

(20487)

Medical Benefit		Effective Date: 01/01/18	Next Review Date: 11/19
Preauthorization	Yes	Review Dates: 01/14, 11/14, 11/15, 11/16, 11/17, 11/18	

Preauthorization is required.

The following protocol contains medical necessity criteria that apply for this service. The criteria are also applicable to services provided in the local Medicare Advantage operating area for those members, unless separate Medicare Advantage criteria are indicated. If the criteria are not met, reimbursement will be denied and the patient cannot be billed. Please note that payment for covered services is subject to eligibility and the limitations noted in the patient's contract at the time the services are rendered.

Populations	Interventions	Comparators	Outcomes
Individuals: <ul style="list-style-type: none"> With suspected hereditary nonsyndromic hearing loss 	Interventions of interest are: <ul style="list-style-type: none"> Genetic testing 	Comparators of interest are: <ul style="list-style-type: none"> Standard clinical management without genetic testing 	Relevant outcomes include: <ul style="list-style-type: none"> Test accuracy Test validity Changes in reproductive decision making Morbid events Resource utilization
Individuals: <ul style="list-style-type: none"> With a family history of hereditary nonsyndromic hearing loss 	Interventions of interest are: <ul style="list-style-type: none"> Preconception genetic testing to determine carrier status 	Comparators of interest are: <ul style="list-style-type: none"> Standard preconception counseling without genetic testing 	Relevant outcomes include: <ul style="list-style-type: none"> Test accuracy Test validity Changes in reproductive decision making Morbid events Resource utilization

DESCRIPTION

Hearing loss is a common birth defect. Approximately one in 500 newborns in developed countries is affected by bilateral, permanent hearing loss of moderate or greater severity (≥ 40 decibels). Syndromic hearing loss refers to hearing loss associated with other medical or physical findings, including visible abnormalities of the external ear. Because syndromic hearing loss occurs as part of a syndrome of multiple clinical manifestations, it is often recognized more readily as hereditary. Nonsyndromic hearing loss (NSHL) is defined as hearing loss not associated with other physical signs or symptoms. NSHL accounts for 70% to 80% of genetically determined deafness, and it is more difficult to determine whether the etiology is hereditary or acquired.

SUMMARY OF EVIDENCE

For individuals who are suspected of having hereditary NSHL who receive genetic testing, the evidence includes small retrospective, single-center studies, case reports, case series, and genotype-phenotype correlation studies evaluating the clinical validity and testing yield for NSHL. Relevant outcomes are test accuracy and validity, changes in reproductive decision making, morbid events, and resource utilization. Genetic variants in GJB2,

GJB6, and numerous other genes are found in a substantial percentage of patients with hereditary hearing loss. Of all patients with suspected hereditary hearing loss after clinical examination, a substantial proportion, in the range of 30% to 60%, will be found to have a genetic variant. The probability of finding a genetic variant is increasing as new variants are identified. False-positive results on genetic testing are expected to be very low. For diagnosis, there are a number of potential benefits of genetic testing, including a reduction in the need for alternative diagnostic tests and monitoring of patients with genetically identified syndromic hearing loss associated with other medical conditions. Clinical guidelines have recommended a tiered genetic testing approach, starting with the most common genes. The evidence is sufficient to determine that the technology results in a meaningful improvement in the net health outcome.

For individuals with a family history of hereditary NSHL who receive preconception genetic testing to determine carrier status, the evidence is limited but includes clinical guidelines. Relevant outcomes are test accuracy and validity, changes in reproductive decision making, morbid events, and resource utilization. Genetic variants in GJB2, GJB6, and numerous other genes are found in a substantial percentage of patients with hereditary hearing loss. The probability of finding a genetic variant is increasing as new gene variants are identified. False-positive results on genetic testing are expected to be very low. There are several situations for which there is potential clinical utility of testing for genes associated with hereditary hearing loss. For parents at high risk of an offspring with hereditary hearing loss, genetic testing can be useful as an aid in reproductive decision making. The evidence is sufficient to determine that the technology results in a meaningful improvement in the net health outcome.

