Genetic Testing for Epilepsy

**POLICY**

Genetic testing for genes associated with infantile- and early-childhood onset epilepsy syndromes in individuals with infantile- and early-childhood-onset epilepsy syndromes in which epilepsy is the core clinical symptom (see Policy Guidelines section) may be considered medically necessary if positive test results may:

1. Lead to changes in medication management; AND/OR
2. Lead to changes in diagnostic testing such that alternative potentially invasive tests are avoided; AND/OR
3. Lead to changes in reproductive decision making.

Genetic testing for epilepsy is considered investigational for all other situations.

**POLICY GUIDELINES**

**Policy Scope**

**Included Tests and Conditions**

This policy addresses testing for epilepsy that might have a genetic etiology. The International League Against Epilepsy has classified epilepsy as having underlying genetic cause or etiology when, as best understood, the epilepsy is the direct result of a known or presumed genetic defect and seizures are the core symptom of the disorder and for which there is no structural or metabolic defect predisposing to epilepsy (Berg et al, 2010).

This policy also addresses the rare epilepsy syndromes that present in infancy or early childhood, in which epilepsy is the core clinical symptom (e.g., Dravet syndrome, early infantile epileptic encephalopathy, generalized epilepsy with febrile seizures plus, epilepsy and intellectual disability limited to females, nocturnal frontal lobe epilepsy). Other clinical manifestations may be present in these syndromes but are generally secondary to the epilepsy itself.

**Excluded Tests and Conditions**
This policy does not address testing for genetic syndromes that have a wider range of symptomatology, of which seizures may be one, such as the neurocutaneous disorders (e.g., neurofibromatosis, tuberous sclerosis) or genetic syndromes associated with cerebral malformations or abnormal cortical development, or metabolic or mitochondrial disorders. Genetic testing for these syndromes may be specifically addressed in other evidence reviews (see Related Policies links).

Testing that is limited to genotyping of CYP450 genes is addressed separately (evidence review 2.04.38).

This policy does not address the use of genotyping for the HLA-B*1502 allelic variant in patients of Asian ancestry prior to considering drug treatment with carbamazepine due to risks of severe dermatologic reactions. This testing is recommended by the U.S. Food and Drug Administration (FDA) labeling for carbamazepine (Food and Drug Administration, 2014).

This policy also does not address the testing for variants in the mitochondrial DNA polymerase gamma (POLG) gene in patients with clinically suspected mitochondrial disorders prior to initiation of therapy with valproate. Valproate’s label contains a black box warning related to increased risk of acute liver failure associated with the use of valproate in patients with POLG gene-related hereditary neurometabolic syndromes. FDA labeling states that valproate “is contraindicated in patients known to have mitochondrial disorders caused by POLG mutations and children under two years of age who are clinically suspected of having a POLG-related disorder” (Food and Drug Administration, 2015).

Medically Necessary Statement Definitions and Testing Strategy

The medically necessary statement refers to epilepsy syndromes that present in infancy or early childhood, are severe, and are characterized by epilepsy as the primary manifestation, without associated metabolic or brain structural abnormalities. As defined by the International League Against Epilepsy, these include epileptic encephalopathies, which are electroclinical syndrome associated with a high probability of encephalopathic features that present or worsen after the onset of epilepsy. Other clinical manifestations, including developmental delay and/or intellectual disability, may be present secondary to the epilepsy itself. Specific clinical syndromes based on the International League Against Epilepsy classification include:

- Dravet syndrome (also known as severe myoclonic epilepsy in infancy or polymorphic myoclonic epilepsy in infancy)
- EFMR syndrome (epilepsy limited to females with mental retardation)
- Epileptic encephalopathy with continuous spike-and-wave during sleep
- GEFS+ syndrome (generalized epilepsies with febrile seizures plus)
- Ohtahara syndrome (also known as early infantile epileptic encephalopathy with burst suppression pattern)
- Landau-Kleffner syndrome
- West syndrome
- Glucose transporter type 1 deficiency syndrome.

Variants in a large number of genes have been associated with early-onset epilepsies. Some of them are summarized in Table PG1.

<table>
<thead>
<tr>
<th>Syndrome</th>
<th>Associated Genes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dravet syndrome</td>
<td>SCN1A, SCN9A, GABRA1, STXBP1, PCDH19, SCN1B, CHD2, HCN1</td>
</tr>
<tr>
<td>Epilepsy limited</td>
<td>PCDH19</td>
</tr>
</tbody>
</table>

Table PG1. Single Genes Associated With Epileptic Syndromes
Application of the Medically Necessary Policy Statement

Although there is no standard definition of epileptic encephalopathies, they are generally characterized by at least some of the following: (1) onset in early childhood (often in infancy); (2) refractory to therapy; (3) associated with developmental delay or regression; and (4) severe electroencephalogram (EEG) abnormalities. There is a challenge in defining the population appropriate for testing given that specific epileptic syndromes may be associated with different EEG abnormalities, which may change over time, and patients may present with severe seizures prior to the onset or recognition of developmental delay or regression. However, for this policy, the medically necessary policy statement would apply for patients with:

1. Onset of seizures in early childhood (i.e., before the age of 5 years); AND
2. Clinically severe seizures that affect daily functioning and/or interictal EEG abnormalities; AND
3. No other clinical syndrome that would potentially better explain the patient’s symptoms.

Testing Strategy

There is clinical and genetic overlap for many of the electroclinical syndromes previously discussed. If there is suspicion for a specific syndrome based on history, EEG findings, and other test results, testing should begin with targeted variant testing for the candidate gene most likely to be involved, followed by sequential testing for other candidate genes. In particular, if an SCN1A-associated syndrome is suspected (Dravet syndrome, GEFS+), molecular genetic testing of SCN1A with sequence analysis of the SCN1A coding region, followed by deletion and duplication analysis if a pathogenic variant is not identified, should be obtained.
Given the genetic heterogeneity of early-onset epilepsy syndromes, a testing strategy that uses a multigene panel may be considered reasonable. In these cases, panels should meet the criteria outlined in evidence review 2.04.92 (general approach to evaluating the utility of genetic panels). Criteria for use of whole exome sequencing are outlined in evidence review 2.04.102 (whole exome and whole genome sequencing for diagnosis of genetic disorders).

**Genetics Nomenclature Update**

The Human Genome Variation Society 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 evidence review updates starting in 2017 (see Table PG2). The Society’s nomenclature is recommended by the Human Variome Project, the HUman Genome Organization, and by the Human Genome Variation Society itself.

The American College of Medical Genetics and Genomics and the 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 PG3 shows the recommended standard terminology—“pathogenic,” “likely pathogenic,” “uncertain significance,” “likely benign,” and “benign”—to describe variants identified that cause Mendelian disorders.

**Table PG2. Nomenclature to Report on Variants Found in DNA**

<table>
<thead>
<tr>
<th>Previous</th>
<th>Updated</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mutation</td>
<td>Disease-associated</td>
<td>Disease-associated change in the DNA sequence</td>
</tr>
<tr>
<td></td>
<td>variant</td>
<td></td>
</tr>
<tr>
<td>Variant</td>
<td>Change in the DNA</td>
<td></td>
</tr>
<tr>
<td></td>
<td>sequence</td>
<td></td>
</tr>
<tr>
<td>Familial variant</td>
<td>Disease-associated</td>
<td>Disease-associated variant identified in a proband for use in</td>
</tr>
<tr>
<td></td>
<td>variant</td>
<td>subsequent targeted genetic testing in first-degree relatives</td>
</tr>
</tbody>
</table>

**Table PG3. ACMG-AMP Standards and Guidelines for Variant Classification**

<table>
<thead>
<tr>
<th>Variant Classification</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pathogenic</td>
<td>Disease-causing change in the DNA sequence</td>
</tr>
<tr>
<td>Likely pathogenic</td>
<td>Likely disease-causing change in the DNA sequence</td>
</tr>
<tr>
<td>Variant of uncertain significance</td>
<td>Change in DNA sequence with uncertain effects on disease</td>
</tr>
<tr>
<td>Likely benign</td>
<td>Likely benign change in the DNA sequence</td>
</tr>
<tr>
<td>Benign</td>
<td>Benign change in the DNA sequence</td>
</tr>
</tbody>
</table>

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.

**Coding**
If the specific gene being tested has been codified in CPT, the appropriate CPT code would be reported. If the specific gene has not been codified in CPT, the unlisted molecular pathology code 81479 would be reported. If a panel of tests not codified in CPT is performed, code 81479 would be reported once.

Some tests related to epilepsy are listed under CPT tier 2 codes. Under CPT code 81401:

**MT-TK (mitochondrially encoded tRNA lysine)** (eg, myoclonic epilepsy with ragged-red fibers [MERRF]), common variants (eg, m.8344A>G, m.8356T>C).

Under CPT code 81403:

**NHLRC1 (NHL repeat containing 1)** (eg, progressive myoclonus epilepsy), full gene sequence

**ARX** (aristaless related homeobox) (eg, X-linked lissencephaly with ambiguous genitalia, X-linked mental retardation) duplication deletion analysis.

Under CPT code 81404:

**ARX** (aristaless related homeobox) (eg, X-linked lissencephaly with ambiguous genitalia, X-linked mental retardation), full gene sequence

**EPM2A (epilepsy, progressive myoclonus type 2A, Lafora disease [laforin])** (eg, progressive myoclonus epilepsy), full gene sequence.

Under CPT code 81405:

**CDKL5** (cyclin-dependent kinase-like 5) (eg, early infantile epileptic encephalopathy), duplication/deletion analysis

**CHRNA4** (cholinergic receptor, nicotinic, alpha 4) (eg, nocturnal frontal lobe epilepsy), full gene sequence

**CHRNβ2** (cholinergic receptor, nicotinic, beta 2 [neuronal]) (eg, nocturnal frontal lobe epilepsy), full gene sequence

**GABRG2** (gamma-aminobutyric acid [GABA] A receptor, gamma 2) (eg, generalized epilepsy with febrile seizures), full gene sequence.

Under CPT code 81406:

**ALDH7A1** (aldehyde dehydrogenase 7 family, member A1) (eg, pyridoxine-dependent epilepsy), full gene sequence

**CDKL5** (cyclin-dependent kinase-like 5) (eg, early infantile epileptic encephalopathy), full gene sequence

**EFHC1** (EF-hand domain [C-terminal] containing 1) (eg, juvenile myoclonic epilepsy), full gene sequence.

Under CPT code 81407:

**SCN1A** (sodium channel, voltage-gated, type 1, alpha subunit) (eg, generalized epilepsy with epilepsy with febrile seizures), full gene sequence.

**BENEFIT APPLICATION**

**BLUE CARD/NATIONAL ACCOUNT ISSUES**

Some Plans may have contract or benefit exclusions for genetic testing.

