Hereditary Ataxia Genetic Testing

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Hereditary ataxia genetic testing is addressed by this guideline.

Procedures addressed

The inclusion of any procedure code in this table does not imply that the code is under management or requires prior authorization. Refer to the specific Health Plan's procedure code list for management requirements.

Procedures addressed by this guideline	Procedure codes
Ataxia gene analysis	81400 81401 81402 81403 81404 81405 81406 81407 81408 81479
ATN1 expansion analysis	81177
ATXN1 gene analysis, evaluation to detect abnormal (eg,expanded) allele	81178
ATXN2 gene analysis, evaluation to detect abnormal (eg,expanded) allele	81179
ATXN3 gene analysis, evaluation to detect abnormal (eg,expanded) allele	81180
ATXN7 gene analysis, evaluation to detect abnormal (eg,expanded) allele	81181
ATXN8 gene analysis, evaluation to detect abnormal (eg, expanded) alleles	81182

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Procedures addressed by this guideline	Procedure codes
ATXN10 gene analysis, evaluation to detect abnormal (eg, expanded) alleles	81183
CACNA1A gene analysis; evaluation to detect abnormal (eg, expanded) alleles	81184
CACNA1A gene analysis; full gene sequence	81185
CACNA1A gene analysis; known familial variant	81186
FXN gene analysis; evaluation to detect abnormal (expanded alleles)	81284
FXN gene analysis; characterization of alleles (e.g. expanded size)	81285
FXN gene analysis; full gene sequence	81286
FXN gene analysis; known familial variant(s)	81289
FXN gene analysis, deletion/duplication	81479
Genomic Unity Ataxia Repeat Expansion and Sequence Analysis	0216U
Genomic Unity Comprehensive Ataxia Repeat Expansion and Sequence Analysis	0217U
Hereditary ataxia multigene panel	81479
Hereditary ataxia multigene panel (including sequencing of at least 15 genes)	81443
PPP2R2B gene analysis, evaluation to detect abnormal (eg, expanded) alleles	81343
TBP gene analysis, evaluation to detect abnormal (eg, expanded) alleles	81344

Criteria

Requests for hereditary ataxia genetic testing are reviewed using the following criteria.

Hereditary Ataxia Known Familial Mutation Testing

- Genetic Counseling:
  - Pre- and post-test genetic counseling by an appropriate provider (as deemed by the Health Plan policy), AND
- Previous Genetic Testing:
  - No previous genetic testing inclusive of the known familial mutation(s), and
  - Disease-causing mutation(s) identified in biological relative with the following degree of relationship to the member:
    - 1st or 2nd degree biological relative for an autosomal dominant disorder, or
    - 1st, 2nd, or 3rd degree biological relative for an autosomal recessive or X-linked disorder, and
  - Member is at risk to have the familial mutation based on the inheritance pattern of the disorder in question, AND
- Predictive Testing for Asymptomatic Individuals:
  - 18 years of age or older, or
  - Under the age of 18 years, and
    - Test results are needed for treatment or medical screening, OR
- Diagnostic Testing for Symptomatic Individuals:
  - Clinical examination and/or biochemical results are suggestive, but not confirmatory, of the familial diagnosis, AND
- Rendering laboratory is a qualified provider of service per the Health Plan policy.

Hereditary Ataxia Single-Gene Testing

- Genetic Counseling:
  - Pre- and post-test genetic counseling by an appropriate provider (as deemed by the Health Plan policy), AND
- Previous Genetic Testing:
  - No known ataxia-related mutation in the member or the member's family that would explain the member's clinical symptoms, AND
  - No previous testing that would have included the requested gene, AND
- Diagnostic Testing for Symptomatic Individuals:
  - Test methodology is appropriate to the disease-causing mutations that are commonly reported for the disorder in question and any recommended previous testing has already been performed (e.g. FRDA trinucleotide repeat testing is completed before sequencing and/or deletion/duplication analysis), and
  - Clinical examination is remarkable for ataxia and other clinical features and/or biochemical results are suggestive, but not confirmatory, of the targeted disorder (see Table: *Select Hereditary Ataxias*), and

  - The member does not have an underlying non-genetic cause for their ataxia (e.g. alcoholism, vitamin deficiencies, multiple sclerosis, vascular disease, tumors, etc) or the clinical suspicion for a gene mutation remains high even in the presence of a non-genetic cause, and
  - When family history is present, inheritance pattern is consistent with the targeted ataxia disorder, and
  - Genetic diagnosis would result in changes to the member's medical management, AND
- Rendering laboratory is a qualified provider of service per the Health Plan policy.

