Genetic Testing for Limb-Girdle Muscular Dystrophies

Policy # 00489  
Original Effective Date: 01/22/2016  
Current Effective Date: 07/19/2017

Applies to all products administered or underwritten by Blue Cross and Blue Shield of Louisiana and its subsidiary, HMO Louisiana, Inc. (collectively referred to as the “Company”), unless otherwise provided in the applicable contract. Medical technology is constantly evolving, and we reserve the right to review and update Medical Policy periodically.

When Services May Be Eligible for Coverage
Coverage for eligible medical treatments or procedures, drugs, devices or biological products may be provided only if:

- Benefits are available in the member’s contract/certificate, and
- Medical necessity criteria and guidelines are met.

Based on review of available data, the Company may consider genetic testing for genes associated with limb-girdle muscular dystrophy (LGMD) to confirm a diagnosis of limb-girdle muscular dystrophy (LGMD) when signs and symptoms of limb-girdle muscular dystrophy (LGMD) are present but a definitive diagnosis cannot be made without genetic testing to be eligible for coverage.

Note: The most common genes associated with LGMD may include CAPN3 (81406), DYSF (81408), SGCA, SGCB, SGCD, SGCG (81405), FKRP (81404), CAV3 (81404), and LMNA (81406).

Patient Selection Criteria
Coverage eligibility for genetic testing for genes associated with limb-girdle muscular dystrophy (LGMD) to confirm a diagnosis of limb-girdle muscular dystrophy (LGMD) when signs and symptoms of limb-girdle muscular dystrophy (LGMD) are present but a definitive diagnosis cannot be made without genetic testing will be considered when at least one of the following criteria are met:

- Results of testing may lead to changes in clinical management that improve outcomes (eg, confirming or excluding the need for cardiac surveillance); OR
- Genetic testing will allow the affected patient to avoid invasive testing, including muscle biopsy.

Targeted genetic testing for a known familial variant associated with limb-girdle muscular dystrophy (LGMD) in an asymptomatic individual to determine future risk of disease may be considered eligible for coverage when the following criteria are met:

- The individual has a close (ie, first- or second-degree) relative with a known familial variant consistent with limb-girdle muscular dystrophy (LGMD);
- Results of testing will lead to changes in clinical management (eg, confirming or excluding the need for cardiac surveillance).

Genetic testing for genes associated with limb-girdle muscular dystrophy (LGMD) in an asymptomatic individual to determine future risk of disease may be considered eligible for coverage when the following criteria are met:

- The individual has a close (ie, first- or second-degree) relative diagnosed with limb-girdle muscular dystrophy (LGMD) whose genetic status is unavailable;
Genetic Testing for Limb-Girdle Muscular Dystrophies

Policy # 00489
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AND

- Results of testing will lead to changes in clinical management (eg, confirming or excluding the need for cardiac surveillance).

Note: The most common genes associated with LGMD may include CAPN3 (81406), DYSF (81408), SGCA, SGCB, SGCD, SGCG (81405), FKRP (81404), CAV3 (81404), and LMNA (81406).

When Services Are Considered Investigational
Coverage is not available for investigational medical treatments or procedures, drugs, devices or biological products.

Based on review of available data, the Company considers Genetic testing for mutations associated with limb-girdle muscular dystrophy (LGMD) in all other situations to be investigational.*

The use of Genetic testing for mutations associated with limb-girdle muscular dystrophy (LGMD) when patient selection criteria are not met is considered to be investigational.*

Background/Overview
MUSCULAR DYSTROPHIES
Muscular dystrophies are a group of inherited disorders characterized by progressive weakness and degeneration of skeletal muscle, cardiac muscle, or both, which may be association with respiratory muscle involvement or dysphagia and dysarthria. Muscular dystrophies (MDs) are associated with a wide spectrum of phenotypes, which may range from rapidly progressive weakness leading to death in the second or third decade of life to clinically asymptomatic disease with elevated creatine kinase (CK) levels. Muscular dystrophies have been classified on the basis of clinical presentation and genetic etiology. The most common are the dystrophinopathies, Duchenne (DMD) and Becker (BMD) muscular dystrophies, which are characterized by pathogenic variants in the dystrophin gene. Other MDs are characterized by the location of onset of clinical weakness and include the LGMDs, facioscapulohumeral MD, oculopharyngeal MD, distal MD, and humeroperoneal MD (also known as Emery-Dreifuss MD). Congenital MD is a genetically heterogeneous group of disorders, which historically included infants with hypotonia and weakness at birth and findings of MD on biopsy. Finally, myotonic dystrophy is a multisystem disorder characterized by skeletal muscle weakness and myotonia in association with cardiac abnormalities, cognitive impairment, endocrinopathies, and dysphagia.