**BACKGROUND**

**Epilepsy**
Epilepsy is defined as the occurrence of two or more unprovoked seizures. It is a common neurologic disorder, with approximately 3% of the population developing the disorder over their entire lifespan.\textsuperscript{1}

**Classification**

Epilepsy is heterogeneous in etiology and clinical expression and can be classified in a variety of ways. Most commonly, classification is done by the clinical phenotype, ie, the type of seizures that occur. The International League Against Epilepsy (ILAE) developed the classification system that is widely used for clinical care and research purposes (see Table 1).\textsuperscript{2} Classification of seizures can also be done on the basis of age of onset: neonatal, infancy, childhood, and adolescent/adult.

**Table 1. Classification of Seizure Disorders by Type**

<table>
<thead>
<tr>
<th>Seizures Disorders</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Partial (focal seizures)</td>
<td></td>
</tr>
<tr>
<td>Simple partial seizures (consciousness not impaired)</td>
<td></td>
</tr>
<tr>
<td>With motor symptoms</td>
<td></td>
</tr>
<tr>
<td>With somatosensory or special sensory symptoms</td>
<td></td>
</tr>
<tr>
<td>With autonomic symptoms or signs</td>
<td></td>
</tr>
<tr>
<td>With psychic symptoms (disturbance of higher cerebral function)</td>
<td></td>
</tr>
<tr>
<td>Complex partial (with impairment of consciousness)</td>
<td></td>
</tr>
<tr>
<td>Simple partial onset followed by impairment of consciousness</td>
<td></td>
</tr>
<tr>
<td>Impairment of consciousness at outset</td>
<td></td>
</tr>
<tr>
<td>Partial seizures evolving to secondarily generalized seizures</td>
<td></td>
</tr>
<tr>
<td>Generalized seizures</td>
<td></td>
</tr>
<tr>
<td>Nonconvulsive (absence)</td>
<td></td>
</tr>
<tr>
<td>Convulsive</td>
<td></td>
</tr>
<tr>
<td>Unclassified seizures</td>
<td></td>
</tr>
</tbody>
</table>

Adapted from Berg et al (2010).\textsuperscript{2}

More recently, the concept of genetic epilepsies has emerged as a way of classifying epilepsy. Many experts now refer to “genetic generalized epilepsy” as an alternative classification for seizures previously called “idiopathic generalized epilepsies.” The ILAE report, published in 2010, offers the following alternative classification (see Table 2).\textsuperscript{2}

**Table 2. Alternative Classifications**

<table>
<thead>
<tr>
<th>Classification</th>
<th>Condition Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genetic epilepsies</td>
<td>Conditions in which the seizures are a direct result of a known or presumed genetic defect(s). Genetic epilepsies are characterized by recurrent unprovoked seizures in patients who do not have demonstrable brain lesions or metabolic disorders</td>
</tr>
</tbody>
</table>

More recently, the concept of genetic epilepsies has emerged as a way of classifying epilepsy. Many experts now refer to “genetic generalized epilepsy” as an alternative classification for seizures previously called “idiopathic generalized epilepsies.” The ILAE report, published in 2010, offers the following alternative classification (see Table 2).\textsuperscript{2}
abnormalities. In addition, seizures are the core symptom of the disorder, and other symptomatology is not present, except as a direct result of seizures. This is differentiated from genetically determined conditions in which seizures are part of a larger syndrome, such as tuberous sclerosis, fragile X syndrome, or Rett syndrome.

### Structural/metabolic Conditions

Conditions having a distinct structural or metabolic condition that increases the likelihood of seizures. Structural conditions include a variety of central nervous system abnormalities such as stroke, tumor or trauma, and metabolic conditions include a variety of encephalopathic abnormalities that predispose to seizures. These conditions may have a genetic etiology, but the genetic defect is associated with a separate disorder that predisposes to seizures.

### Unknown cause

Conditions for which the underlying etiology for the seizures cannot be determined and may include both genetic and nongenetic causes.

For this evidence review, the ILAE classification for genetic epilepsies is most useful. The review focuses on the category of genetic epilepsies in which seizures are the primary clinical manifestation. This category does not include syndromes that have multiple clinical manifestations, of which seizures may be one. Examples of syndromes that include seizures are Rett syndrome and tuberous sclerosis. Genetic testing for these syndromes will not be assessed herein but may be included in separate reviews that specifically address genetic testing for that syndrome.

Genetic epilepsies can be further broken down by type of seizures. For example, genetic generalized epilepsy refers to patients who have convulsive (grand mal) seizures, while genetic absence epilepsy refers to patients with nonconvulsive (absence) seizures. The disorders are also sometimes classified by the age of onset.

The category of genetic epilepsies includes a number of rare epilepsy syndromes that present in infancy or early childhood. These syndromes are characterized by epilepsy as the primary manifestation, without associated metabolic or brain structural abnormalities. They are often severe and sometimes refractory to medication treatment. They may involve other clinical manifestations such as developmental delay and/or intellectual disability, which in many cases are thought to be caused by frequent uncontrolled seizures. In these cases, the epileptic syndrome may be classified as an epileptic encephalopathy, which is described by ILAE as disorders in which the epileptic activity itself may contribute to severe cognitive and behavioral impairments above and beyond what might be expected from the underlying pathology alone and that these can worsen over time. A partial list of severe early-onset epilepsy syndromes is as follows:

- Dravet syndrome (also known as severe myoclonic epilepsy in infancy or polymorphic myoclonic epilepsy in infancy)
- EFMR syndrome (epilepsy limited to females with mental retardation)
- Nocturnal frontal lobe epilepsy
- GEFS+ syndrome (generalized epilepsies with febrile seizures plus)
- EIEE syndrome (early infantile epileptic encephalopathy with burst suppression pattern)
- West syndrome
- Ohtahara syndrome.

Dravet syndrome falls on a spectrum of SCN1A-related seizure disorders, which includes febrile seizures at the mild end to Dravet syndrome and intractable childhood epilepsy with generalized tonic-clonic seizures at the severe end. The spectrum may be associated with multiple seizure phenotypes, with a
Genetic Testing for Epilepsy

broad spectrum of severity; more severe seizure disorders may be associated with cognitive impairment, or deterioration. Ohtahara syndrome is a severe early-onset epilepsy syndrome characterized by intractable tonic spasms, other seizures, interictal electroencephalography abnormalities, and developmental delay. It may be secondary to structural abnormalities but has been associated with variants in the STXBP1 gene in rare cases. West syndrome is an early-onset seizure disorder associated with infantile spasms and the characteristic electroencephalography finding of hypsarrhythmia. Other seizure disorders presenting early in childhood may have a genetic component but are characterized by a more benign course, including benign familial neonatal seizures and benign familial infantile seizures.

Genetic Etiology

Most genetic epilepsies are primarily believed to involve multifactorial inheritance patterns. This follows the concept of a threshold effect, in which any particular genetic defect may increase the risk of epilepsy, but is not by itself causative. A combination of risk-associated genes, together with environmental factors, determines whether the clinical phenotype of epilepsy occurs. In this model, individual genes that increase the susceptibility to epilepsy have a relatively weak impact. Multiple genetic defects, and/or a particular combination of genes, probably increase the risk by a greater amount. However, it is not well understood how many abnormal genes are required to exceed the threshold to cause clinical epilepsy, nor is it understood which combination of genes may increase the risk more than others.

Early-onset epilepsy syndromes may be single-gene disorders. Because of the small amount of research available, the evidence base for these rare syndromes is incomplete, and new variants are currently being frequently discovered.

Some of the most common genes associated with genetic epileptic syndromes are listed in Table 3.

Table 3. Selected Genes Most Commonly Associated With Genetic Epilepsy

<table>
<thead>
<tr>
<th>Genes</th>
<th>Physiologic Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>KCNQ2</td>
<td>Potassium channel</td>
</tr>
<tr>
<td>KCNQ3</td>
<td>Potassium channel</td>
</tr>
<tr>
<td>SCN1A</td>
<td>Sodium channel α-subunit</td>
</tr>
<tr>
<td>SCN2A</td>
<td>Sodium channel α-subunit</td>
</tr>
<tr>
<td>SCN1B</td>
<td>Sodium channel β-subunit</td>
</tr>
<tr>
<td>GABRG2</td>
<td>γ-aminobutyrate A-type subunit</td>
</tr>
<tr>
<td>GABRRA1</td>
<td>γ-aminobutyrate A-type subunit</td>
</tr>
<tr>
<td>GABRD</td>
<td>γ-aminobutyrate subunit</td>
</tr>
<tr>
<td>CHRNA2</td>
<td>Acetylcholine receptor α2 subunit</td>
</tr>
<tr>
<td>CHRNA4</td>
<td>Acetylcholine receptor α4 subunit</td>
</tr>
</tbody>
</table>
MP 2.04.109  
Genetic Testing for Epilepsy

<table>
<thead>
<tr>
<th>Genes</th>
<th>Physiologic Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>CHRNB2</td>
<td>Acetylcholine receptor β2 subunit</td>
</tr>
<tr>
<td>STXBP1</td>
<td>Synaptic vesicle release</td>
</tr>
<tr>
<td>ARX</td>
<td>Homeobox gene</td>
</tr>
<tr>
<td>PCDH19</td>
<td>Protocadherin cell-cell adhesion</td>
</tr>
<tr>
<td>EFHC1</td>
<td>Calcium homeostasis</td>
</tr>
<tr>
<td>CACNB4</td>
<td>Calcium channel subunit</td>
</tr>
<tr>
<td>CLCN2</td>
<td>Chloride channel</td>
</tr>
<tr>
<td>LGI1</td>
<td>G-protein component</td>
</tr>
</tbody>
</table>

Adapted from Williams and Battaglia (2013).\(^1\)

For the severe early epilepsy syndromes, the disorders most frequently reported to be associated with single-gene variants include generalized epilepsies with febrile seizures plus syndrome (associated with SCN1A, SCN1B, and GABRG2 variants), Dravet syndrome (associated with SCN1A variants, possibly modified by SCN9A variants), and epilepsy and intellectual disability limited to females (associated with PCDH19 variants). Ohtahara syndrome has been associated with variants in STXBP1 in cases where patients have no structural or metabolic abnormalities. West syndrome is often associated with chromosomal abnormalities or tuberous sclerosis or may be secondary to an identifiable infectious or metabolic cause, but when there is no underlying cause identified, it is thought to be due to a multifactorial genetic predisposition.\(^7\)

Targeted testing for individual genes is available. Several commercial epilepsy genetic panels are also available. The number of genes included in the tests varies widely, from about 50 to over 450. The panels frequently include genes for other disorders such as neural tube defects, lysosomal storage disorders, cardiac channelopathies, congenital disorders of glycosylation, metabolic disorders, neurologic syndromes, and multisystemic genetic syndromes. Some panels are designed to be comprehensive while other panels target specific subtypes of epilepsy. Chambers et al (2016) reviewed comprehensive epilepsy panels from 7 U.S.-based clinical laboratories and found that between 1% and 4% of panel contents were genes not known to be associated with primary epilepsy.\(^8\) Between 1% and 70% of the genes included on an individual panel were not on any other panel.