POLICY

Genetic testing for hereditary hearing loss genes (*GJB2*, *GJB6* and other hereditary hearing loss-related genes) in individuals with suspected hearing loss to confirm the diagnosis of hereditary hearing loss (see Policy Guidelines) may be considered **medically necessary**.

Preconception genetic testing (carrier testing) for hereditary hearing loss genes (*GJB2*, *GJB6* and other hereditary hearing loss-related genes) in parents may be considered **medically necessary** when at least one of the following conditions has been met:

- Offspring with hereditary hearing loss *OR*
- One or both parents with suspected hereditary hearing loss *OR*
- First- or second-degree relative affected with hereditary hearing loss *OR*
- First-degree relative with offspring who is affected with hereditary hearing loss.

Genetic testing for hereditary hearing loss genes is considered **investigational** for all other situations, including, but not limited to, testing in patients without hearing loss (except as addressed in related protocols, e.g., Preimplantation Genetic Testing).

POLICY GUIDELINES

Hereditary hearing loss can be classified as syndromic or nonsyndromic. The definition of NSHL is hearing loss not associated with other physical signs and symptoms at the time of hearing loss presentation. It is differentiated from syndromic hearing loss, which is hearing loss associated with other signs and symptoms characteristic of a specific syndrome. Physical signs of a syndrome often include dysmorphic changes in the maxillofacial region and/or malformations of the external ears. Malfunction of internal organs may also be part of a syndrome. The physical signs can be subtle and easily missed on physical exam, therefore exclusion of syndromic

findings is ideally done by an individual with expertise in identifying dysmorphic physical signs. The phenotypic presentation of nonsyndromic hearing loss varies, but generally involves the following features:

- Sensorineural hearing loss
- Mild-to-profound (more commonly) degree of hearing impairment
- Congenital onset
- Usually nonprogressive.

This protocol primarily focuses on the use of genetic testing to identify a cause of suspected hereditary hearing loss. The diagnosis of syndromic hearing loss can be made on the basis of associated clinical findings. However, at the time of hearing loss presentation, associated clinical findings may not be apparent; furthermore variants in certain genetic loci may cause both syndromic and NSHL. Given this overlap this protocol focuses on genetic testing for hereditary hearing loss more generally.

In addition to pathogenic variants in the *GJB6* and *GJB2* genes, there are many less common pathogenic variants found in other genes. They include: *ACTG1*, *CDH23*, *CLDN14*, *COCH*, *COL11A2*, *DFNA5*, *DFNB31*, *DFNB59*, *ESPN*, *EYA4*, *GJB2*, *GJB6*, *KCNQ4*, *LHFPL5*, *MT-TS1*, *MYO15A*, *MYO6*, *MYO7A*, *OTOF*, *PCDH15*, *POU3F4*, *SLC26A4*, *STRC*, *TECTA*, *TMC1*, *TMIE*, *TMPRSS3*, *TRIOBP*, *USH1C*, and *WFS1* genes.

Targeted testing for variants associated with hereditary hearing loss should be confined to known pathogenic variants. While research studies using genome-wide associations have uncovered numerous single-nucleotide polymorphisms variants and copy number variations associated with hereditary hearing loss the clinical significance of these findings is unclear.

For carrier testing, outcomes are expected to improve if parents alter their reproductive decision-making as a result of genetic test results. This may occur through the use of preimplantation genetic testing in combination with in vitro fertilization. Other ways that prospective parents may alter their reproductive choices are to proceed with attempts at pregnancy, or to avoid attempts at pregnancy, based on carrier testing results.

TESTING STRATEGY

Evaluation of a patient with suspected hereditary hearing loss should involve a careful physical exam and family history to assess for associated clinical findings that may point to a specific syndromic or nonsyndromic cause of hearing loss (e.g., infectious, toxic, autoimmune, other causes). Consideration should also be given to temporal bone computed tomography scanning in cases of progressive hearing loss and to testing for cytomegalovirus in infants with sensorineural hearing loss.