Limb-Girdle Muscular Dystrophies
The term limb-girdle muscular dystrophy is a clinical descriptor for a group of MDs characterized by predominantly proximal muscle weakness (pelvic and shoulder girdles) that may be included in the differential diagnosis of DMD and BMD. Onset can be in childhood or adulthood. The degree of disability depends on the location and degree of weakness. Some LGMD subtypes are characterized by only mild, slowly progressive weakness, while others are associated with early-onset, severe disease with loss of ambulation. Limb-girdle muscular dystrophies may be associated with cardiac dysfunction, cardiomyopathy.
Genetic Testing for Limb-Girdle Muscular Dystrophies

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(dilated or hypertrophic), respiratory depression, and dysphagia or dysarthria. Of particular note is the risk of cardiac complications, which is a feature of many but not all LGMDs. Most patients have an elevated CK.

Limb-girdle muscular dystrophies have an estimated prevalence ranging from 2.27 to 4 per 100,000 in the general population, constituting the fourth most prevalent MD type after the dystrophinopathies (DMD and BMD), facioscapulohumeral MD, and myotonic dystrophy. The prevalence of specific types increases in populations with founder pathogenic variants (eg, Finland, Brazil).

**Genetic Basis and Clinical Correlation**

As the genetic basis of the LGMDs has been elucidated, it has been recognized that there is tremendous heterogeneity in genetic variants that cause the LGMD phenotype. Limb-girdle muscular dystrophies were initially classified based on a clinical and locus-based system. As of 2015, at least 9 autosomal dominant types (designated LGMD1A through LGMD1H) and at least 23 autosomal recessive types (designated LGMD2A through LGMD2W) have been identified. Subtypes vary in inheritance, pathophysiology, age of onset, and severity. Table 1 summarizes involved gene and protein, clinical characteristics (if known), and proportions of all cases represented by a specific genotype (if known).

**Table 1. Summary of Genetic Basis of LGMD (Adapted From Norwood et al [2007], Mahmood et al [2014], Nigro et al [2011], Nigro et al [2014], Pegoraro & Hoffman [2000])**