**Treatment**

The condition is generally chronic, requiring treatment with one or more medications to adequately control symptoms. Seizures can be controlled by antiepileptic medications in most cases, but some patients are resistant to medications, and further options such as surgery, vagus nerve stimulation, and/or the ketogenic diet can be used.\(^9\)

**Pharmacogenomics**

Another area of interest for epilepsy is the pharmacogenomics of antiepileptic medications. There are a wide variety of these medications, from numerous different classes. The choice of medications, and the combinations of medications for patients who require treatment with more than 1 agent is complex.
Approximately one-third of patients are considered refractory to medications, defined as inadequate control of symptoms with a single medication. These patients often require escalating doses and/or combinations of different medications. At present, selection of agents is driven by the clinical phenotype of seizures but has a large trial-and-error component in many refractory cases. The current focus of epilepsy pharmacogenomics is in detecting genetic markers that identify patients likely to be refractory to the most common medications. This may lead to directed treatment that will result in a more efficient process for medication selection, and potentially more effective control of symptoms.

Of note, genotyping for the HLA-B*1502 allelic variant in patients of Asian ancestry, prior to considering drug treatment with carbamazepine due to risks of severe dermatologic reactions, is recommended by the U.S. Food and Drug Administration labeling for carbamazepine.

Regulatory Status

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

RATIONALE

This evidence review was created in November 2013 and has been updated regularly with searches of the MEDLINE database. The most recent literature update was performed through December 6, 2018.

Evidence reviews assess whether a medical test is clinically useful. A useful test provides information to make a clinical management decision that improves the net health outcome. That is, the balance of benefits and harms is better when the test is used to manage the condition than when another test or no test is used to manage the condition.

The first step in assessing a medical test is to formulate the clinical context and purpose of the test. The test must be technically reliable, clinically valid, and clinically useful for that purpose. Evidence reviews assess the evidence on whether a test is clinically valid and clinically useful. Technical reliability is outside the scope of these reviews, and credible information on technical reliability is available from other sources.

This evidence review does not address testing for genetic syndromes that have a wider range of symptomatology (eg, neurofibromatosis, tuberous sclerosis) or genetic syndromes associated with cerebral malformations or abnormal cortical development, or metabolic or mitochondrial disorders.

The genetic epilepsies are discussed in 2 categories: the rare epileptic syndromes that may be caused by a single-gene variant and are classified as epileptic encephalopathies and the epilepsy syndromes that are thought to have a multifactorial genetic basis.

Early-Onset Epilepsy and Epileptic Encephalopathies

Clinical Context and Test Purpose

Numerous rare syndromes have seizures as their primary symptom which generally present in infancy or early childhood and may be classified as epileptic encephalopathies. Many are thought to be caused by single-gene variants. The published literature on these syndromes generally consists of small cohorts of
patients treated in tertiary care centers, with descriptions of genetic variants that are detected in affected individuals.

Table 4 lists some of these syndromes, with the putative causative genetic variants.

Table 4. Early-Onset Epilepsy Syndromes Associated With Single-Gene Variants

<table>
<thead>
<tr>
<th>Syndrome</th>
<th>Implicated Genes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dravet syndrome (severe myoclonic epilepsy of infancy)</td>
<td>SCN1A</td>
</tr>
<tr>
<td>Early infantile epileptic encephalopathy</td>
<td>STXBP1</td>
</tr>
<tr>
<td>Generalized epilepsy with febrile seizures plus</td>
<td>SCN1A, SCN2A, SCN1B, GABRG2</td>
</tr>
<tr>
<td>Epilepsy and mental retardation limited to females</td>
<td>PCDH19</td>
</tr>
<tr>
<td>Nocturnal frontal lobe epilepsy</td>
<td>CHRNA4, CHRNB2, CHRNA2</td>
</tr>
</tbody>
</table>

Other less commonly reported single-gene variants have been evaluated in childhood-onset epilepsies and early-onset epileptic encephalopathies, including ASAHI1, FOLR1, GRIN2A, SCN8A, SYNGAP1, and SYNJ1 variants in families with early-onset epileptic encephalopathies and SLC13A5 variants in families with pedigrees consistent with autosomal recessive epileptic encephalopathy.

The purpose of genetic testing in patients who have epileptic encephalopathies is to determine the etiology of the epilepsy syndrome and thereby possibly limit further invasive investigation (eg, epilepsy surgery), to define prognosis, and to help guide therapy.

The question addressed in this evidence review is: Does genetic testing improve health outcomes in individuals with infantile- or early-childhood-onset epileptic encephalopathy?

The following PICOTS were used to select literature to inform this review.

Patients

The relevant population of interest is patients with clinical features (age of onset, seizure semiology, electroencephalography features) consistent with epileptic encephalopathies, including conditions such as Dravet syndrome, Ohtahara syndrome, early-onset myoclonic encephalopathy, and West syndrome, who do not present with evidence of a structural or metabolic condition that increases the likelihood of seizures and for whom seizures are the primary clinical manifestation.

Interventions

Commercial testing is available from numerous companies. Testing for individual genes is available for most, or all, or the genes listed in Table 4, as well as for a wider range of genes. Lists of genes that may lead to genetic epilepsy and testing laboratories in the United States are provided at the GeneTests website funded by BioReference Laboratories and the Genetic Testing Registry of the National Center for Biotechnology Information website.

Because of the large number of potential genes, panel testing is available from a number of genetic companies. These panels include a variable number of genes implicated in diverse disorders. Some panels are designed to be comprehensive while other panels test for specific subtypes of epilepsy. Testing using whole exome sequencing is reviewed in 2.04.102 (whole exome and whole genome sequencing for diagnosis of genetic disorders).

Comparators

The following practice is currently used: standard clinical care without genetic testing.

Outcomes
Specific outcomes in each of these categories are listed in Table 5.

The potential beneficial outcomes of primary interest would be an improvement in symptoms (particularly reduction in seizure frequency), functioning, and quality of life. A genetic diagnosis may also limit further invasive investigations into seizure etiology that have associated risks and resource utilization (eg, a genetic diagnosis may spare patients the burden and morbidity of unnecessary epilepsy surgery).

The potential harmful outcomes are those resulting from a false test result. False-positive test results can lead to initiation of unnecessary treatment and adverse events from that treatment. False-negative test results could lead to unnecessary surgeries.

**Table 5. Outcomes of Interest for Individuals with Symptomatic Epilepsy**

<table>
<thead>
<tr>
<th>Outcomes</th>
<th>Details</th>
</tr>
</thead>
<tbody>
<tr>
<td>Symptoms</td>
<td>Seizure frequency; reduction in seizure frequency by 50%; proportion</td>
</tr>
<tr>
<td></td>
<td>seizure-free</td>
</tr>
<tr>
<td>Functional outcomes</td>
<td>Measurement of development delays (eg, Bayley Scales of Infant and Toddler Development)</td>
</tr>
<tr>
<td>Quality of life</td>
<td>Validated quality of life assessment tools</td>
</tr>
<tr>
<td>Medication use</td>
<td>Number of unsuccessful medication trials, number of medications needed</td>
</tr>
<tr>
<td>Resource utilization</td>
<td>Number of surgeries</td>
</tr>
<tr>
<td>Treatment-related morbidity</td>
<td>Adverse events of epilepsy medication and surgery</td>
</tr>
</tbody>
</table>

**Timing**

The primary outcomes of interest would be related to seizure frequency over a 6-month to 2-year period.

**Setting**

Infants or young children with a first seizure may be initially evaluated by emergency physicians and referred to a primary care physician or neurologist for further diagnosis and management. Patients who are refractory to first-line antiepileptic drugs (AEDs) are frequently referred to a neurologist. Care of patients with medically refractory epilepsy may be managed by an epileptologist. Referral for genetic counseling is important for the explanation of genetic disease, heritability, genetic risk, test performance, and possible outcomes.

**Simplifying Test Terms**

There are 3 core characteristics for assessing a medical test. Whether imaging, laboratory, or other, all medical tests must be:

- Technically reliable
- Clinically valid
- Clinically useful.

Because different specialties may use different terms for the same concept, we are highlighting the core characteristics. The core characteristics also apply to different uses of tests, such as diagnosis, prognosis, and monitoring treatment.

Diagnostic tests detect presence or absence of a condition. Surveillance and treatment monitoring are essentially diagnostic tests over a time frame. Surveillance to see whether a condition develops or
progresses is a type of detection. Treatment monitoring is also a type of detection because the purpose is to see if treatment is associated with the disappearance, regression, or progression of the condition.

Prognostic tests predict the risk of developing a condition in the future. Tests to predict response to therapy are also prognostic. Response to therapy is a type of condition and can be either a beneficial response or adverse response. The term predictive test is often used to refer to response to therapy. To simplify terms, we use prognostic to refer both to predicting a future condition or to predicting a response to therapy.

**Technically Reliable**

Assessment of technical reliability focuses on specific tests and operators and requires review of unpublished and often proprietary information. Review of specific tests, operators, and unpublished data are outside the scope of this evidence review, and alternative sources exist. This evidence review focuses on the clinical validity and clinical utility.

**Clinically Valid**

A test must detect the presence or absence of a condition, the risk of developing a condition in the future, or treatment response (beneficial or adverse).

The literature on the clinical validity of genetic testing for these rare syndromes is limited and, for most syndromes, the clinical sensitivity and specificity are not defined. Dravet syndrome is probably the most well studied, and some evidence on the clinical validity of SCN1A variants is available. The clinical sensitivity has been reported to be in the 70% to 80% range. In a 2006 series of 64 patients, 51 (79%) were found to have SCN1A pathogenic variants. Among 8 infants who met clinical criteria for Dravet syndrome in a 2015 population-based cohort, 6 had a pathogenic SCN1A variant, all of which were de novo.

A number of studies have reported on the genetic testing yield in cohorts of pediatric patients with epilepsy, typically in association with other related symptoms. Table 6 summarizes examples of diagnostic yield in children with epileptic encephalopathy.

Esterhuizen et al (2018) analyzed data from 22 South African infants with provisional diagnoses of Dravet syndrome (DS) who underwent targeted resequencing of DS-associated genes. Disease-causing variants (SCN1A = 9, PCDH19 = 1) were identified in 10 children (45.5%), and results suggested that a clinical DS risk score of >6 and seizure onset before age 6 months were highly predictive of SCN1A-associated DS. For 10 of the 12 variant-negative children, clinical reassessment resulted in a revised diagnosis. No limitations to the analysis were reported.