If there is no high suspicion for a specific hearing loss etiology, ideally the evaluation should occur in a step-wise fashion. About 50% of individuals with autosomal recessive hereditary hearing loss have pathogenic variants in the *GJB2* gene. In the remainder of patients with apparent autosomal recessive hereditary hearing loss, numerous other genes are implicated. In autosomal dominant hereditary hearing loss, there is no single identifiable gene responsible for most cases. If there is suspicion for autosomal recessive congenital hearing loss, it would be reasonable to begin with testing of *GJB2* and *GJB6*. If this is negative, screening for the other genes associated with hearing loss with a multigene panel would be efficient. An alternative strategy for suspected autosomal recessive or autosomal dominant hearing loss would be to obtain a multigene panel that includes *GJB2* and *GJB6* as a first step. Given the extreme heterogeneity in genetic causes of hearing loss, these two strategies may be considered reasonably equivalent.

GENETICS NOMENCLATURE UPDATE

The Human Genome Variation Society (HGVS) nomenclature is used to report information on variants found in DNA and serves as an international standard in DNA diagnostics. It is being implemented for genetic testing

medical protocol updates starting in 2017 (see Table PG1). The society's nomenclature is recommended by the Human Variome Project, the HUGO and by HGVS itself.

The American College of Medical Genetics and Genomics and Association for Molecular Pathology standards and guidelines for interpretation of sequence variants represent expert opinion from both organizations in addition to the College of American Pathologists. These recommendations primarily apply to genetic tests used in clinical laboratories, including genotyping, single genes, panels, exomes, and genomes. Table PG 2 shows the recommended standard terminology—"pathogenic," "likely pathogenic," "uncertain significance," "likely benign," and "benign"—to describe variants identified that cause Mendelian disorders.

Table PG1. Nomenclature to Report on Variants Found in DNA

Previous	Updated	Definition
Mutation	Disease-associated variant	Disease-associated change in the DNA sequence
	Variant	Change in the DNA sequence
	Familial variant	Disease-associated variant identified in a proband for use in subsequent targeted genetic testing in first-degree relatives

Table PG2. ACMG-AMP Standards and Guidelines for Variant Classification

Variant Classification	Definition
Pathogenic	Disease-causing change in the DNA sequence
Likely pathogenic	Likely disease-causing change in the DNA sequence
Variant of uncertain significance	Change in DNA sequence with uncertain effects on disease
Likely benign	Likely benign change in the DNA sequence
Benign	Benign change in the DNA sequence

ACMG: American College of Medical Genetics and Genomics; AMP: Association for Molecular Pathology

GENETIC COUNSELING

Experts recommend formal genetic counseling for patients who are at risk for inherited disorders and who wish to undergo genetic testing. Interpreting the results of genetic tests and understanding risk factors can be difficult for some patients; genetic counseling helps individuals understand the impact of genetic testing, including the possible effects the test results could have on the individual or their family members. It should be noted that genetic counseling may alter the utilization of genetic testing substantially and may reduce inappropriate testing; further, genetic counseling should be performed by an individual with experience and expertise in genetic medicine and genetic testing methods.

MEDICARE ADVANTAGE

For Medicare advantage genetic testing for hereditary hearing loss genes is unlikely to impact therapeutic decision-making in the clinical management of the patient and is considered **not medically necessary**.

BACKGROUND

HEREDITARY HEARING LOSS

Hearing loss is a common birth defect. Approximately one in 500 newborns in developed countries is affected by bilateral, permanent hearing loss of moderate or greater severity (≥ 40 decibels).¹

Syndromic hearing loss refers to hearing loss associated with other medical or physical findings, including visible abnormalities of the external ear. Because syndromic hearing loss occurs as part of a syndrome of multiple clinical manifestations, it is often recognized more readily as hereditary.

Nonsyndromic hearing loss (NSHL) is defined as hearing loss not associated with other physical signs or symptoms. For NSHL, it is more difficult to determine whether the etiology is hereditary or acquired, because, by definition, there are no other clinical manifestations at the time of the hearing loss presentation. NSHL accounts for 70% to 80% of genetically determined deafness.²

Autosomal recessive patterns of inheritance predominate and account for 80% of congenital NSHL. A typical clinical presentation of autosomal recessive NSHL involves the following characteristics:

- Sensorineural hearing loss
- Mild-to-profound (more commonly) degree of hearing impairment
- Congenital onset
- Usually nonprogressive
- No associated medical findings.