<table>
<thead>
<tr>
<th>LGMD Type</th>
<th>Involved Gene</th>
<th>Involved Protein</th>
<th>Age at Onset</th>
<th>Rate of Progression</th>
<th>Cardiac Involvement?</th>
<th>Percent AR LGMD Cases</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Autosomal dominant</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1A</td>
<td>MYOT</td>
<td>Myotilin</td>
<td>Adulthood</td>
<td>Slow</td>
<td>Yes</td>
<td></td>
</tr>
<tr>
<td>1B</td>
<td>LMNA</td>
<td>Lamin A/C</td>
<td>Adolescence or variable</td>
<td>Slow</td>
<td>Yes</td>
<td></td>
</tr>
<tr>
<td>1C</td>
<td>CAV3</td>
<td>Caveolin-3</td>
<td>Variable</td>
<td>Slow</td>
<td>Yes</td>
<td></td>
</tr>
<tr>
<td>1D</td>
<td>DNAJB6</td>
<td>DNAJ/Hsp40 homolog</td>
<td>Adulthood</td>
<td>Slow</td>
<td>No</td>
<td></td>
</tr>
<tr>
<td>1E</td>
<td>DES</td>
<td>Desmin</td>
<td>Adulthood</td>
<td>Slow</td>
<td>Yes</td>
<td></td>
</tr>
<tr>
<td>1F</td>
<td>TNPO3</td>
<td>Transportin3</td>
<td>Variable</td>
<td>Slow</td>
<td>No</td>
<td></td>
</tr>
<tr>
<td>1G</td>
<td>HNRPDL</td>
<td>Heterogeneous nuclear ribonucleoprotein D-like protein</td>
<td>Adulthood</td>
<td>Slow</td>
<td>No</td>
<td></td>
</tr>
<tr>
<td>1H</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Autosomal recessive</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2A</td>
<td>CAPN3</td>
<td>Calpain 3</td>
<td>Adolescence to adulthood</td>
<td>Moderate</td>
<td>Rare</td>
<td>=10% to =40%</td>
</tr>
<tr>
<td>2B</td>
<td>DYSF</td>
<td>Dysferlin</td>
<td>Adolescence to adulthood</td>
<td>Slow</td>
<td>Yes</td>
<td>=5% to =25%</td>
</tr>
<tr>
<td>2C</td>
<td>SGCG</td>
<td>γ-sarcoglycan</td>
<td>Early childhood</td>
<td>Rapid</td>
<td>Yes</td>
<td>68% with childhood</td>
</tr>
<tr>
<td>2D</td>
<td>SGCA</td>
<td>α-sarcoglycan</td>
<td>Early childhood</td>
<td>Rapid</td>
<td>Yes</td>
<td>onset; =10%</td>
</tr>
<tr>
<td>2E</td>
<td>SGCB</td>
<td>β-sarcoglycan</td>
<td>Early childhood</td>
<td>Rapid</td>
<td>Yes</td>
<td>with adult onset</td>
</tr>
<tr>
<td>2F</td>
<td>SGCD</td>
<td>δ-sarcoglycan</td>
<td>Early childhood</td>
<td>Rapid</td>
<td>Yes</td>
<td></td>
</tr>
<tr>
<td>2G</td>
<td>TCAP</td>
<td>Telethonin</td>
<td>Adolescence</td>
<td>Slow</td>
<td>Yes</td>
<td>3%</td>
</tr>
<tr>
<td>2H</td>
<td>TRIM32</td>
<td>Tripartite motif containing 32</td>
<td>Adulthood</td>
<td>Slow</td>
<td>No</td>
<td></td>
</tr>
<tr>
<td>2I</td>
<td>FKRP</td>
<td>Fukutin-related protein</td>
<td>• &lt;10 to &gt;40 y • Late childhood or variable</td>
<td>Moderate</td>
<td>Yes</td>
<td>6%</td>
</tr>
<tr>
<td>2J</td>
<td>TTN</td>
<td>Titin</td>
<td>Young adulthood</td>
<td>Rapid</td>
<td>No</td>
<td></td>
</tr>
<tr>
<td>2K</td>
<td>POMT1</td>
<td>Protein-O-mannosyltransferase 1</td>
<td>Childhood</td>
<td>Slow</td>
<td>No</td>
<td></td>
</tr>
</tbody>
</table>
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<table>
<thead>
<tr>
<th>LGMD Type</th>
<th>Involved Gene</th>
<th>Involved Protein</th>
<th>Age at Onset</th>
<th>Rate of Progression</th>
<th>Cardiac Involvement?</th>
<th>Percent AR LGMD Cases</th>
</tr>
</thead>
<tbody>
<tr>
<td>2L</td>
<td>ANO5</td>
<td>Anoctamin-5</td>
<td>Variable</td>
<td>Slow</td>
<td>No</td>
<td>25% in U.K.</td>
</tr>
<tr>
<td>2M</td>
<td>FKTN</td>
<td>Fukutin</td>
<td>Early childhood</td>
<td>Slow/moderate</td>
<td>Yes</td>
<td></td>
</tr>
<tr>
<td>2N</td>
<td>POMT2</td>
<td>Protein-O-</td>
<td>Early childhood</td>
<td>Slow/moderate</td>
<td>Rare</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>mannosyltransferase 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2O</td>
<td>POMGnT1</td>
<td>Protein O-linked</td>
<td>Late childhood</td>
<td>Moderate</td>
<td>No</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>mannose beta1, 2-Nacetyl-</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>glucosaminyl-transferase</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2P</td>
<td>DAG1</td>
<td>Dystroglycan</td>
<td>Early childhood</td>
<td>Moderate</td>
<td>No</td>
<td></td>
</tr>
<tr>
<td>2Q</td>
<td>PLEC1</td>
<td>Plectin</td>
<td>Early childhood</td>
<td>Slow</td>
<td>No</td>
<td></td>
</tr>
<tr>
<td>2R</td>
<td>DES</td>
<td>Desmin</td>
<td>Young adulthood</td>
<td></td>
<td>Yes (AV conduction block)</td>
<td></td>
</tr>
<tr>
<td>2S</td>
<td>TRAPPC1</td>
<td>Transport protein particle</td>
<td>Young adulthood</td>
<td>Slow</td>
<td>No</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>complex 11</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2T</td>
<td>GMPPB</td>
<td>GDP-mannose</td>
<td>Early childhood to</td>
<td>Yes</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>pyrophosphorylase B</td>
<td>young adulthood</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2U</td>
<td>ISPD</td>
<td>Isoprenoid</td>
<td>Variable</td>
<td>Moderate/rapid</td>
<td>Yes</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>synthase domain containing</td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>2V</td>
<td>GAA</td>
<td>Glucosidase, α-1</td>
<td>Variable</td>
<td>Variable</td>
<td>Yes</td>
<td></td>
</tr>
<tr>
<td>2W</td>
<td>LIMS2</td>
<td>Lim and senescent cell</td>
<td>Childhood</td>
<td></td>
<td>Yes</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>antigen-like domains 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>