Peng et al (2018) published an analysis of 273 pediatric patients with drug-resistant epilepsy who underwent genetic testing using whole exome sequencing (WES; n=74), epilepsy-related gene panel testing (n=141), or clinical WES gene panel testing (n=58). Ninety-three likely disease-causing mutations in 33 genes were identified in 86 individuals (31.5%). The most frequently mutated genes were SCN1A (24.4%), TSC2 (8.1%), SCN8A (5.8%), CDKL5 (5.8%), KCNMA1 (4.6%), TSC1 (4.6%), KCNQ2 (3.5%), MECP2 (3.5%), PCDH19 (3.5%), and STXBP1(3.5%). Of the 34 individuals who accepted corrective therapy according to their mutant genes, 52.9% became seizure-free and 38.2% achieved seizure reduction. No limitations to the analysis were reported.

**Table 6. Genetic Testing Yields in Pediatric Patients with Epilepsy**

<table>
<thead>
<tr>
<th>Study</th>
<th>Population</th>
<th>Genetic Testing</th>
<th>Results</th>
</tr>
</thead>
</table>

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Original Policy Date: November 2013  
Page: 13
<table>
<thead>
<tr>
<th>Study</th>
<th>Population</th>
<th>Methodology</th>
<th>Results</th>
</tr>
</thead>
<tbody>
<tr>
<td>Esterhuizen et al (2018)</td>
<td>22 infants with provisional diagnosis of DS</td>
<td>Target resequencing of DS-associated genes</td>
<td>Disease-causing variants (SCN1A and PCDH) identified in 45.5% of patients</td>
</tr>
<tr>
<td>Peng et al (2018)</td>
<td>273 pediatric patients with drug-resistant epilepsy</td>
<td>WES, epilepsy panel, or clinical WES panel</td>
<td>93 likely disease-causing variants found in 31.5% of patients:</td>
</tr>
<tr>
<td>Berg et al (2017)</td>
<td>327 infants and young children with newly diagnosed with epilepsy</td>
<td>Various forms</td>
<td>Diagnostic yield: 40.4% overall</td>
</tr>
<tr>
<td>Moller et al (2016)</td>
<td>216 patients with epileptic encephalopathy phenotypes or familial epilepsy</td>
<td>Epilepsy panel of 46 genes</td>
<td>Diagnostic yield: 23% patients overall</td>
</tr>
<tr>
<td>Trump et al (2016)</td>
<td>400 patients with early-onset seizures and/or severe developmental delay</td>
<td>Epilepsy and development delay panel of 46 genes</td>
<td>Diagnostic yield: 18% patients overall</td>
</tr>
<tr>
<td>Wirrell et al (2015)</td>
<td>81 patients with infantile spasms and no obvious cause at diagnosis</td>
<td>Various forms</td>
<td>Diagnostic yield:</td>
</tr>
<tr>
<td>Mercimek-Mahmutoglu et al (2015)</td>
<td>110 patients with epileptic encephalopathies</td>
<td>aCGH, NGS</td>
<td>Diagnostic yield:</td>
</tr>
<tr>
<td>Hrabik et al (2015)</td>
<td>147 children with epilepsy</td>
<td>SNV microarray</td>
<td>Diagnostic yield: 7.5% clinically significant abnormal results</td>
</tr>
</tbody>
</table>

DS: Dravet syndrome; WES: whole exome sequencing; aCGH: array comparative genomic hybridization; NGS: next-generation sequencing; SNV: single-nucleotide variant.

**Clinically Useful**

A test is clinically useful if the use of the results informs management decisions that improve the net health outcome of care. The net health outcome can be improved if patients receive correct therapy, or more effective therapy, or avoid unnecessary therapy, or avoid unnecessary testing.
Direct Evidence

Direct evidence of clinical utility is provided by studies that have compared health outcomes for patients managed with and without the test. Because these are intervention studies, the preferred evidence would be from randomized controlled trials.

For the early-onset epilepsies that may have a genetic component, interventions to reduce the risk of having an affected offspring may be a potential area for clinical utility. Genetic counseling and consideration of preimplantation genetic testing combined with in vitro fertilization are available options. For Dravet syndrome, most pathogenic variants are sporadic, making the clinical utility of testing for the purposes of counseling parents and intervening in future pregnancies low. However, when there is a familial disease with a pathogenic variant present in 1 parent, then preimplantation genetic testing may reduce the likelihood of having an affected offspring. For other syndromes, the risk in subsequent pregnancies for families with 1 affected child may be higher, but the utility of genetic counseling is not well-established in the literature.

Another potential area of clinical utility for genetic testing may be in making a definitive diagnosis and avoiding further testing. For most of these syndromes, the diagnosis is made by clinical criteria. However, there may be significant overlap across syndromes regarding seizure types. It is not known how often genetic testing leads to a definitive diagnosis when the diagnosis cannot be made by clinical criteria.

There is no direct evidence of utility, ie, there are no studies that report on whether the efficacy of treatment directed by genetic testing is superior to the efficacy of treatment without genetic testing.

Chain of Evidence

Indirect evidence on clinical utility rests on clinical validity. If the evidence is insufficient to demonstrate test performance, no inferences can be made about clinical utility.

A chain of evidence could be constructed to demonstrate the utility of genetic testing for epileptic encephalopathies. As mentioned, the differential diagnosis of infants presenting with clinical features of epileptic encephalopathies cannot always be made by phenotype alone; however, treatment may differ depending on the diagnosis. For Dravet syndrome, the seizures are often refractory to common medications. Some experts have suggested that diagnosis of Dravet syndrome may, therefore, prompt more aggressive treatment, and/or avoidance of certain medications known to be less effective (eg, carbamazepine).17,27 Also, some experts suggest that patients with Dravet syndrome may be more susceptible to particular AEDs, including clobazam and stiripentol.4 In contrast, the usual medical treatment of infantile spasms is hormonal therapy with corticotropin (adrenocorticotropic hormone),28,29,30 and usual first-line treatment of Lennox-Gastaut is sodium valproate.31 Therefore, confirming the specific diagnosis leads to changes in therapy expected to improve outcomes.

Ream et al (2014) retrospectively reviewed a single center’s use of clinically available genetic tests in the management of pediatric drug-resistant epilepsy.32 The study included 25 newly evaluated patients with pediatric drug-resistant epilepsy. Fourteen (56%) of tested patients had epileptic encephalopathies; 17 (68%) had generalized epilepsy syndromes. Of the 25 patients in the newly evaluated group, 15 had positive findings on genetic testing (defined as a “potentially significant” result), with 10 of the 15 considered to be diagnostic (consisting of variants previously described to be disease-causing for epilepsy syndromes or variants predicted to be disease-causing.) The genetic testing yield was higher in patients with epileptic encephalopathies (p=0.005) and generalized epilepsy (p=0.028). Patients with a clinical phenotype suggestive of an epilepsy syndrome were more likely to have positive results on testing: both patients with Dravet syndrome phenotypes had pathologic variants in SCN1A; 3 of 9
patients with Lennox-Gastaut syndrome had identified variants (1 with a \textit{CDKL5} variant, 1 with an \textit{SCL9A6} variant, 1 with both \textit{SCN1A} and \textit{EFHC1} variants). Two (6.9\%) patients had diagnostic variants not suspected based on their clinical phenotypes. In 8 (27.6\%) patients, genetic test results had potential therapeutic implications. However, only 1 patient had significantly reduced seizure frequency; the patient received stiripentol following a positive \textit{SCN1A} variant test.

\textbf{Section Summary: Early-Onset Epilepsy Syndromes and Epileptic Encephalopathies}

For early-onset epilepsy syndromes and epileptic encephalopathies, the diagnostic yield is highest for Dravet syndrome (70\%-80\%). The yield in epileptic encephalopathies and early infancy onset is between 30\% and 60\% in the studies reporting in those subsets. There is no direct evidence of the clinical utility of genetic testing. However, a chain of evidence can be constructed to demonstrate the utility of genetic testing for early-onset epilepsy syndromes and epileptic encephalopathies. The differential diagnosis of infants presenting with clinical features of epileptic encephalopathies cannot always be made by phenotype alone, and genetic testing can yield a diagnosis in some cases. Management differs depending on the differential diagnosis so correct diagnosis is expected to improve outcomes.

\textbf{Presumed Genetic Epilepsy}

\textbf{Clinical Context and Test Purpose}

Most genetic epilepsy syndromes present in childhood, adolescence, or early adulthood. They include generalized or focal and may be convulsant (grand mal) or absence type. They are generally thought to have a multifactorial genetic component.

The purpose of genetic testing in patients who are presumed to have genetic epilepsy is to determine etiology of the epilepsy syndrome and thereby possibly limit further invasive investigation (eg, epilepsy surgery), define prognosis, and help guide therapy.

The question addressed in this evidence review is: Does genetic testing improve health outcomes in individuals with presumed genetic epilepsy?

The following PICOTS were used to select literature to inform this review.

\textbf{Patients}

The relevant population of interest is patients with clinical features (age of onset, seizure semiology, electroencephalography features) consistent with genetic epilepsies, such as generalized epilepsy, childhood absence epilepsy, juvenile absence epilepsy, juvenile myoclonic epilepsy, and epilepsy with tonic-clonic seizures alone, who do not have evidence of a structural or metabolic condition that increases the likelihood of seizures and for whom seizures are the primary clinical manifestation.

\textbf{Interventions}

As mentioned, commercial tests are available from many companies. Testing using whole exome sequencing is reviewed in 2.04.102 (whole exome and whole genome sequencing for diagnosis of genetic disorders).

\textbf{Comparators}

The following practice is currently used: standard clinical care without genetic testing.

\textbf{Outcomes}

The outcomes of interest are similar to those described in the previous section. Specific outcomes are listed in Table 7. The National Institute of Neurological Disorders and Stroke Common Data Elements for
Epilepsy describes a minimum set of data elements, including outcome measures, that should ideally be collected in research of epilepsy.33

**Table 7. Outcomes of Interest for Individuals with Symptomatic Epilepsy**

<table>
<thead>
<tr>
<th>Outcome</th>
<th>Details</th>
</tr>
</thead>
<tbody>
<tr>
<td>Symptoms</td>
<td>Seizure frequency; reduction in seizure frequency by 50%; proportion</td>
</tr>
<tr>
<td></td>
<td>seizure-free; Child Symptom Inventory, Adolescent Symptom Inventory</td>
</tr>
<tr>
<td>Functional outcomes</td>
<td>Validated measures of cognitive functioning (eg, Wechsler scales, California</td>
</tr>
<tr>
<td></td>
<td>Verbal Learning Test)</td>
</tr>
<tr>
<td>Quality of life</td>
<td>Validated measure of quality of life (eg, Quality of Life in Epilepsy Inventory</td>
</tr>
<tr>
<td></td>
<td>for Adolescents, Quality of Life in Childhood Epilepsy)</td>
</tr>
<tr>
<td>Medication use</td>
<td>Number of unsuccessful medication trials, number of medications needed</td>
</tr>
<tr>
<td>Resource utilization</td>
<td>Number of surgeries</td>
</tr>
<tr>
<td>Treatment-related morbidity</td>
<td>Adverse effects of epilepsy medication and surgery</td>
</tr>
</tbody>
</table>

**Timing**

The primary outcomes of interest would be related to seizure frequency over a 6-month to 2-year period.