Multigene Panel Testing

- Genetic Counseling:
  - Pre- and post-test genetic counseling by an appropriate provider (as deemed by the Health Plan policy), AND
- Previous Genetic Testing:
  - No previous testing of the requested genes, and
  - No known ataxia-related mutation in the member or the member's family that would explain the member's clinical symptoms, AND
- Diagnostic Testing for Symptomatic Individuals:
  - Test methodology is appropriate to the disease-causing mutations that are commonly reported for the disorder in question (e.g., sequencing-only panels will not detect triplet repeat or large deletion/duplication mutations), and
  - Individual has been diagnosed with cerebellar ataxia, regardless of age of onset, and
  - The member does not have an underlying non-genetic cause for their ataxia (e.g. alcoholism, vitamin deficiencies, multiple sclerosis, vascular disease, tumors, etc) or the clinical suspicion for a gene mutation remains high even in the presence of a non-genetic cause, and
  - Family and medical histories do not point to a specific genetic diagnosis (see Table: *Select Hereditary Ataxias* for specific examples) or pattern of inheritance for which a more focused test would be appropriate, and
  - The requested hereditary ataxia multigene panel and genetic diagnosis would result in changes to the member's medical management, AND
- Rendering laboratory is a qualified provider of service per the Health Plan policy.

Exclusions and Other Considerations

- This guideline may not apply to genetic testing for indications that are specifically addressed elsewhere. Please refer to test-specific guidelines when available (see Table: *Select Hereditary Ataxias*).

- Gene panels that are specific to hereditary ataxias will be considered for medical necessity according to the criteria outlined in this guideline.
- Broad hereditary ataxia panels may not be medically necessary when a narrower panel (e.g., a single-syndrome panel) is available and more appropriate based on the clinical findings.
- Germline genetic testing is only medically reimbursable once per lifetime. Therefore, a single gene included in a multigene panel may not be medically necessary if testing has been performed previously. Exceptions may be considered if technical advances in testing demonstrate significant advantages that would support a medical need to retest.

Billing and Reimbursement

This section outlines the billing requirements for tests addressed in this guideline. These requirements will be enforced during the case review process whenever appropriate. Examples of requirements may include specific coding scenarios, limits on allowable test combinations or frequency and/or information that must be provided on a claim for automated processing. Any claims submitted without the necessary information to allow for automated processing (e.g. ICD code, place of service, etc.) will not be reimbursable as billed. Any claim may require submission of medical records for post service review.

- Any individual gene or multi-gene panel is only reimbursable once per lifetime.
- When otherwise reimbursable, the following limitations apply:
  - When a panel is being performed, it is only reimbursable when billed with a single, appropriate panel procedure code (e.g., 81443, 81479, 0216U, or 0217U)*.
  - Analysis of individual genes will not be reimbursed separately when performed as part of a multi-gene panel (i.e. multiple stacked codes are not eligible for reimbursement of panels).

Note: *The panel code(s) listed here may not be all-inclusive. For further discussion of what is considered an appropriate panel code, please refer to the guideline *Laboratory Billing and Reimbursement*.

What are hereditary ataxias?

The hereditary ataxias are a group of genetic disorders characterized by slowly progressive uncoordinated, unsteady movement and gait, and often poor coordination of hands, abnormal eye movements, and slurred speech. Cerebellar atrophy is also frequently seen via brain imaging.[1] Hereditary ataxias include, but are not limited to, ataxia telangiectasia (A-T), dentatorubral-pallidoluysian atrophy (DRPLA), fragile X-associated tremor/ataxia syndrome (FXTAS), Friedreich ataxia (FRDA), and

spinocerebellar ataxias (SCAs). Specific features may vary with each subtype of hereditary ataxia.[1-19]

Prevalence

Prevalence estimates vary. The prevalence is approximately 2.7/100,000 and 3.3/100,000 for autosomal dominant and autosomal recessive hereditary ataxias, respectively.[20] One study in Norway estimated the prevalence of hereditary ataxia at 6.5 per 100,000 people.[21] Founder mutations may account for a higher prevalence of certain hereditary ataxias in specific regions.[2,17,18,22-24]

Symptoms

The hereditary ataxias are made up of multiple different conditions. Common symptoms include slowly progressive uncoordinated, unsteady movement and gait, and poor coordination of hands, abnormal eye movements, and slurred speech. Brain imaging is often remarkable for cerebellar atrophy.[1] The table below summarizes some of the clinical features of the more common hereditary ataxias.