The prevalence of different variants and LGMD subtypes can differ widely by country, but the autosomal recessive forms are generally more common. Pathogenic variants in **CAPN3** represent 20% to 40% of LGMD cases, and LGMD2A is the most frequent LGMD in most countries. **DYSF** pathogenic variants leading to LGMD2B are the second most common LGMD in many, but not all, areas (15%-25%). Sarcoglycanopathies constitute about 10% to 15% of all LGMDs, but 68% of the severe forms.

In an evaluation of 370 patients with suspected LGMD enrolled in a registry from 6 U.S. university centers, 312 of whom had muscle biopsy test results available, Moore et al (2006) reported the distribution of LGMD subtypes based on muscle biopsy results as follows: 12% LGMD2A, 18% LGMD2B, 15% LGMD2C-2F, and 1.5% LGMD1C.

**Clinical Variability**

Other than presentation with proximal muscle weakness, LGMD subtypes can have considerable clinical variability in terms of weakness severity and associated clinical conditions. The sarcoglycanopathies (LGMD2C-2F) cause a clinical picture similar to that of the intermediate forms of DMD and BMD, with risk of cardiomyopathy in all forms of the disease.

Of particular clinical importance is that fact that while most, but not all, LGMD subtypes are associated with an increased risk of cardiomyopathy, arrhythmia, or both, the risk of cardiac disorders varies across subtypes. LGMD1A, LGMD1B, LGMB2C-K, and LGMD2M-P have all been associated with cardiac involvement. Sarcoglycan variants tend to be associated with severe cardiomyopathy. Similarly, patients with the LGMD subtypes of LGMD2I and 2C-2F are at higher risk of respiratory failure.
Many of the genes associated with LGMD subtypes have allelic disorders, both with neuromuscular disorder phenotypes and clinically unrelated phenotypes. Variants in the lamin A/C proteins, which are caused by splice-site variants in the *LMNA* gene, are associated with different neuromuscular disorder phenotypes, including Emery-Dreifuss MD, a clinical syndrome characterized by childhood-onset elbow, posterior cervical, and ankle contractures and progressive humeroperoneal weakness, autosomal dominant LGMD (LGMD1B), and congenital MD. All forms have been associated with cardiac involvement, including atrial and ventricular arrhythmias and dilated cardiomyopathy.

**Clinical Diagnosis**

A diagnosis of LGMD is suspected in patients who have myopathy in the proximal musculature in the shoulder and pelvic girdles, but the distribution of weakness and the degree of involvement of distal muscles varies, particularly early in the disease course. Certain LGMD subtypes may be suspected on the basis of family history, patterns of weakness, CK levels, and associated clinical findings. However, there is considerable clinical heterogeneity and overlap across the LGMD subtypes.

