka-Ikeda M, Shoji M, Tanaka M, Izatt L, Shaw CE, M'Zahem A, Dunne E, Bomont P, Benhassine T, Bouslam N, Stevanin G, Brice A, Guimaraes J, Mendonca P, Barbot C, Coutinho P, Sequeiros J, Durr A, Warter JM, Koenig M. Senataxin, the ortholog of a yeast RNA helicase, is mutant in ataxia-ocular apraxia 2. *Nat Genet.* 2004;36:225–7. [PubMed: [14770181](#)]

Musumeci O, Naini A, Slonim AE, Skavin N, Hadjigeorgiou GL, Krawiecki N, Weissman BM, Tsao CY, Mendell JR, Shanske S, De Vivo DC, Hirano M, DiMauro S. Familial cerebellar ataxia with muscle coenzyme Q10 deficiency. *Neurology.* 2001;56:849–55. [PubMed: [11294920](#)]

Nemeth AH, Bochukova E, Dunne E, Huson SM, Elston J, Hannan MA, Jackson M, Chapman CJ, Taylor AM. Autosomal recessive cerebellar ataxia with oculomotor apraxia (ataxia-telangiectasia-like syndrome) is linked to chromosome 9q34. *Am J Hum Genet.* 2000;67:1320–6. [PubMed: [11022012](#)]

Pulst SM, Nechiporuk A, Nechiporuk T, Gispert S, Chen XN, Lopes-Cendes I, Pearlman S, Starkman S, Orozco-Diaz G, Lunkes A, DeJong P, Rouleau GA, Auburger G, Korenberg JR, Figueroa C, Sahba S. Moderate expansion of a normally biallelic trinucleotide repeat in spinocerebellar ataxia type 2. *Nat Genet.* 1996;14:269–76. [PubMed: [8896555](#)]

Rabin BA, Griffin JW, Crain BJ, Scavina M, Chance PF, Cornblath DR. Autosomal dominant juvenile amyotrophic lateral sclerosis. *Brain* 122 (Pt. 1999;8):1539–50. [PubMed: [10430837](#)]

- Rasmussen TP, Culbertson MR. The putative nucleic acid helicase Sen1p is required for formation and stability of termini and for maximal rates of synthesis and levels of accumulation of small nucleolar RNAs in *Saccharomyces cerevisiae*. *Mol Cell Biol*. 1998;18:6885–96. [PubMed: [9819377](#)]
- Sekijima Y, Hashimoto T, Onodera O, Date H, Okano T, Naito K, Tsuji S, Ikeda S. Severe generalized dystonia as a presentation of a patient with aprataxin gene mutation. *Mov Disord*. 2003;18:1198–200. [PubMed: [14534929](#)]
- Shiloh Y. ATM and related protein kinases: safeguarding genome integrity. *Nat Rev Cancer*. 2003;3:155–68. [PubMed: [12612651](#)]
- Shimazaki H, Takiyama Y, Sakoe K, Ikeguchi K, Nijima K, Kaneko J, Namekawa M, Ogawa T, Date H, Tsuji S, Nakano I, Nishizawa M. Early-onset ataxia with ocular motor apraxia and hypoalbuminemia: the aprataxin gene mutations. *Neurology*. 2002;59:590–5. [PubMed: [12196655](#)]
- Stewart GS, Maser RS, Stankovic T, Bressan DA, Kaplan MI, Jaspers NG, Raams A, Byrd PJ, Petrini JH, Taylor AM. The DNA double-strand break repair gene hMRE11 is mutated in individuals with an ataxia-telangiectasia-like disorder. *Cell*. 1999;99:577–87. [PubMed: [10612394](#)]
- Tachi N, Kozuka N, Ohya K, Chiba S, Sasaki K. Hereditary cerebellar ataxia with peripheral neuropathy and mental retardation. *Eur Neurol*. 2000;43:82–7. [PubMed: [10686465](#)]
- Takashima H, Boerkoel CF, John J, Saifi GM, Salih MA, Armstrong D, Mao Y, Quijcho FA, Roa BB, Nakagawa M, Stockton DW, Lupski JR. Mutation of TDP1, encoding a topoisomerase I-dependent DNA damage repair enzyme, in spinocerebellar ataxia with axonal neuropathy. *Nat Genet*. 2002;32:267–72. [PubMed: [12244316](#)]
- Tranchant C, Fleury M, Moreira MC, Koenig M, Warter JM. Phenotypic variability of aprataxin gene mutations. *Neurology*. 2003;60:868–70. [PubMed: [12629250](#)]
- Ursic D, Himmel KL, Gurley KA, Webb F, Culbertson MR. The yeast SEN1 gene is required for the processing of diverse RNA classes. *Nucleic Acids Res*. 1997;25:4778–85. [PubMed: [9365256](#)]
- Wang W, Czaplinski K, Rao Y, Peltz SW. The role of Upf proteins in modulating the translation read-through of nonsense-containing transcripts. *EMBO J*. 2001;20:880–90. [PubMed: [11179232](#)]
- Watanabe M, Sugai Y, Concannon P, Koenig M, Schmitt M, Sato M, Shizuka M, Mizushima K, Ikeda Y, Tomidokoro Y, Okamoto K, Shoji M. Familial spinocerebellar ataxia with cerebellar atrophy, peripheral neuropathy, and elevated level of serum creatine kinase, gamma-globulin, and alpha-fetoprotein. *Ann Neurol*. 1998;44:265–9. [PubMed: [9708552](#)]