**Setting**

Infants or young children with a first seizure may be initially evaluated by emergency physicians and referred to primary care physician or neurologist for further diagnosis and management. Patients who are refractory to first-line AEDs are frequently referred to a neurologist. Care of patients with medically refractory epilepsy may be managed by an epileptologist. Referral for genetic counseling is important for the explanation of genetic disease, heritability, genetic risk, test performance, and possible outcomes.

**Technically Reliable**

Assessment of technical reliability focuses on specific tests and operators and requires review of unpublished and often proprietary information. Review of specific tests, operators, and unpublished data are outside the scope of this evidence review, and alternative sources exist. This evidence review focuses on the clinical validity and clinical utility.

**Clinically Valid**

A test must detect the presence or absence of a condition, the risk of developing a condition in the future, or treatment response (beneficial or adverse).

The literature on clinical validity includes many studies that have reported on the association between various genetic variants and epilepsy. A large number of case-control studies have compared the frequency of genetic variants in patients who have epilepsy with the frequency in patients without epilepsy. There is a smaller number of genome-wide association studies (GWAS) that evaluate the presence of SNVs associated with epilepsy across the entire genome. No studies were identified that reported on the clinical sensitivity and specificity of genetic variants in various clinically defined groups of patients with epilepsy. In addition to these studies on the association of genetic variants with the diagnosis of epilepsy, numerous other studies have evaluated the association between genetic variants and pharmacogenomics of AEDs.

**Diagnosis of Epilepsy**
Hesse et al (2018) published a retrospective analysis of 305 patients (age range <1–69 years old with 88% <18 years old) referred for genetic testing with a targeted epilepsy panel between 2014 and 2016. Positive yield was 15.1%, with pathogenic, likely pathogenic, predicted deleterious mutations identified in 46 individuals. Twenty-nine distinct genes were present, and known pathogenic variants were identified in 7 genes (BRAF, DPYD, GABRG2, PAX6, SCN1A, SLC2A1, and SLC46A1). No limitations to the analysis were reported.

Lindy et al (2018) published an industry sponsored analysis of 8565 consecutive individuals with epilepsy and/or neurodevelopmental disorders who underwent genetic testing with multigene panels. Positive results were reported in 1315 patients (15.4%), and, of 22 genes with high positive yield, SCN1A (24.8%) and KCNQ2 (13.2%) accounted for the greatest number of positive findings. Results found 14 distinct genes with recurrent pathogenic or likely pathogenic (P/LP) variants (most commonly in MECP2, KCNQ2, SCN1A, SCN2A, STXBP1, and PRRT2). Greater than 30% of positive cases had parental testing performed; all variants found in CDKL5, STXBP1, SCN8A, GABRA1, and FOXG1 were de novo, however, 85.7% of variants in PRRT2 were inherited. No P/LP variants were found in ATP6AP2, CACNB4, CHRNA2, DNAJC5, EFHC1, MAGI2, and SRPX2. No limitations to the analysis were reported.

Miao et al (2018) published an analysis of 141 Chinese patients under 14 years of age with epilepsy who underwent genotype and phenotype analysis using an epilepsy-associated gene panel between 2015 and 2017. Certain diagnoses were obtained in 39 probands (27.7%); these causative variants were related to 21 genes. The most frequently mutated gene was SCN1A (5.6%), but others included KCNQ2, KCNT1, PCDH19, STXBP1, SCN2A, TSC2, and PRRT2. The treatments for 18 patients (12.8%) were altered based on their genetic diagnosis and on genotype-phenotype analysis. No limitations to the analysis were reported.

Butler et al (2017) published a retrospective analysis of epilepsy patients screened using a 110-gene panel between 2013 and 2016; 339 unselected individuals (age range 2.5 months to 74 years, with more than 50% <5 years old) were included. Pathogenic and likely pathogenic variants were identified in 62 patients (18%), and another 21 individuals (6%) had potentially causative variants. SCN1A (n=15) and KCNQ2 (n=10) were the frequently identified potentially causative variants. However, other genes in which variants were identified in multiple individuals included CDKL5, SCN2A, SCN8A, SCN1B, STXBP1, TPP1, PCDH19, CACNA1A, GABRA1, GRIN2A, SLC2A1, and TSC2. The study was limited by the lack of clinical information available for approximately 20% of participants.

Table 8. Summary of Key Nonrandomized Study Characteristics

<table>
<thead>
<tr>
<th>Study</th>
<th>Study Type</th>
<th>Country</th>
<th>Dates</th>
<th>Participants</th>
<th>Treatment1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lindy (2018)</td>
<td>Cohort</td>
<td>US</td>
<td>2011-2015</td>
<td>Individuals with epilepsy and/or neurodevelopmental disorders (n=8565)</td>
<td>Genetic testing with multiple gene panels</td>
</tr>
<tr>
<td>Miao (2018)</td>
<td>Retrospective</td>
<td>China</td>
<td>2015-2017</td>
<td>Patients with epilepsy &lt;14 years old (n=141)</td>
<td>Epilepsy-associated gene panel</td>
</tr>
<tr>
<td>Butler (2017)</td>
<td>Retrospective</td>
<td>US</td>
<td>2013-2016</td>
<td>Patients with epilepsy (n=339)</td>
<td>110-gene epilepsy and seizure disorders panel</td>
</tr>
</tbody>
</table>

Table 9. Summary of Key Nonrandomized Study Results

<table>
<thead>
<tr>
<th>Study</th>
<th>Positive Yield</th>
<th>Genes with Identified Pathogenic Variants</th>
</tr>
</thead>
<tbody>
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</table>

Original Policy Date: November 2013
Tan and Berkovic (2010) published an overview of genetic association studies using records from Epilepsy Genetic Association Database. Reviews identified 165 case-control studies published between 1996 and 2008. There were 133 studies that examined the association between 77 different genetic variants and the diagnosis of epilepsy. Approximately half (65/133) focused on patients with genetic generalized epilepsy (GGE). Most studies had relatively small sample sizes, with a median of 104 cases (range, 8-1361) and 126 controls (range, 22-1390). There were fewer than 200 case patients in 80% of the studies. Most did not show a statistically significant association. Using a cutoff of \( p \) less than 0.01 as the threshold for significance, 35 studies (21.2%) reported a statistically significant association.

According to standard definitions for genetic association, all associations were in the weak-to-moderate range, with no associations considered strong.

In 2014, the International League Against Epilepsy Consortium on Complex Epilepsies published a meta-analysis of GWAS studies for all epilepsy and 2 epilepsy clinical subtypes, GGE and focal epilepsy. The authors combined GWAS data from 12 cohorts of patients with epilepsy and controls (ethnically matched to cases) from population-based datasets, for a total of 8696 cases and 26,157 controls. Cases with epilepsy were categorized as having GGE, focal epilepsy, or unclassified epilepsy. For all cases, loci at 2q24.3 (\( \text{SCN1A} \)) and 4p15.1 (\( \text{PCDH7} \), which encodes a protocadherin molecule) were significantly associated with epilepsy (\( p = 8.71 \times 10^{-10} \) and \( 5.44 \times 10^{-9} \), respectively). For those with GGE, a locus at 2p16.1 (\( \text{VRK2} \) or \( \text{FANCL} \)) was significantly associated with epilepsy (\( p = 9.99 \times 10^{-9} \)). No SNVs were significantly associated with focal epilepsy.

Some of the larger GWAS are described here. The EPICURE Consortium published one of the larger GWAS of GGE in 2012. It included 3020 patients with GGE and 3954 control patients, all of European ancestry. A 2-stage approach was used, with a discovery phase and a replication phase, to evaluate a total of 4.56 million SNVs. In the discovery phase, 40 candidate SNVs were identified that exceeded the significance for the screening threshold (\( 1 \times 10^{-5} \)), although none reached the threshold defined as statistically significant for GWAS (\( 1 \times 10^{-8} \)). After stage 2 analysis, 4 SNVs identified had suggestive associations with GGE on genes \( \text{SCN1A} \), \( \text{CHRM3} \), \( \text{ZEB2} \), and \( \text{NLE2F1} \).

A second GWAS with a relatively large sample size of Chinese patients was also published in 2012. Using a similar 2-stage methodology; this study evaluated 1087 patients with epilepsy and 3444 matched controls. Two variants were determined to have the strongest association with epilepsy. One was on the \( \text{CAMSAP1L1} \) gene and the second was on the \( \text{GRIK2} \) gene. There were several other loci on genes suggestive of an association that coded for neurotransmitters or other neuron function.

In addition to the individual studies reporting general genetic associations with epilepsy, a number of meta-analyses have evaluated the association of particular genetic variants with different types of epilepsy. Most have not shown a significant association. For example, Cordoba et al (2012) evaluated the association between \( \text{SLC6A4} \) gene variants and temporal lobe epilepsy in 991 case patients and 1202 controls and failed to demonstrate a significant association on combined analysis. Nurmohamed et al (2010) performed a meta-analysis of 9 case-control studies that evaluated the association between the \( \text{ABC1} \) gene variants and epilepsy. It included 2454 patients with epilepsy and 1542 control patients. No significant associations were found.
One meta-analysis that did report a significant association was published by Kauffman et al (2008).\textsuperscript{44} They evaluated the association between variants in the \textit{IL1B} gene and temporal lobe epilepsy and febrile seizures, using data from 13 studies (1866 patients with epilepsy, 1930 controls). Combined analysis showed a significant relation between 1 SNV (511T) and temporal lobe epilepsy, with a strength of association considered modest (odds ratio [OR], 1.48; 95% confidence interval [CI], 1.1 to 2.0; \textit{p}=0.01). Another meta-analysis reporting a positive association was published by Tang et al (2014).\textsuperscript{45} The authors evaluated the association between the \textit{SCN1A} IVS5N+5GNA variant and susceptibility to epilepsy with febrile seizures. The analysis included 6 studies with 2719 cases and 2317 controls. There was a significant association between \textit{SCN1A} variant and epilepsy with febrile seizures (A vs G: OR=1.5; 95% CI, 1.1 to 2.0).

**Prognosis of Epilepsy**

A smaller body of literature has evaluated whether specific genetic variants are associated with epilepsy phenotypes or prognosis. Van Podewils et al (2015) evaluated the association between sequence variants in \textit{EFHC1} and phenotypes and outcomes in 38 probands with juvenile myoclonic epilepsy, along with 3 family members.\textsuperscript{46} Several \textit{EFHC1} gene variants, including F229L, R294H, and R182H, were associated with earlier onset of generalized tonic-clonic seizures (66.7% vs 12.5%, OR=13, \textit{p}=0.022), high risk of status epilepticus (\textit{p}=0.001), and decreased risk of bilateral myoclonic seizures (\textit{p}=0.05).