Without genetic testing, diagnostic evaluation can typically lead to a general diagnosis of a LGMD, with limited ability to determine the subcategory. Most cases of LGMD will have elevated CK levels, with some variation in the degree of elevation based on subtype. Muscle imaging with computed tomography (CT) or magnetic resonance imaging (MRI) may be obtained to assess areas of involvement and guide muscle biopsy. Magnetic resonance imaging or CT may be used to evaluate patterns of muscle involvement. At least for calpainopathy (LGMD2A) and dysferlinopathy (LGMD2B), MRI may show patterns distinct from other neuromuscular disorders, including hyaline body myopathy and myotonic dystrophy. In 1 study (2012) that evaluated muscle CT in 118 patients with LGMD and 32 controls, there was generally poor overall interobserver agreement ($\kappa=0.27$), and low sensitivity (40%) and specificity (58%) for LGMD.

Electromyography (EMG) has limited value in LGMD, although it may have clinical utility if there is clinical concern for type III spinal muscular atrophy. Electromyography typically shows myopathic changes with small polyphasic potentials.

Muscle biopsy may be used in suspected LGMD to rule out other, treatable causes of weakness (in some cases), and to attempt to identify a LGMD subtype. All LGMD subtypes are characterized on muscle biopsy by dystrophic features, with degeneration and regeneration of muscle fibers, variation in fiber size, fiber splitting, increased numbers of central nuclei, and endomysial fibrosis. Certain subtypes, particularly in dysferlin deficiency (LGMD2B), may show inflammatory infiltrates, which may lead to an inaccurate diagnosis of polymyositis.

Following standard histologic analysis, immunohistochemistry and immunoblotting are typically used to evaluate myocyte protein components, which may include sarcolemma-related proteins (eg, α-dystroglycan, sarcoglycans, dysferlin, caveolin-3), cytoplasmic proteins (eg, calpain-3, desmin), or nuclear proteins (eg, lamin A/C). Characteristic findings on muscle biopsy immunostaining or immunoblotting can be seen for calpainopathy (LGMD2A), sarcoglycanopathies (LGMD2C-2F), dysferlinopathy (LGMD2B), and O-linked glycosylation defects (dystroglycanopathies; LGMD2I, LGMD2K, LGMD2M, LGMD2O, LGMD2N). However, muscle biopsy is imperfect: secondary deficiencies in protein expression can be seen in some LGMD. In the
Genetic Testing for Limb-Girdle Muscular Dystrophies

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2006 Moore study (previously described), 9% of all muscle biopsy samples had reduced expression of more than 1 protein tested. In some types of variants, muscle immunohistochemistry results may be misleading because the variant leads to normal protein amounts but abnormal function. For example, Western blot analysis for calpain 3, with loss of all calpain 3 bands, may be diagnostic of LGMD2A, but the test is specific but not sensitive, because some LGMD2A patients may retain normal amounts of nonfunctional protein.

A blood-based dysferlin protein assay, which evaluates dysferlin levels in peripheral blood CD14+ monocytes, has been evaluated in a sample of 77 individuals with suspected dysferlinopathy. However, the test is not yet in widespread use.

Treatment
At present, no therapies have been clearly shown to slow the progression of muscle weakness for the LGMDs. Treatment is focused on supportive care to improve muscle strength, slow decline in strength, preserve ambulation, and treat and prevent musculoskeletal complications that may result from skeletal muscle weakness (eg, contractures, scoliosis). Clinical management guidelines are available from the American Academy of Neurology (AAN) and Association of Neuromuscular & Electrodiagnostic Medicine (AANEM).

Monitoring for Complications
Different genetic variants associated with clinical LGMD are associated with different rates of complications and the speed and extent of disease progression.

Monitoring for respiratory depression and cardiac dysfunction is indicated for LGMD subtypes associated with respiratory or cardiac involvement, because patients are often asymptomatic until they have significant organ involvement. When respiratory depression is present, patients may be candidates for invasive or noninvasive mechanical ventilation. Treatments for cardiac dysfunction potentially include medical or device-based therapies for heart failure or conduction abnormalities.