Table: Select Hereditary Ataxias

This table is not intended to be all-inclusive; other conditions not listed here may have coverage under this guideline.

Syndrome Name	Clinical Features	Cause	Inheritance
Ataxia-telangiectasia (A-T)[*16,27,28]	Age of onset for classic A-T: early childhood, usually between 1 and 4 years of age. Signs and symptoms of classic A-T include: • cerebellar ataxia; • extrapyramidal movement disorders such as chorea, myoclonus, dystonia and tremor; • peripheral neuropathy; • dysarthria; • dysphagia; • eye movement disorders such as gaze-evoked nystagmus and oculomotor apraxia; • telangiectasias, particularly of conjunctiva and sun-exposed skin; • immunodeficiencies and frequent non-opportunistic infections; • pulmonary disease; • respiratory infections;	Biallelic mutations in the ATM gene.	AR

Syndrome Name	Clinical Features	Cause	Inheritance
	• malignancies, especially leukemias and lymphomas in children or solid tumors in adults; • endocrine abnormalities such as growth impairment, gonadal dysfunction, and insulin resistance, and • radiation sensitivity. Variant A-T has a less progressive disease course and may present in childhood to adulthood; most individuals have first manifestations by age 10 years. Immunodeficiency, respiratory infections, and pulmonary disease are typically absent.		

Syndrome Name	Clinical Features	Cause	Inheritance
Dentatorubral-pallidoluysian atrophy (DRPLA)[18,28,29]	Age of onset: ranges from one year of age to 72 years of age; the mean age of onset is 31.5 years of age. Signs and symptoms of the juvenile onset form (under ~age 20 years) include: • progressive intellectual deterioration; • behavior changes; ◦ ataxia; ◦ chorea; ◦ myoclonus, and ◦ seizures. Signs and symptoms of the juvenile onset form (over ~age 20 years) include: • ataxia; • choreoathetosis; • dementia, and • psychiatric disturbance.	Monoallelic expansion of a CAG trinucleotide repeat in the ATN1 gene.	AD

Syndrome Name	Clinical Features	Cause	Inheritance
Fragile X-associated tremor/ ataxia syndrome (FXTAS)**[19]	Age of onset: typically, older than 50 years. Signs and symptoms of FXTAS include: • progressive cerebellar ataxia; • intention tremor; • psychiatric disturbances; • short term memory loss; • executive function deficits; • cognitive decline; • dementia; • parkinsonism; • autonomic dysfunction, and • neuropathy in lower extremities.	Monoallelic expansion of a CGG trinucleotide repeat in the premutation range (55-200 CGG repeats) in the FMR1 gene.	X-linked

Syndrome Name	Clinical Features	Cause	Inheritance
Friedreich ataxia (FRDA)[17,30]	Age of onset for typical FRDA: typically, before age 25 years with the mean age of onset between 10 and 15 years. Signs and symptoms of typical FRDA include: • progressive ataxia of the limbs and gait; • dysarthria; • dysphagia; • absent lower limb reflexes; • peripheral motor and sensory neuropathy; • spasticity; • autonomic disturbance; • abnormal eye movements; • optic atrophy; • muscle weakness; • cardiomyopathy; • diabetes mellitus; • scoliosis; • pes cavus, and • sensorineural hearing loss. Approximately 25% of affected individuals have an atypical form that includes late-onset	Most often due to biallelic expansions of a GAA trinucleotide repeat in the FXN gene. Approximately 4% of affected individuals have a trinucleotide repeat expansion in one allele and a sequence variant or large deletion in the other allele.	AR

Syndrome Name	Clinical Features	Cause	Inheritance
	FRDA, very-late onset FRDA, and FRDA with retained reflexes.		