**Pharmacogenomics of Antiepileptic Medications**

**Pharmacogenomic of AED Response**

Numerous case-control studies have reported on the association between various genetic variants and response to medications in patients with epilepsy. The Epilepsy Genetic Association Database identified 32 case-control studies of 20 different genes and their association with medication treatment.\textsuperscript{38} The most common comparison was between responders to medication and nonresponders. Some of the larger representative studies are discussed next.

Kwan et al (2008) compared the frequency of SNVs on the \textit{SCN1A}, \textit{SCN2A}, and \textit{SCN3A} genes in 272 drug-responsive patients and 199 drug-resistant patients.\textsuperscript{47} Twenty-seven candidate SNVs were evaluated, selected from a large database of previously identified SNVs. One SNV identified on the \textit{SCN2A} gene (rs2304016) had a significant association with drug resistance (OR=2.1; 95% CI, 1.2 to 3.7; \textit{p}=0.007).

Jang et al (2009) compared the frequency of variants on the \textit{SCN1A}, \textit{SCN1B}, and \textit{SCN2B} genes in 200 patients with drug-resistant epilepsy and 200 patients with drug-responsive epilepsy.\textsuperscript{48} None of the individual variants tested showed a significant relation with drug resistance. In a further analysis for gene-gene interactions associated with drug resistance, the authors reported a possible interaction of 2 variants, one on the \textit{SCN2A} gene and the other on the \textit{SCN1B} gene, though falling below their cutoff for statistical significance (\textit{p}=0.055).

Li et al (2015) conducted a meta-analysis of 28 articles reporting on 30 case-control studies to evaluate the association between the \textit{ABCB1} gene C3435T variant and AED resistance.\textsuperscript{49} The included studies had a total of 4124 drug-resistant epileptic patients and 4480 control epileptic patients for whom drug treatment was effective. In a pooled random-effects model, the 3435C allele was not significantly associated with drug resistance, with a pooled odds ratio of 1.07 in an allele model (95% CI, 0.95 to 1.19; \textit{p}=0.26) and 1.05 in a genotype model (95% CI, 0.89 to 1.24; \textit{p}=0.55).

Other representative studies that have reported associations between genetic variants and AED response are summarized in Table 10.

**Table 10. Genetic Variants and Antiepileptic Drug Response**
<table>
<thead>
<tr>
<th>Study</th>
<th>Population</th>
<th>Genes</th>
<th>Overview of Findings</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lu et al (2017)</td>
<td>124 epileptic Chinese patients receiving OXC monotherapy</td>
<td>· UGT1A4 142T&gt;G (rs2011425)</td>
<td>· UGT1A9 variant allele 1399C&gt;T had significantly lower monohydroxylated derivative plasma concentrations (TT 13.28 mg/L, TC 16.41 mg/L vs CC 22.24 mg/L, p&lt;0.05) and poorer seizure control than noncarriers (p=0.01)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>· UGT1A6 19T&gt;G (rs6759892)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>· UGT1A9 1399C&gt;T (rs2741049)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>· UGT2B15 253T&gt;G (rs1902023)</td>
<td></td>
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</tbody>
</table>
| Hashi et al (2015) | 50 epileptic adults treated with stable clobazam dose                      | CYP2C19                                                              | · Clobazam metabolite N-desmethylclobazam serum concentration:dose ratio was higher in PMs (median, 16,300 [ng/ml]/[mg/kg/d]) than in EMs (median, 1760 [ng/ml]/[mg/kg/d]) or IMs (median, 4640 [ng/ml]/[mg/kg/d])  
Patients with EM or IM status had no change in seizure frequency with clobazam therapy                                                                                                                                                                                                                     |
| Ma et al (2015)    | 184 epileptic patients receiving OXC monotherapy and 156 healthy volunteers | · SCN1A c.3184A>G (rs2298771)                                         | · SCN1A IVS5-91G>A, UGT2B7 c.802T>C, and ABCC2 c.1249G>A variants showed significant associations with OXC maintenance doses  
Patients with the ABCC2 c.1249G>A allele variant more likely to require higher OXC maintenance doses than noncarriers (p=0.002, uncorrected), which remained significant after Bonferroni correction                                                                                                      |
|                    |                                                                           | · SCN2A c.56G>A (rs17183814)                                          |                                                                                                                                                                                                                                                                                                                                                     |
|                    |                                                                           | · SCN2A IVS7-32A>G (rs2304016)                                        |                                                                                                                                                                                                                                                                                                                                                     |
|                    |                                                                           | · ABCC2 3972C>T (rs3740066)                                           |                                                                                                                                                                                                                                                                                                                                                     |
|                    |                                                                           | · ABCC2 c.1249G>A (rs2273697)                                         |                                                                                                                                                                                                                                                                                                                                                     |
|                    |                                                                           | · UGT2B7 c.802T>C (rs7439366)                                         |                                                                                                                                                                                                                                                                                                                                                     |
| Guo et al (2015)   | 483 Chinese patients with genetic generalized epilepsies                  | KCNJ10                                                               | · Frequency of rs12402969 C allele and the CC+CT genotypes were higher in the drug-responsive patients than that in the drug-resistant patients (9.3% vs 5.6%, OR=1.7, 95% CI, 1.1 to 2.9, p=0.026)                                                                                                         |
| Ma et al (2014)    | 453 epileptic patients, classified as drug-responsive (n=207) or drug-resistant (n=246) | · SCN1A c.3184A>G (rs2298771)                                         | · SCN1A IVS5-91G>A AA genotype more prevalent in drug-resistant than drug-responsive patients receiving multidrug therapy (OR=3.41; 95% CI, 1.73 to 6.70; p<0.001, uncorrected)                                                                                                           |
|                    |                                                                           | · SCN2A c.56G>A (rs17183814)                                          | · SCN1A IVS5-91G>A AA more prevalent in drug-resistant than drug-responsive patients receiving carbamazepine/OXC (OR=3.55; 95% CI, 1.62 to 7.78; p=0.002, uncorrected)                                                                                                                      |
|                    |                                                                           | · SCN2A IVS7-32A>G (rs2304016)                                        | · ABCC2 c.1249G>A GA genotype and allele A significantly associated with drug response (OR=2.14; 95% CI, 1.23 to 3.71; p=0.007;                                                                                                                                      |
### Overview of Findings

**Radisch et al (2014)**\(^{55}\) 229 epileptic patients treated with carbamazepine monotherapy

- ABCC2: variant rs717620 (-24G4A), rs2273697 (c.1249G4A) and rs3740067

- OR\(=2.05; 95\%\) CI, 1.31 to 3.19; \(p=0.001\), respectively, uncorrected

- **ABCC2 variants not associated with time to first seizure or time to 12-mo remission**

**Yun et al (2013)**\(^{56}\) 38 epileptic patients treated with carbamazepine monotherapy

- EPHX1 c.337T>C
- EPHX1 c.416A>G
- SCN1A IVS5-91G>A
- CYP3A4*1G

- Patients EPHX1 c.416A>G genotypes had higher adjusted plasma carbamazepine concentrations vs those with wild-type genotype \(p<0.05\)
- Other studied variants not associated with carbamazepine pharmaco-resistance

**Taur et al (2014)**\(^{52}\) 115 epileptic patients treated with phenytoin, phenobarbital, and/or carbamazepine

- ABCB1 (c.3435T)
- CYP2C9 (416C>T)
- CYP2C9 (1061A>T)
- CYP2C19 (681G>A)
- CYP2C19 (636G>A)

- **ABCB1 C3435T genotype and allele variants significantly associated with drug response** \(OR=4.5; 95\%\) CI, 1.04 to 20.99; \(OR=1.73; 95\%\) CI, 1.02 to 2.95, respectively

---

CI: confidence interval; EM: extensive metabolizer; IM: intermediate metabolizer; OR: odds ratio; OXC: oxcarbazepine; PM: poor metabolizer.

Several meta-analyses evaluating pharmacogenomics were identified. Haerian et al (2010) examined the association between SNVs on the ABCB1 gene and drug resistance in 3231 drug-resistant patients and 3524 controls from 22 studies. \(^{58}\) Reviewers reported no significant relation between variants of this gene and drug resistance (combined OR=1.06; 95\% CI, 0.98 to 1.14; \(p=0.12\)). There was also no significant association for subgroup analysis by ethnicity.

In a separate meta-analysis, Sun et al (2014) evaluated 8 studies evaluating the association between variants in the multidrug resistance 1 (MDR1) gene and childhood medication-refractory epilepsy, including 634 drug-resistant patients, 615 drug-responsive patients, and 1052 healthy controls. \(^{59}\) In the pooled analysis, the MDR1 C3435T variant was not significantly associated with risk of drug resistance.

### Table 11. Pharmacogenomic of AED Response SR & M-A of Characteristics

<table>
<thead>
<tr>
<th>Study</th>
<th>Dates</th>
<th>Trials</th>
<th>Participants</th>
<th>N (Range)</th>
<th>Design</th>
<th>Duration</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sun (2014)</td>
<td>2007-2013</td>
<td>8</td>
<td>Children (&lt;18 years old) with intractable epilepsy</td>
<td>634 drug-resistant patients, 615 drug-responsive, and 1052 healthy controls</td>
<td>Case-controlled or cohort studies</td>
<td>NR</td>
</tr>
</tbody>
</table>

### Table 12. Pharmacogenomic of AED Response SR & M-A Results

<table>
<thead>
<tr>
<th>Study</th>
<th>Association of ABCB1 C3435T with risk of DR</th>
<th>Association of MDR1 C3435T with risk of DR</th>
</tr>
</thead>
<tbody>
<tr>
<td>Haerian (2010)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>OR</td>
<td>1.06</td>
<td></td>
</tr>
</tbody>
</table>
Shazadi et al (2014) assessed the validity of a gene classifier panel consisting of 5 SNVs for predicting initial AED response and overall seizure control in 2 cohorts of patients with newly diagnosed epilepsy. A cohort of 115 Australian patients with newly diagnosed epilepsy was used to develop the classifier from a sample of 4041 SNVs in 279 candidate genes via a $k$-nearest neighbor machine learning algorithm, resulting in a 5-SNV classifier. The classifier was validated in 2 separate cohorts. One cohort included 285 newly diagnosed patients in Glasgow, of whom a large proportion had participated in randomized trials of AED monotherapy. Drug-response phenotypes in this cohort were identified by retrospectively reviewing prospectively collected clinical trial and/or hospital notes. The second cohort was drawn from patients who had participated in the Standard and New Epileptic Drugs (SANAD) trial, a multicenter RCT comparing standard with newer AEDs. The trial included 2400 patients, of whom 520 of self-described European ancestry who provided DNA samples were used in the present analysis. The $k$-nearest neighbor machine model derived from the original Australian cohort did not predict treatment response in either the Glasgow or the SANAD cohorts. Investigators redeveloped a $k$-nearest neighbor machine learning algorithm based on SNV genotypes and drug responses in a training dataset (n=343) derived from the SANAD cohort. None of the 5 SNVs used in the multigenic classifier was independently associated with AED response in the Glasgow or the SANAD cohort after correction for multiple tests. When applied to a test dataset (n=148) derived from the SANAD cohort, the classifier correctly identified 26 responders and 52 nonresponders but incorrectly identified 26 nonresponders as responders (false positives) and 44 responders as nonresponders (false negatives), corresponding to a positive predictive value of 50% (95% CI, 32.8% to 67.2%) and a negative predictive value of 54% (95% CI, 41.1% to 66.7%). In a cross-validation analysis, the 5-SNV classifier was significantly predictive of treatment responses among Glasgow cohort patients initially prescribed either carbamazepine or valproate (positive predictive value, 67%; negative predictive value, 60%; corrected p=0.018), but not among those prescribed lamotrigine (corrected p=1.0) or other AEDs (corrected p=1.0). The 5-SNV classifier was significantly predictive of treatment responses among SANAD cohort patients initially prescribed carbamazepine or valproate (positive predictive value, 69%; negative predictive value, 56%; corrected p=0.048), but not among those prescribed lamotrigine (corrected p=0.36) or other AEDs (corrected p=0.36).