Suggested Readings

- Amouri R, Moreira MC, Zouari M, El Euch G, Barhoumi C, Kefi M, Belal S, Koenig M, Hentati F. Aprataxin gene mutations in Tunisian families. *Neurology*. 2004;63:928–9. [PubMed: [15365154](#)]
- Caldecott KW. DNA single-strand break repair and spinocerebellar ataxia. *Cell*. 2003;112:7–10. [PubMed: [12526788](#)]
- Clements PM, Breslin C, Deeks ED, Byrd PJ, Ju L, Bieganski P, Brenner C, Moreira MC, Taylor AM, Caldecott KW. The ataxia-oculomotor apraxia 1 gene product has a role distinct from ATM and interacts with the DNA strand break repair proteins XRCC1 and XRCC4. *DNA Repair (Amst)*. 2004;3:1493–502. [PubMed: [15380105](#)]
- Criscuolo C, Mancini P, Sacca F, De Michele G, Monticelli A, Santoro L, Scarano V, Banfi S, Filla A. Ataxia with oculomotor apraxia type 1 in Southern Italy: late onset and variable phenotype. *Neurology*. 2004;63:2173–5. [PubMed: [15596775](#)]
- Gros-Louis F, Dupre N, Dion P, Fox MA, Laurent S, Verreault S, Sanes JR, Bouchard JP, Rouleau GA. Mutations in SYNE1 lead to a newly discovered form of autosomal recessive cerebellar ataxia. *Nat Genet*. 2007;39:80–5. [PubMed: [17159980](#)]
- Gueven N, Becherel OJ, Kijas AW, Chen P, Howe O, Rudolph JH, Gatti R, Date H, Onodera O, Taucher-Scholz G, Lavin MF. Aprataxin, a novel protein that protects against genotoxic stress. *Hum Mol Genet*. 2004;13:1081–93. [PubMed: [15044383](#)]
- Kijas AW, Harris JL, Harris JM, Lavin MF. Aprataxin forms a discrete branch in the HIT (histidine triad) superfamily of proteins with both DNA/RNA binding and nucleotide hydrolase activities. *J Biol Chem*. 2006;281:13939–48. [PubMed: [16547001](#)]
- Le Ber I, Brice A, Durr A. New autosomal recessive cerebellar ataxias with oculomotor apraxia. *Curr Neurol Neurosci Rep*. 2005;5:411–7. [PubMed: [16131425](#)]

- Mosesso P, Piane M, Palitti F, Pepe G, Penna S, Chessa L. The novel human gene aprataxin is directly involved in DNA single-strand-break repair. *Cell Mol Life Sci.* 2005;62:485–91. [PubMed: [15719174](#)]
- Sano Y, Date H, Igarashi S, Onodera O, Oyake M, Takahashi T, Hayashi S, Morimatsu M, Takahashi H, Makifuchi T, Fukuhara N, Tsuji S. Aprataxin, the causative protein for EAOH is a nuclear protein with a potential role as a DNA repair protein. *Ann Neurol.* 2004;55:241–9. [PubMed: [14755728](#)]
- Sekijima Y, Ohara S, Nakagawa S, Tabata K, Yoshida K, Ishigame H, Shimizu Y, Yanagisawa N. Hereditary motor and sensory neuropathy associated with cerebellar atrophy (HMSNCA): clinical and neuropathological features of a Japanese family. *J Neurol Sci.* 1998;158:30–7. [PubMed: [9667774](#)]
- Whitehouse CJ, Taylor RM, Thistlethwaite A, Zhang H, Karimi-Busheri F, Lasko DD, Weinfeld M, Caldecott KW. XRCC1 stimulates human polynucleotide kinase activity at damaged DNA termini and accelerates DNA single-strand break repair. *Cell.* 2001;104:107–17. [PubMed: [11163244](#)]

Author Information

Acknowledgments

The authors wish to thank all patients and their families for their collaboration, as well as all the physicians involved in the clinical study of the families. Genetic studies were supported by funds from the Fundação para a Ciência e a Tecnologia (Portuguese Ministry of Science), the Portuguese Ministry of Health (projects STRDA/C/SAU/277/92 and PECS/C/SAU/219/95), the Institut National de la Santé et de la Recherche Médicale, the Centre National de la Recherche Scientifique, the Hôpitaux Universitaires de Strasbourg (PHRC regional), and the GIS-Maladies Rares (SPATAX Research Network. Grant 4MR12FA004DS). M.C.M. has a post-graduate fellowship SFRH/BPD/11502/2002 from Fundação para a Ciência e a Tecnologia (Portuguese Ministry of Science).

Revision History

- 5 March 2007 (me) Comprehensive update posted to live Web site
- 31 May 2005 (mcm) Revision: Sequence analysis clinically available
- 15 November 2004 (me) Review posted to live Web site
- 23 June 2004 (mcm) Original submission