Patients may need monitoring and treatment for swallowing dysfunction, if it is present, along with physical and occupational therapy and bracing for management of weakness.

Investigational Therapies
A number of therapies are under investigation for LGMD. Glucocorticoids have been reported to have some benefit in certain subtypes (LGMD2D, LGMD2I, LGMD2L). However, 1 small (N=25) randomized, double-blind, placebo-controlled trial (2013) of the glucocorticoid deflazacort in patients with genetically confirmed LGMD2B (dysferlinopathy) showed no benefit and a trend toward worsening strength associated with deflazacort therapy. Autologous bone marrow transplant has been investigated for LGMD, but is not in general clinical use. Adeno-associated virus-mediated gene transfer to the extensor digitorum brevis muscle has been investigated in LGMD2D, and in a phase 1 trial in LGMD2C. Exon-skipping therapies have been investigated as a treatment for dysferlin gene variants (LGMD2B) given the gene’s large size.
Molecular Diagnosis

Because most variants leading to LGMD are single-nucleotide variants, the primary method of variant detection is gene sequencing using Sanger sequencing or next generation sequencing (NGS) methods. In cases in which a LGMD is suspected but gene sequencing is normal, deletion/duplication analysis through targeted comparative genomic hybridization or multiplex ligation–dependent probe amplification (MLPA) may also be obtained.

A number of laboratories offer panels of tests for LGMD that rely on Sanger sequencing or NGS. The following list is not exhaustive.

- GeneDx (LGMD Panel; Gaithersburg, MD): NGS, with reporting only on panel genes, with concurrent targeted array comparative genomic hybridization (aCGH) analysis to evaluate for deletions/duplications for most genes (exceptions, GMPPB and TNPO3). Multiplex polymerase chain reaction (PCR) assay is performed to assess for the presence of the 3’ untranslated region insertion in the FKTN gene. All reported sequence variants are confirmed by conventional di-deoxy DNA sequence analysis, quantitative PCR, MLPA, repeat PCR analysis, or another appropriate method.
- Prevention Genetics offers several LGMD tests. They include an autosomal dominant LGMD Sanger sequencing panel, which includes MYOT, LMNA, DNAJB6, and CAV3 sequencing either individually or as a panel, followed by aCGH for deletions/duplications. The company also offers an autosomal recessive LGMD Sanger sequencing panel, which includes sequencing of SGCG, SGCA, SGCB, SGCD, TRIM32, CAPN3, DYSF, FKRP, TTN, TCAP, GMPPB, ANO5, and TRAPPC11, either individually or as a panel, followed by aCGH for deletions/duplications. In addition, Prevention Genetics offers 2 NGS panels for LGMD, which involve NGS followed by aCGH if variant analysis is negative. Additional Sanger sequencing is performed for any regions not captured or with insufficient number of sequence reads. All pathogenic, undocumented and questionable variant calls are confirmed by Sanger sequencing.
- Counsyl offers a Family Prep Screen, which includes testing for multiple diseases that may require early intervention or cause shortened life or intellectual disability and is designed to be used for carrier testing in reproductive planning. Testing for LGMD2D and LGMD2E may be added to the panel. Testing is conducted by NGS, without evaluation for large duplications or deletions
- Centogene (Rostock, Germany) offers an NGS panel for LGMD, which includes sequencing of the included variants (with hot spot testing for TTN), followed by deletion/duplication testing by MLPA (if ordered), with whole exome sequencing if no variants are identified.
- Athena Diagnostics offers NGS testing for FKRP, LMNA, DYSF, CAV3, and CAPN3 (NGS followed by dosage analysis), along with a NGS panel, with deletion/duplication testing for SGCA, SGCG, and CAPN3.

Variants included in some of the currently available NGS testing panels are summarized in Table 2.