Pharmacogenomics of AED Adverse Events

Many AEDs have a relatively narrow therapeutic index, with the potential for dose-dependent or idiosyncratic adverse events. Several studies have evaluated genetic predictors of adverse events from AEDs, particularly severe skin reactions including Stevens-Johnson syndrome (SJS) and toxic epidermal necrolysis (TEN).

Chung et al (2014) evaluated genetic variants associated with phenytoin-induced severe cutaneous adverse events (SJS/TEN, drug reactions with eosinophilia and systemic symptoms) and maculopapular exanthema. This GWAS included 60 cases with phenytoin-related severe cutaneous adverse events and 412 population controls, and was followed by a case-control study of 105 cases with phenytoin-related severe cutaneous adverse events (61 with SJS/TEN, 44 with drug reactions with eosinophilia and
systemic symptoms), 78 cases with maculopapular exanthema, 130 phenytoin-tolerant control participants, and 3655 population controls from Taiwan, Japan, and Malaysia. In the GWAS analysis, a missense variant of CYP2C9*3 (rs1057910) was significantly associated with phenytoin-related severe cutaneous adverse events (OR=12; 95% CI, 6.6 to 20; p=1.1´10^-17). In a case-control comparison between the subgroups of 168 patients with phenytoin-related cutaneous adverse events and 130 phenytoin-tolerant controls, CYP2C9*3 variants were significantly associated with SJS/TEN (OR=30; 95% CI, 8.4 to 109; p=1.2´10^-19), drug reactions with eosinophilia and systemic symptoms (OR=19; 95% CI, 5.1 to 71; p=7.0´10^-7), and maculopapular exanthema (OR=5.5; 95% CI, 1.5 to 21; p=0.01).

He et al (2014) conducted a case-control study to evaluate the association between carbamazepine-induced SJS/TEN and 10 SNVs in the ABCB1, CYP3A4, EPHX1, FAS, SNC1A, MICA, and BAG6 genes. The study included 28 cases with carbamazepine-induced SJS/TEN and 200 carbamazepine-tolerant controls. The authors reported statistically significant differences in the allelic and genotypic frequencies of EPHX1 c.337T>C variants between patients with carbamazepine-induced SJS/TEN and carbamazepine-tolerant controls (p=0.011 and p=0.007, respectively). There were no significant differences between SJS/TEN cases and carbamazepine-tolerant controls for the remaining SNVs evaluated.

Wang et al (2014) evaluated the association between HLA genes and cross-reactivity of cutaneous adverse drug reactions to aromatic AEDs (carbamazepine, lamotrigine, oxcarbazepine, phenytoin, phenobarbital). The study included 60 patients with a history of aromatic AED-induced cutaneous adverse drug reactions, including SJS/TEN and maculopapular eruption, who were reexposed to an aromatic AED, 10 of whom had a recurrence of the cutaneous adverse drug reaction on re-exposure (cross-reactive group). Subjects tolerant to re-exposure were more likely to carry the HLA-A*2402 allele than cross-reactive subjects (OR=0.13; 95% CI, 0.015 to 1.108; p=0.040). Frequency distributions for testing other HLA genes did not differ significantly between groups.

### Table 13. Summary of Key Observational Study Characteristics for Pharmacogenomics of AED Adverse Events

<table>
<thead>
<tr>
<th>Study</th>
<th>Study Type</th>
<th>Country</th>
<th>Dates</th>
<th>Participants</th>
<th>Treatment 1</th>
<th>Treatment 2</th>
<th>Follow-Up</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chung (2014)</td>
<td>Case-control</td>
<td>Taiwan, Malaysia, Japan</td>
<td>2002-2014</td>
<td>Individuals with PRSCARs (n=60) and tolerant controls (n=130)</td>
<td>GWAS</td>
<td></td>
<td>NR</td>
</tr>
<tr>
<td>He (2014)</td>
<td>Case-control</td>
<td>China</td>
<td>NR</td>
<td>Chinese Han patients with CBZ-SJS/TEN (n=28) and CBZ-tolerant controls (n=200)</td>
<td>Polymerase chain reaction amplification and direct sequencing</td>
<td>Fluorescence polarization immunoassay</td>
<td>NR</td>
</tr>
<tr>
<td>Wang (2014)</td>
<td></td>
<td>China</td>
<td>2009-2013</td>
<td>Patients with a history of aromatic AED-induced cADRs reexposed to an aromatic AED (n=60)</td>
<td>High-resolution HLA-A, -B, -DRB1 genotyping</td>
<td></td>
<td>NR</td>
</tr>
</tbody>
</table>


### Table 14. Summary of Key Observational Study Results for Pharmacogenomics of AED Adverse Events
Predictive of Sudden Unexplained Death in Epilepsy

Sudden unexplained death in epilepsy (SUDEP) is defined as a sudden, unexpected, nontraumatic, and nondrowning death in patients with epilepsy, excluding documented status epilepticus, with no cause of death identified following comprehensive postmortem evaluation. It is the most common cause of epilepsy-related premature death, accounting for 15% to 20% of deaths in patients with epilepsy.\(^64\) Given uncertainty related to the underlying causes of SUDEP, there has been interest in identifying genetic associations with SUDEP.

Bagnall et al. (2014) evaluated the prevalence of sequence variations in the PHOX2B gene in 68 patients with SUDEP.\(^64\) Large polyalanine repeat expansions in the PHOX2B gene are associated with congenital central hypoventilation syndrome, a potentially lethal autonomic dysfunction syndrome, but smaller PHOX2B expansions may be associated with nocturnal hypoventilation. In a cohort of patients with SUDEP, 1 patient was found to have a 15-nucleotide deletion in the PHOX2B gene, but no PHOX2B polyalanine repeat expansions were found.

Coll et al. (2016) evaluated the use of a custom resequencing panel including genes related to sudden death, epilepsy, and SUDEP in a cohort of 14 patients with focal or generalized epilepsy and a personal or family history of SUDEP, including 2 postmortem cases.\(^65\) In 4 cases, rare variants were detected with complete segregation in the SCN1A, FBN1, HCN1, SCN4A, and EFHC1 genes, and in 1 case a rare variant in KCNQ1 with an incomplete pattern of inheritance was detected. New potential candidate genes for SUDEP were detected: FBN1, HCN1, SCN4A, EFHC1, CACNA1A, SCN11A, and SCN10A.

Bagnall et al. (2016) performed an exome-based analysis of rare variants related to cardiac arrhythmia, respiratory control, and epilepsy to search for genetic risk factors in 61 SUDEP cases compared with 2936 controls.\(^66\) Mean epilepsy onset of the SUDEP cases was 10 years and mean age at death was 28 years. De novo variants, previously reported pathogenic variants, or candidate pathogenic variants were identified in 28 (46%) of 61 SUDEP cases. Four (7%) SUDEP cases had variants in common genes responsible for long QT syndrome and a further 9 (15%) cases had candidate pathogenic variants in
dominant cardiac arrhythmia genes. Fifteen (25%) cases had variants or candidate pathogenic variants in epilepsy genes; 6 cases had a variant in *DEPDC5*. *DEPDC5* (p=0.00015) and *KCNH2* (p=0.0037) were highly associated with SUDEP. However, using a rare variant collapsing analysis, no gene reached criteria for genome-wide significance.

**Table 15. Summary of Nonrandomized Study Characteristics for Prediction of Sudden Unexplained Death in Epilepsy**

<table>
<thead>
<tr>
<th>Study</th>
<th>Study Type</th>
<th>Country</th>
<th>Dates</th>
<th>Participants</th>
<th>Treatment</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bagnall (2014)</td>
<td>Retrospective</td>
<td>Australia</td>
<td>1993-2009</td>
<td>Patients with SUDEP (n=68)</td>
<td>DNA sequencing analysis of PHOX2B</td>
</tr>
<tr>
<td>Coll (2016)</td>
<td>Cohort</td>
<td>Italy</td>
<td>NR</td>
<td>Patients with focal or generalized epilepsy and a personal or family history of SUDEP (n=14)</td>
<td>Custom resequencing panel</td>
</tr>
<tr>
<td>Bagnall (2016)</td>
<td>Cohort</td>
<td>Australia</td>
<td>1993-2010</td>
<td>Patients with SUDEP (n=61) and controls (n=2936)</td>
<td>Exome sequencing and rare variant collapsing analysis</td>
</tr>
</tbody>
</table>

SUDEP: sudden unexplained death in epilepsy; NR: not reported.

**Table 16. Summary of Key Nonrandomized Study Results for Prediction of Sudden Unexplained Death in Epilepsy**

<table>
<thead>
<tr>
<th>Study</th>
<th>Patients with a 15-nucleotide deletion in PHOX2B gene, n/N</th>
<th>Patients with PHOX2B polyalanine repeat expansions, n/N</th>
<th>Rare variants detected with complete segregation</th>
<th>New potential candidate genes for SUDEP</th>
<th>Variants highly associated with SUDEP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bagnall (2014)</td>
<td>1/68</td>
<td>0/68</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Coll (2016)</td>
<td>4 cases: SCN1A, FBN1, HCN1, SCN4A, EFHC1</td>
<td>1 case: KCNQ1</td>
<td></td>
<td>FBN1, HCNI, SCN4A, EFHC1, CACNA1A, SCN11A, SCN10A</td>
<td></td>
</tr>
<tr>
<td>Bagnall (2016)</td>
<td></td>
<td></td>
<td></td>
<td>DEPDC5 (p&lt;0.001), KCNH2 (p&lt;0.004)</td>
<td></td>
</tr>
</tbody>
</table>

**Clinically Useful**

A test is clinically useful if the use of the results informs management decisions that improve the net health outcome of care. The net health outcome can be improved if patients receive correct therapy, or more effective therapy, or avoid unnecessary therapy, or avoid unnecessary testing.