Most of the remaining 20% of patients have an autosomal dominant inheritance pattern, with a small number having X-linked or mitochondrial inheritance. Patients with autosomal dominant inheritance typically show progressive NSHL, which begins in the second through fourth decades of life.³

Diagnosis

Diagnosis of NSHL requires an evaluation by appropriate core medical personnel with expertise in the genetics of hearing loss, dysmorphology, audiology, otolaryngology, genetic counseling, and communication with deaf patients. The evaluation should include a family history, as well as a physical examination consisting of otologic examination, airway examination, documentation of dysmorphisms, and neurologic evaluation.⁴ However, the clinical diagnosis of NSHL is nonspecific because there are a number of underlying etiologies, and often it cannot be determined with certainty whether a genetic cause for hearing loss exists.

Treatment

Treatment of congenital and early-onset hearing loss typically involves enrollment in an educational curriculum for hearing impaired persons and fitting with an appropriate hearing aid. In some patients with profound deafness, a cochlear implant can be performed. Early identification of infants with hearing impairment may be useful in facilitating early use of amplification by six months of age and early intervention to achieve age-appropriate communication, speech, and language development.⁵ Delays in the development of hearing treatment have been shown to delay development of communication. The primary method for identification of hearing impairment has been newborn screening with audiometry. Genetic testing has not been proposed as a primary screen for hearing loss.

Genetics of Hereditary Hearing Loss

Genes associated with hereditary hearing loss may be associated with an autosomal dominant, autosomal recessive, X-linked, or mitochondrial inheritance pattern. The genetic loci on which variants associated with hereditary hearing loss are usually found are termed DFN, and hereditary hearing loss is sometimes called DFN-associated hearing loss. DFN loci are named based on their mode of inheritance: DFNA associated with autosomal dominant inheritance; DFNB with autosomal recessive inheritance; and DFNX with X-linked inheritance.

Two DFN loci commonly associated with hereditary hearing loss are DFNA3 and DFNB1, both of which map to chromosome 13q12. DFNA3-associated hereditary hearing loss is caused by autosomal dominant pathogenic variants present in the GJB2 or GJB6 genes.⁶ DFNB1-associated hereditary hearing loss relates to autosomal recessive syndromes in which more than 99% of cases are caused by pathogenic variants in the GJB2 gene, and less than 1% of remaining cases arise from pathogenic variants to GJB6.⁷ A list of available tests for genes at the DFNA3 and DFNB1 loci are provided in Table 1.

Two of the most commonly disease-associated genes are GJB2 and GJB6. GJB2 is a small gene with a single coding exon. Variants of this gene are most common in hereditary hearing loss, causing an estimated 50% of the cases of hereditary NSHL.⁸ The carrier rate in the general population for a recessive deafness-causing GJB2 variant is approximately one in 33.¹ Specific variants have been observed to be more common in certain ethnic populations.^{9,10} Variants in the GJB2 gene will impact the expression of the Cx26 connexin protein and almost always cause prelingual, but not necessarily congenital, deafness.¹¹ Different variants of GJB2 can present high phenotypic variation, but it has been demonstrated that it is possible to correlate the type of associated hearing loss with findings on molecular analysis. A systematic review by Chan and Chang (2014), reporting on GJB2 variant prevalence, suggested that the overall prevalence of GJB2 variants is similar around the world, although specific variants differ.¹²

Variants in the GJB6 gene lead to similar effects on abnormal expression of connexin protein Cx30. However, GJB6 variants are much less common than GJB2 variants. Of all patients with hereditary hearing loss, approximately 3% have a variant in the GJB6 gene.