Syndrome Name	Clinical Features	Cause	Inheritance
Spinocerebellar ataxia (SCA)[3-15] The most common subtypes are 1, 2, 3, 6, and 7.***	Age of onset: typically, adult onset. Common signs and symptoms for SCAs include progressive cerebellar ataxia, dysarthia, ophthalmologic involvement (depending on the subtype of SCA, this may include nystagmus, slow saccadic eye movements, ophthalmoparesis, dysconjugate eye movements, diplopia, and lid retraction). Subtype-specific features include: SCA1: deterioration of bulbar functions, pyramidal signs, cognitive dysfunction, and peripheral neuropathy. SCA2: peripheral neuropathy, decreased deep tendon reflexes, and dementia. SCA3: vestibular dysfunction, pyramidal and extrapyramidal	SCA1: Monoallelic expansion of a CAG trinucleotide repeat in the ATNX1 gene. SCA2: Monoallelic expansion of a CAG trinucleotide repeat in the ATNX2 gene. SCA3: Monoallelic expansion of a CAG trinucleotide repeat in the ATNX3 gene. SCA6: Monoallelic expansion of a CAG trinucleotide repeat in the CACNA1A gene. SCA7: Monoallelic expansion of a CAG trinucleotide repeat in the ATNX7 gene.	AD

Syndrome Name	Clinical Features	Cause	Inheritance
	signs, amyotrophy, fasciculations, and sensory loss. SCA6: sometimes episodic ataxia and very slow progression. SCA7: Onset may be infantile, early-childhood, or adult. • Infantile or early-childhood onset: Failure to thrive, loss of motor milestones, multiorgan failure, rapid deterioration, and early death. • Adult onset: progressive cerebellar ataxia, dysarthria, dysphagia, dysmetria, dysdiadochokinesia, cone-rod and retinal dystrophy with progressive central visual loss resulting in blindness.		

AD: autosomal dominant inheritance; **AR**: autosomal recessive inheritance; **XL**: X-linked inheritance

*If testing of this gene is requested for hereditary cancer risk assessment due to a monoallelic mutation, please refer to the guideline, *Genetic Testing for Cancer Susceptibility and Hereditary Cancer Syndromes,* or *Hereditary Cancer Syndrome Multigene Panels*, as this testing is not addressed here.

**For information on fragile X-associated tremor/ataxia syndrome testing, please refer to the guideline *FMR1-Related Disorders (Fragile X) Genetic Testing*, as this testing is not addressed here.

***SCAs are due to mutations in numerous genes. This table in not all inclusive and includes information on the most common subtypes of SCAs.

Cause

Pathogenic mutations in one of numerous genes cause hereditary ataxias [1-19] Several of the ataxias are caused by nucleotide repeat expansions. Testing for these conditions is performed by expansion analysis to identify the number of repeats. Anticipation is observed for some hereditary ataxias due to nucleotide repeat expansion. This means that as the disease passes through generations, the severity can increase and the age of onset can decrease. Other hereditary ataxias are due to single nucleotide substitutions or small deletions and duplications. Next generation sequencing is used to identify these pathogenic mutations.[1-19]

Inheritance

Hereditary ataxias may be inherited in an autosomal dominant (AD), autosomal recessive (AR), or X-linked (XL) manner, depending on the gene involved.[1-19]

Diagnosis

The diagnosis and classification of a hereditary ataxia may include a combination of clinical assessment, family history, laboratory testing, and physical examination in addition to specialized testing, such as molecular diagnostics.[1] Molecular genetic testing can be used to establish a specific diagnosis. In the absence of a family history, it can be difficult to differentiate the type or subtype of hereditary ataxia based on clinical features.[1] One study found that in approximately 13% of apparently sporadic ataxias, a causative genetic change was identified.[25]

Acquired causes of ataxia — including alcoholism, vitamin deficiencies, multiple sclerosis, vascular disease, and tumors — should be ruled out.[1] Timely genetic testing may help establish a diagnosis in the individual and guide appropriate management. Genetic testing can allow not only for diagnostic testing but also presymptomatic testing and prenatal testing.[1]

Management

Individuals with a hereditary ataxia are best cared for by a multidisciplinary team. Care is largely supportive and may include speech therapy, occupational therapy, physical therapy, and the use of mobility aids and other assistive devices.[1-19,26] Some pharmacologic treatments may be effective in decreasing the presence of associated

symptoms. Certain hereditary ataxias may require disease specific interventions (e.g. immunodeficiency and increased risk for malignancy seen with ataxia-telangiectasia).[1,16]

Survival

The survival range of the hereditary ataxias varies across the multiple conditions included in this group. Specific symptoms and a genetically determined diagnosis can assist with determining predicted survival and prognosis.[1]

Test Information

Testing for hereditary ataxias may include known familial mutation analysis, trinucleotide repeat testing, next generation sequencing, deletion/duplication analysis and/or multigene panel testing.