### Table 2. LGMD Variants Included in Commercial NGS Test Panels

<table>
<thead>
<tr>
<th>Gene</th>
<th>GeneDx</th>
<th>Prevention Genetics</th>
<th>Centogene</th>
<th>Athena Diagnostics^b</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Autosomal Dominant^a</td>
<td>Autosomal Recessive</td>
<td></td>
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</tr>
</tbody>
</table>

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<table>
<thead>
<tr>
<th>Gene</th>
<th>X</th>
<th>X</th>
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<th>X</th>
</tr>
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<tbody>
<tr>
<td>MYOT</td>
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<tr>
<td>CAV3</td>
<td>X</td>
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<td>X</td>
</tr>
<tr>
<td>DNAJB6</td>
<td>X</td>
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LGMD: limb-girdle muscular dystrophy; NGS: next-generation sequencing.

a This panel also includes testing for SMCHD1, which is associated with facioscapulohumeral muscular dystrophy

b This panel also includes testing for PNPLA2, which is associated with neutral lipid storage disease with myopathy, and TOR1AIP1.

FDA or Other Governmental Regulatory Approval

U.S. Food and Drug Administration (FDA)
Clinical laboratories may develop and validate tests in-house and market them as a laboratory service; laboratory-developed tests (LDTs) must meet the general regulatory standards of the Clinical Laboratory Improvement Amendments (CLIA). Tests from laboratories such as GeneDx, Prevention Genetics, Centogene, Counsyl, and Athena Diagnostics are offered under the auspices of CLIA. Laboratories that offer LDTs must be licensed by CLIA for high-complexity testing. To date, the U.S. FDA has chosen not to require any regulatory review of this test.

Centers for Medicare and Medicaid Services (CMS)
There is no national coverage determination (NCD). In the absence of an NCD, coverage decisions are left to the discretion of local Medicare carriers.
Genetic Testing for Limb-Girdle Muscular Dystrophies

Policy # 00489
Original Effective Date: 01/22/2016
Current Effective Date: 07/19/2017

**Rationale/Source**
Validation of the clinical use of any diagnostic test focuses on 3 main principles: (1) analytic validity of the test (ie, the technical performance of the test); (2) clinical validity (ie, the diagnostic performance of the test, eg, sensitivity, specificity, and positive and negative predictive values) in different populations of patients and compared with the criterion standard; and (3) clinical utility of the test (ie, how the results of the diagnostic test will be used to improve patient management). Following is a summary of the key literature to date.

**TESTING INDIVIDUALS WITH SIGNS OR SYMPTOMS OF LIMB-GIRDLE MUSCULAR DYSTROPHY**

**Clinical Context and Test Purpose**
The purpose of genetic testing of individuals with suspected LGMD is to establish the diagnosis of LGMD, direct treatment, and monitor based on a genetic diagnosis. Changes in management may include discontinuation of routine cardiac and/or respiratory surveillance in the absence of a specific genetic diagnosis with specific complications, avoidance of therapies not known to be efficacious for LGMD, potential avoidance of invasive testing, and informing reproductive decision making.

The question addressed in this evidence review is: In individuals with suspected LGMD, does use of the genetic testing result eliminate or reduce the need for a muscle biopsy, need for cardiac and/or respiratory surveillance, and lead to improved health outcomes?

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

**Patients**
The relevant population of interest includes individuals with signs or symptoms of LGMD.

**Interventions**
Genetic testing of genes associated with LGMD.

**Comparators**
Standard diagnostic workup without genetic testing.

**Outcomes**
The general outcomes of interest include overall survival, test accuracy and validity, changes in reproductive decision making, change in disease status, and morbidity events.

The potential beneficial outcomes of primary interest would be reductions in muscle biopsies to confirm diagnosis of LGMD and whether changes in management are initiated based on confirming a genetic diagnosis of LGMD.

Potential harmful outcomes are those resulting from a false-positive or false-negative test results. False-positive test results can lead to inappropriate initiation of treatments or psychological harm after receiving positive test results. False-negative test results can lead to lack of cardiac and/or respiratory surveillance.
Genetic Testing for Limb-Girdle Muscular Dystrophies

Policy # 00489
Original Effective Date: 01/22/2016
Current Effective Date: 07/19/2017

Setting
The time frame for outcomes measures varies from short-term changes in disease status or changes in cardiac and/or respiratory surveillance to long-term changes in outcomes.