Table 1. Clinical Characteristics and Testing Methods for GJB2 and GJB6 Variants at the DFNA3 and DFNB1 Loci

Locus	Gene	Onset	Audioprofile	Test Method	Variants Detected
DFNA3	GJB2	Prelingual	High-frequency progressive	<ul style="list-style-type: none"> Sequence analysis/variant scanning Targeted variant analysis Deletion/duplication analysis 	<ul style="list-style-type: none"> Sequence variants Specified sequence variants Exonic or whole-gene deletions/duplications
DFNA3	GJB6	Prelingual	High-frequency progressive	<ul style="list-style-type: none"> Sequence analysis/variant scanning Targeted variant analysis Deletion/duplication analysis 	<ul style="list-style-type: none"> Sequence variants Specified sequence variants Exonic or whole-gene deletions/duplications
DFNB1	GJB2	Prelingual	Usually stable	<ul style="list-style-type: none"> Targeted variant analysis Deletion/duplication 	<ul style="list-style-type: none"> GJB2 sequence variants Exon(s) or whole-gene deletions
DFNB1	GJB6	Prelingual	Usually stable	<ul style="list-style-type: none"> Deletion/duplication 	<ul style="list-style-type: none"> GJB6 deletions

Analysis for GJB6 and GJB2 variants can be performed by Sanger sequencing of individual genes. This method has a high degree of validity and reliability but is limited by the ability to sequence one gene at a time. With Sanger sequencing, the genes with the most common pathogenic variants are generally sequenced first, followed by sequencing of additional genes if a pathogenic variant is not found.

In addition to the most common genes associated with hereditary hearing loss (GJB6, GJB2), there are many less common disease-associated genes. Some are: ACTG1, CDH23, CLDN14, COCH, COL11A2, DFNA5, DFNB31, DFNB59, ESPN, EYA4, GJB2, GJB6, KCNQ4, LHFPL5, MT-TS1, MYO15A, MYO6, MYO7A, OTOF, PCDH15, POU3F4, SLC26A4, STRC, TECTA, TMC1, TMIE, TMPRSS3, TRIOBP, USH1C, and WFS1 genes. Novel genetic variants continue to be identified in cases of hereditary hearing loss.^{13,14} For example, as of 2014, over 2000 pathogenic deafness variants in approximately 130 genes had been reported.^{15,16} In contrast, only 18 pathogenic copy number variants (CNVs) had been identified by 2014.¹⁷ CNVs, caused by insertions, deletions, or recombination, can lead to hearing loss from gene disruption or changes in the number of dose-sensitive genes. The gene most commonly associated with pathogenic CNVs in hearing loss is STRC, which encodes stereocilin and is the most frequent cause of autosomal recessive causes of NSHL after pathogenic variants in GJB2.¹⁷

Because a large number of genes are associated with hereditary hearing loss, there are various genetic panels for hereditary deafness. Next-generation sequencing technology allows targeted sequencing of multiple genes simultaneously, expanding the ability to examine multiple genes. These panels are alternatives to the sequencing of individual genes such as GJB6 and GJB2. Some examples of these panels are shown in Table 2. These panels include the most common genes associated with NSHL. They may also include many of the less common

genes associated with NSHL, as well as genes associated with syndromic hearing loss. Also, whole exome sequencing and whole genome sequencing have been used to identify novel variants in subjects with a history suggestive of genetic hereditary hearing loss.¹⁸⁻²⁰ Targeted genomic enrichment coupled with massively parallel sequencing can be used to identify both single nucleotide variants and CNVs.

Table 2. Gene Panels for Hereditary Hearing Loss

Test	Technology	Genes Tested	Analytic Sensitivity
Partners Healthcare (OtoGenome™ Test for Hearing Loss and Related Syndromes)	NGS, followed by confirmation with Sanger sequencing or PCR	87	99%
University of Iowa Healthcare (OtoSCOPE® V8) ²¹	NGS/massive parallel sequencing	152	99%

Adapted from Linden Phillips et al (2013).¹¹

NGS: next-generation sequencing; PCR: polymerase chain reaction.

Overlap Between NSHL and Recognized Syndromes

There is overlap between hereditary NSHL and syndromic hearing loss associated with recognized syndromes. Some genetic variants may be associated with clinical findings other than hearing loss, but they are not necessarily manifest at the time of presentation with hearing loss. For example, Jervell and Lange-Nielsen syndrome is associated with congenital deafness and prolonged QT interval, but it may present only with deafness without an apparent history to suggest cardiac dysfunction. Additionally, some genes associated with NSHL are associated with recognized syndromes. Some genetic syndromes and genes that may overlap with NSHL are shown in Table 3.