Known Familial Mutation (KFM) Testing

Known familial mutations analysis is performed when a causative mutation has been identified in a close biological relative of the individual requesting testing. Analysis for known familial mutations typically includes only the single mutation. However, if available, a targeted mutation panel that includes the familial mutation may be performed.

Trinucleotide Repeat Testing

Repeat expansion genetic testing allows for the determination of the size of a repeated DNA sequence. This testing may involve more than one test methodology. Smaller repeat expansions are typically identified using certain types of polymerase chain reaction (PCR), while larger expansions may require Southern blot. More comprehensive repeat expansion testing that utilizes next generation sequencing and exome sequencing methods is under development.

Next Generation Sequencing Assay

Next generation sequencing (NGS), which is also sometimes called massively parallel sequencing, was developed in 2005 to allow larger scale and more efficient gene sequencing. NGS relies on sequencing many copies of small pieces of DNA simultaneously and using bioinformatics to assemble the sequence. Sequence analysis detects single nucleotide substitutions and small (several nucleotide) deletions and insertions. Regions analyzed typically include the coding sequence and intron/exon boundaries. Promoter regions and intronic sequences may also be sequenced if disease-causing mutations are known to occur in these regions of a gene.

Deletion and Duplication Analysis

Analysis for deletions and duplications can be performed using a variety of technical platforms including exon array, Multiplex ligation-dependent probe amplification (MLPA), and NGS data analysis. These assays detect gains and losses too large to be identified through standard sequence analysis, often single or multiple exons or whole genes.

Multi-Gene Testing Panels

The efficiency of NGS has led to an increasing number of large, multi-gene testing panels. NGS panels that test several genes at once are particularly well-suited to conditions caused by more than one gene or where there is considerable clinical overlap between conditions making it difficult to reliably narrow down likely causes. Additionally, tests should be chosen to maximize the likelihood of identifying mutations in the genes of interest, contribute to alterations in management for an individual, and/or minimize the chance of finding variants of uncertain clinical significance.

Guidelines and Evidence

American College of Medical Genetics and Genomics

An overview published by the American College of Medical Genetics (ACMG, 2013) stated the following regarding testing for hereditary ataxias:[2]

"Establishing the diagnosis of hereditary ataxia requires:

- Detection on neurological examination of typical clinical signs including poorly coordinated gait and finger/hand movements, dysarthria (incoordination of speech), and eye movement abnormalities such as nystagmus, abnormal saccade movements, and ophthalmoplegia.
- Exclusion of nongenetic causes of ataxia (see Differential Diagnosis below).
- Documentation of the hereditary nature of the disease by finding a positive family history of ataxia, identifying an ataxia-causing mutation, or recognizing a clinical phenotype characteristic of a genetic form of ataxia."

"Differential diagnosis of hereditary ataxia includes acquired, nongenetic causes of ataxia, such as alcoholism, vitamin deficiencies, multiple sclerosis, vascular disease, primary or metastatic tumors, and paraneoplastic diseases associated with occult carcinoma of the ovary, breast, or lung, and the idiopathic degenerative disease multiple system atrophy (spinal muscular atrophy). The possibility of an acquired cause of ataxia needs to be considered in each individual with ataxia because a specific treatment may be available."

"Testing strategy when the family history suggests autosomal recessive inheritance:

- A family history in which only sibs are affected and/or when the parents are consanguineous suggests autosomal recessive inheritance. Because of their frequency and/or treatment potential, FRDA, A-T, AOA1, AOA2, AVED, and metabolic or lipid storage disorders such as Refsum disease and mitochondrial diseases should be considered."

"Testing simplex cases. A simplex case is a single occurrence of a disorder in a family, sometimes incorrectly referred to as a 'sporadic' case.

- If no acquired cause of the ataxia is identified, the probability is ~13% that the affected individual has SCA1, SCA2, SCA3, SCA6, SCA8, SCA17, or FRDA, and mutations in rare ataxia genes are even less common.
- Other possibilities to consider are a de novo mutation in a different autosomal dominant ataxia, decreased penetrance, alternative paternity, or a single occurrence of an autosomal recessive or X-linked disorder in a family such as fragile X-associated tremor/ataxia syndrome.
- Although the probability of a positive result from molecular genetic testing is low in an individual with ataxia who has no family history of ataxia, such testing is usually justified to establish a specific diagnosis for the individual's medical evaluation and for genetic counseling.
- Always consider a possible nongenetic cause such as multiple system atrophy, cerebellar type in simplex cases."