**Direct Evidence**

Direct evidence of clinical utility is provided by studies that have compared health outcomes for patients managed with and without the test. Because these are intervention studies, the preferred evidence would be from randomized controlled trials.

There is a lack of evidence on the clinical utility of genetic testing for the genetic epilepsies. Association studies are insufficient evidence to determine whether genetic testing can improve the clinical diagnosis.
of GGE. There are no studies reporting the accuracy regarding sensitivity, specificity, or predictive value; therefore, it is not possible to determine the impact of genetic testing on diagnostic decision making.

The evidence on pharmacogenomics has suggested that genetic factors may play a role in the pharmacokinetics of antiepileptic medications. However, how genetic information might be used to tailor medication management in ways that will improve efficacy, reduce adverse events, or increase the efficiency of medication trials is not yet well-defined.

Section Summary: Presumed Genetic Epilepsy

The evidence on genetic testing for genetic epilepsies is characterized by a large number of studies that have evaluated associations between many different genetic variants and the various categories of epilepsy. The evidence on the clinical validity of testing for the diagnosis of epilepsy is not consistent in showing an association between any specific genetic variant and any specific type of epilepsy. Where associations have been reported, they are not of strong magnitude and, in most cases, have not been replicated independently or through the available meta-analyses. Because of the lack of established clinical validity, the clinical utility of genetic testing for the diagnosis of genetic epilepsies is also lacking. Several studies have reported associations between a number of genes and response to AEDs or AED adverse events. How this information should be used to tailor medication management is not yet well-defined, and no studies were identified that provide evidence for clinical utility.

Summary of Evidence

For individuals who have infantile- or early-childhood-onset epileptic encephalopathy who receive testing for genes associated with epileptic encephalopathies, the evidence includes prospective and retrospective cohort studies describing the testing yield. Relevant outcomes are test validity, symptoms, quality of life, functional outcomes, medication use, resource utilization, and treatment-related morbidity. For Dravet syndrome, which appears to have the largest body of associated literature, the sensitivity of testing for SCN1A disease-associated variants is high (≥80%). For other early-onset epileptic encephalopathies, the true clinical sensitivity and specificity of testing are not well-defined. However, studies reporting on the overall testing yield in populations with epileptic encephalopathies and early-onset epilepsy have reported detection rates for clinically significant variants ranging from 7.5% to 57%. The clinical utility of genetic testing occurs primarily when there is a positive test for a known pathogenic variant. The presence of a pathogenic variant may lead to targeted medication management, avoidance of other diagnostic tests, and/or informed reproductive planning. The evidence is sufficient to determine that the technology results in a meaningful improvement in the net health outcome.

For individuals who have presumed genetic epilepsy who receive testing for genetic variants associated with genetic epilepsies, the evidence includes prospective and retrospective cohort studies describing testing yields. Relevant outcomes are test validity, changes in reproductive decision making, symptoms, quality of life, functional outcomes, medication use, resource utilization, and treatment-related morbidity. For most genetic epilepsies, which are thought to have a complex, multifactorial basis, the association between specific genetic variants and the risk of epilepsy is uncertain. Despite a large body of literature on associations between genetic variants and epilepsies, the clinical validity of genetic testing is poorly understood. Published literature is characterized by weak and inconsistent associations, which have not been replicated independently or by meta-analyses. A number of studies have also reported associations between genetic variants and AED treatment response, AED adverse effect risk, epilepsy phenotype, and risk of sudden unexplained death in epilepsy. The largest number of these studies is related to AED pharmacogenomics, which has generally reported some association between
variants in a number of genes (including \textit{SCN1A}, \textit{SCN2A}, \textit{ABCC2}, \textit{EPHX1}, \textit{CYP2C9}, \textit{CYP2C19}) and AED response. Similarly, genetic associations between a number of genes and AED-related adverse events have been reported. However, no empirical evidence on the clinical utility of testing for the genetic epilepsies was identified, and the changes in clinical management that might occur as a result of testing are not well-defined. The evidence is insufficient to determine the effects of the technology on health outcomes.

\textbf{SUPPLEMENTAL INFORMATION}

\textbf{Clinical Input from Physician Specialty Societies and Academic Medical Centers}

While the various physician specialty societies and academic medical centers may collaborate with and make recommendations during this process, through the provision of appropriate reviewers, input received does not represent an endorsement or position statement by the physician specialty societies or academic medical centers, unless otherwise noted.

In response to requests, input was received from 4 specialty societies and 2 academic medical centers, for a total of 8 reviewers, while this policy was under review for 2015. The review was limited to input related to the use of genetic testing for infantile- and early-childhood-onset epileptic encephalopathies. There was a consensus that genetic testing for early-onset epileptic encephalopathies is medically necessary. Particular areas of clinical utility noted by reviewers included making specific treatment decisions in \textit{SCN1A}-related epilepsies and avoiding other diagnostic tests and for reproductive planning for multiple types of early-onset epilepsies.

\textbf{Practice Guidelines and Position Statements}

\textbf{American Academy of Neurology et al}

In 2006, the American Academy of Neurology and Child Neurology Society published joint guidelines on the diagnostic assessment of children with status epilepticus.\textsuperscript{57} These guidelines were reviewed and reaffirmed in 2016. With regard to whether genetic testing should be routinely ordered for children with status epilepticus, the guidelines stated: “There is insufficient evidence to support or refute whether such studies should be done routinely.”

In 2000, American Academy of Neurology, Child Neurology Society, and the American Epilepsy Society published joint guidelines for evaluating a first nonfebrile seizure in children.\textsuperscript{58} This guidance was reviewed and reaffirmed in 2014. Routine electroencephalography was recommended as part of the diagnostic evaluation; genetic testing was not addressed.

\textbf{International League Against Epilepsy}

In 2015, the International League Against Epilepsy issued a report with recommendations on the management of infantile seizures, which included the following related to genetic testing in epilepsy\textsuperscript{30}:

- “Genetic screening should not be undertaken at a primary or secondary level of care, as the screening to identify those in need of specific genetic analysis is based on tertiary settings.”
- “Standard care should permit genetic counseling by trained personnel to be undertaken at all levels of care (primary to quaternary).”
- “Genetic evaluation for Dravet syndrome and other infantile-onset epileptic encephalopathies should be available at tertiary and quaternary levels of care (optimal intervention would permit an extended genetic evaluation).”
- “Early diagnosis of some mitochondrial conditions may alter long-term outcome, but whether screening at quaternary level is beneficial is unknown.”
European Federation of Neurological Societies

In 2010, the European Federation of Neurological Societies issued guidelines on the molecular diagnosis of channelopathies, epilepsies, migraine, stroke, and dementias. The guidelines made the following recommendations on epilepsy:

“There is good evidence to suggest that a thorough clinical and electrophysiological investigation may lead to the choice of the gene to be tested in patients with periodic paralysis (Level B). In myotonic disorders, it is recommended to first search for myotonic dystrophy and use clinical and electrophysiological phenotype characterization to guide for molecular genetic testing (Level B).

Molecular investigations are possible and may help in some cases to diagnose the condition but cannot be considered as a routine procedure with regard to the large number of different mutations [variants] in different genes. Furthermore, diagnosis can be made more easily by clinical and physiological investigation (Good Practice Point). One exception of note is the diagnosis of severe myoclonic epilepsy of infancy (SMEI), in which mutations [variants] are found in SCN1A in 80% of the patients (Level B).”

U.S. Preventive Services Task Force Recommendations

Not applicable.

Medicare National Coverage

There is no national coverage determination. In the absence of a national coverage determination, coverage decisions are left to the discretion of local Medicare carriers.

Ongoing and Unpublished Clinical Trials

Three ongoing trials that might influence this review are listed in Table 17.

Table 17. Summary of Key Trials

<table>
<thead>
<tr>
<th>NCT No.</th>
<th>Trial Name</th>
<th>Planned Enrollment</th>
<th>Completion Date</th>
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</thead>
<tbody>
<tr>
<td>Ongoing</td>
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<td></td>
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<tr>
<td>NCT02883712</td>
<td>Study of Predictors of Response to Anti-Epilepsy in Epilepsy (RESISTANT)</td>
<td>1000</td>
<td>Dec 2019</td>
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<tr>
<td>NCT01858285</td>
<td>Genetics of Epilepsy and Related Disorders</td>
<td>1000</td>
<td>Dec 2020</td>
</tr>
<tr>
<td>Unpublished</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>NCT00552045</td>
<td>Epilepsy Phenome/Genome Project: a Phenotype/Genotype Analysis of Epilepsy</td>
<td>4150</td>
<td>Oct 2018 (completed)</td>
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</table>

NCT: national clinical trial.

REFERENCES


CODES

<table>
<thead>
<tr>
<th>Codes</th>
<th>Number</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>CPT</td>
<td></td>
<td>See Policy Guidelines</td>
</tr>
</tbody>
</table>

Original Policy Date: November 2013
**ICD-10-CM** | G40.001-G40.919 | Epilepsy code range  
**ICD-10-PCS** |  | Not applicable. ICD-10-PCS codes are only used for inpatient services. There are no ICD procedure codes for laboratory tests.  
**Type of service** | Laboratory  
**Place of service** | Outpatient  

**POLICY HISTORY**

<table>
<thead>
<tr>
<th>Date</th>
<th>Action</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>03/12/15</td>
<td>Replace policy</td>
<td>Policy updated with results of clinical input. Policy statement added that genetic testing for early-onset epileptic encephalopathy syndromes may be considered medically necessary with conditions. References 1 and 40 added.</td>
</tr>
<tr>
<td>11/12/15</td>
<td>Replace policy</td>
<td>Policy updated with literature review through October 12, 2015; references 15-18, 32, 35-37, 44, and 49-50 added. Medically necessary policy statement edited to clarify that testing refers to testing for mutations associated with early-onset epileptic encephalopathies.</td>
</tr>
<tr>
<td>02/24/17</td>
<td>Replace policy</td>
<td>Policy updated with literature review through December 21, 2016; references 9, 15-16, 20-21, 26-29, 31, 39, 44, 47, and 59-61 added. The policy is revised with updated genetics nomenclature. Policy statements unchanged.</td>
</tr>
<tr>
<td>06/08/17</td>
<td>Replace policy – correction only</td>
<td>Tables 4 and 7 removed.</td>
</tr>
<tr>
<td>02/26/18</td>
<td>Replace policy</td>
<td>Blue Cross of Idaho adopted changes as noted. Policy updated with literature review through December 11, 2017; reference 19 added; reference 29 updated. Policy statements unchanged.</td>
</tr>
<tr>
<td>02/21/19</td>
<td>Replace policy</td>
<td>Blue Cross of Idaho adopted changes as noted, effective 02/21/2019. Policy updated with literature review through December 6, 2018; references 19-20, and 34-37 added. Policy statements unchanged.</td>
</tr>
</tbody>
</table>

**Original Policy Date:** November 2013