Table 3. Genes With Overlap Between Syndromic and Nonsyndromic Hearing Loss

Syndrome	Inheritance	Clinical Description	Gene	Reason for Overlap With NSHL
Usher syndrome	For all types: autosomal recessive	For all types: sensorineural HL with retinitis pigmentosa		<ul style="list-style-type: none"> Retinitis pigmentosa usually not apparent in 1st decade
Type 1		<ul style="list-style-type: none"> Congenital severe-to-profound HL Abnormal vestibular function 	MYO7A, USH1C, CDH23, PCDH15, SANS, CIB2	<ul style="list-style-type: none"> DFNB18 (nonsyndromic) may also be caused by variants in USH1C DFNB12 (nonsyndromic) may also be caused by variants in CDH23 DFNB2 (nonsyndromic) and DFNA11 (nonsyndromic) may also be caused by variants in MYO7A
Type 2		<ul style="list-style-type: none"> Congenital mild-to-severe HL Normal vestibular function 	USH2A, VLGR1, WHRN	
Type 3		<ul style="list-style-type: none"> Progressive HL Progressive vestibular dysfunction 	CLRN1i PDZD7	
Pendred syndrome	Autosomal recessive	<ul style="list-style-type: none"> Congenital sensorineural HL Bony labyrinth abnormalities (Mondini dysplasia or dilated vestibular aqueduct) Euthyroid goiter 	SLC26A4 (50%)	<ul style="list-style-type: none"> Goiter not present until early puberty or adulthood Variants in SLC26A4 may also cause NSHL
Jervell and Lange-Nielsen	Autosomal recessive	<ul style="list-style-type: none"> Congenital deafness Prolongation of the QT 	KCNQ1, KCNE1	<ul style="list-style-type: none"> HL may present without personal or family history of cardiac symptoms

Syndrome	Inheritance	Clinical Description	Gene	Reason for Overlap With NSHL
syndrome		interval		(sudden death, SIDS, syncopal episodes, or long QT syndrome)
Wolfram syndrome	Autosomal recessive	<ul style="list-style-type: none"> Progressive sensorineural HL Diabetes Optic atrophy Progressive neurologic abnormalities 	WFS1	<ul style="list-style-type: none"> WFS1-associated HL (DFNA6, DFNA4, DFNA38; congenital HL without associated findings) may also be caused by variants in WFS1

HL: hearing loss; NSHL: nonsyndromic hearing loss; SIDS: sudden infant death syndrome.

REGULATORY STATUS

Clinical laboratories may develop and validate tests in-house and market them as a laboratory service; laboratory-developed tests (LDTs) must meet the general regulatory standards of the Clinical Laboratory Improvement Amendments (CLIA). Molecular diagnostic testing is available under the auspices of the CLIA. Laboratories that offer LDTs must be licensed by the CLIA for high-complexity testing. To date, the U.S. Food and Drug Administration has chosen not to require any regulatory review of this test.

RELATED PROTOCOLS

Cochlear Implant

Preimplantation Genetic Testing

Whole Exome and Whole Genome Sequencing for Diagnosis of Genetic Disorders

Services that are the subject of a clinical trial do not meet our Technology Assessment Protocol criteria and are considered investigational. *For explanation of experimental and investigational, please refer to the Technology Assessment Protocol.*

It is expected that only appropriate and medically necessary services will be rendered. We reserve the right to conduct prepayment and postpayment reviews to assess the medical appropriateness of the above-referenced procedures. **Some of this protocol may not pertain to the patients you provide care to, as it may relate to products that are not available in your geographic area.**

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We are not responsible for the continuing viability of web site addresses that may be listed in any references below.

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34. National Government Services, Inc. (Primary Geographic Jurisdiction 06 & K - Illinois, Minnesota, Wisconsin, Connecticut, New York - Entire State, Maine, Massachusetts, New Hampshire, Rhode Island, Vermont) Local Coverage Determination (LCD): Molecular Pathology Procedures (L35000), Revision Effective Date for services performed on or after 01/01/2018.