European Federation of Neurological Sciences

The European Federation of Neurological Sciences (EFNS, 2014) stated the following regarding testing for hereditary ataxias:[31]

- “In the case of a family history that is compatible with an autosomal dominant cerebellar ataxia, screening for SCA1, SCA2, SCA3, SCA6, SCA7, and SCA17 is recommended (Level B). In Asian patients, DRPLA should also be tested for.”
- “If mutation analysis is negative, we recommend contact with or referral to a specialized clinic for reviewing the phenotype and further genetic testing (good practice point).”
- “In the case of sporadic ataxia and independent from onset age, we recommend routine testing for SCA1, SCA2, SCA3, SCA6, and DRPLA (in Asian patients) (level B), the step one panel of the recessive ataxia workup, i.e. mutation analysis of the FRDA gene (level B), and biochemical testing that includes cholestanol, vitamin E, cholesterol, albumin, CK, and alpha-fetoprotein.”

Selected Relevant Publications

Peer-reviewed publications stated that diagnostic evaluations for ataxia may include assessments for acquired, other nongenetic, and genetic etiologies. [2,26] Establishing the diagnosis of a hereditary ataxia may include demonstration of typical clinical signs

on neurological examination and exclusion of acquired or other nongenetic causes. Additionally, a positive family history, documentation of a hereditary ataxia disease causing mutation, and/or the presence of a characteristic clinical phenotype of a specific hereditary ataxia may solidify the diagnosis.[26]

The results of additional evaluations, such as brain imaging, may increase the suspicion of a hereditary etiology. These additional studies may indicate that an ataxia is slowly progressive and long standing which may signify early onset.[25] Furthermore, findings on MR spectroscopy may indicate that a hereditary etiology is more likely compared to an immune-mediated ataxia.[25]

The likelihood of a hereditary etiology is higher in those with early age of onset (81%) compared to late onset (55%) idiopathic ataxia.[25] The presence of other clinical features also increases the likelihood of detecting a mutation.[25] In those with a family history consistent with autosomal dominant inheritance, a mutation was detected in 50-60% with testing for SCA1, 2, 3, 6, 7, 8, 10, 12, 17 and dentatorubral-pallidoluysian atrophy (DRPLA).[2] In a simplex case with no known acquired cause, according to one study, the likelihood an individual has SCA1, 2, 3, 6, 8, 17, or Friedreich ataxia (FRDA) is approximately 13% and the likelihood of a mutation in a different hereditary ataxia gene is more rare.[2] In another study utilizing targeted exome analysis of 441 genes in individuals with ataxia of unknown etiology, a positive result was detected in 52% of individuals. Forty percent of the positive cases were due to mutations in SPG7, SYNE1, ADCK3, CACNA1A, ATP1A3, and SPTBN2.[32] Even in those with an unremarkable family history, genetic testing may aid in their medical evaluation and in genetic counseling.[2]

It was suggested that genetic testing for progressive ataxias should include evaluation of the genes for FRDA, SCA 1, 2, 3, 6, 7 (12, 17) and fragile X-associated tremor/ataxia syndrome.[26] Testing may proceed in a sequential fashion. For those with a family history suggestive of autosomal dominant inheritance, first round testing for the most common hereditary ataxias (SCA1, SCA2, SCA3, SCA6, and SCA7) may be completed followed by testing for less common hereditary etiologies, which may be guided by ethnic background and/or specific clinical features.[2] In those with a family history suggestive of autosomal recessive inheritance, the following may be tested due to "frequency and/or treatment potential": FRDA, ataxia telangiectasia, ataxia with oculomotor apraxia type 1, ataxia with oculomotor apraxia type 2, ataxia with vitamin E deficiency, and metabolic or lipid storage disorders.[2] Single-gene testing may be pursued if the clinical examination is consistent with a specific diagnosis or if a specific type is known in the family.[2]

Note:

This benefit/harm statement only applies to those jurisdictions that do not have Medicare guidance. Based upon the guidelines and evidence provided in the clinical policy, following EviCore's criteria for hereditary ataxia multigene panel testing will ensure that testing will be available to those members most likely to benefit from a genetic

diagnosis. For those not meeting criteria, it ensures alternate diagnostic strategies are considered. However, it is possible that some members who would benefit from the testing, but do not meet clinical criteria, will not receive an immediate approval for testing.

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