Setting
Patients suspected of LGMD are actively managed by neurologists. Genetic testing is used to confirm a diagnosis of LGMD. Referral for genetic counseling is important for explanation of genetic disease, heritability, genetic risk, test performance, and possible outcomes.

Analytic Validity
Analytic validity refers to the technical accuracy of a test in detecting a variant that is present or in excluding a variant that is absent.

Sanger sequencing is expected to have high analytic validity. For next-generation sequencing (NGS) panels, the analytic validity is expected to be very high. One laboratory offering NGS panel has reported an analytic sensitivity that exceeds 99% for single-nucleotide variants (SNVs) and insertions and deletions of less than 20 base pairs. Other laboratories offering NGS panels have similarly reported sensitivities greater than 99%.

Less information was identified on the analytic validity of MLPA or comparative genomic hybridization (CGH) for the detection of large deletions and duplications. Piluso et al (2011) described the development and analytic validation of a customized exon-specific oligonucleotide CGH array focusing on genes involved in neuromuscular disorders, including 26 MD–related genes (specific variants not specified), 34 DYSF-interacting variants and 10 TRIM32-interacting variants. They reported 100% concordance between variants detected with the novel array and those detected by other methods.

Section Summary: Analytic Validity
The analytic validity of genetic testing for LGMD is expected to be high with Sanger sequencing and NGS for the detection of SNVs in LGMD-associated genes. Given that most variants for LGMD are SNVs, initial genetic testing with Sanger or NGS is also expected to be high. When genetic testing with Sanger or NGS is negative, information on other molecular techniques (MLPA, CGH) to detect other classes of genetic variants (eg, copy number variants) is limited.

Clinical Validity
Clinical validity refers to the diagnostic performance of a test (sensitivity, specificity, positive and negative predictive values).

For LGMD, clinical validity may refer to the overall yield of testing for any LGMD-associated variant in patients with clinically suspected disease, or the yield of testing for specific variants. The genetic test is generally considered the criterion standard for determining a specific LGMD subtype.
Unselected LGMD Populations

One potential role for genetic testing in LGMD is assessment of patients with clinically suspected LGMD, but who do not necessarily have results of a muscle biopsy available.

In 2014, the AAN and AANEM published joint guidelines on the diagnosis and treatment of limb-girdle and distal dystrophies, which included a systematic review of studies that assessed the yield of genetic testing for LGMD in patients who present with suspected MD. The available studies for each gene variant are heterogeneous, but the types of studies available, and the study size and population included (if described), are summarized in Table 3. Class I studies include statistical, population-based samples of patients studied at a uniform point in time (usually early) during the course of the condition, with all patients undergoing the intervention of interest, and with outcomes determined in an evaluation that is masked to patients’ clinical presentations. Class II studies are similar to class I, but the patient population is a non-referral-clinic-based sample, and most, not all, patients undergo the intervention of interest. Class III studies include samples of patients studied during the course of the condition, some of whom undergo the intervention of interest, and in whom the outcome is determined by someone other than the treating physician.

Table 3. Genetic Testing Yield in Patients With Suspected LGMD (Adapted From Narayanaswami et al)²¹

<table>
<thead>
<tr>
<th>LGMD Type</th>
<th>Involved Protein</th>
<th>Evidence Base</th>
<th>Population</th>
<th>Variant Detection Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>LGMD1A</td>
<td>Myotilin</td>
<td>1 class I study</td>
<td>1105 patients with genetic muscle disorders; 68 with LGMD</td>
<td>No myotilin variants among patients with LGMD</td>
</tr>
<tr>
<td></td>
<td></td>
<td>3 class III studies</td>
<td>Not described</td>
<td>&lt;1% to 1.7%</td>
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<tr>
<td>LGMD1B</td>
<td>Lamin A/C</td>
<td>1 class I study</td>
<td>1105 patients with genetic muscle disorders; 68 with LGMD</td>
<td>8.8% of all muscle disorder cases</td>
</tr>
<tr>
<td></td>
<td></td>
<td>9 class III studies</td>
<td>Patients with clinical LGMD</td>
<td>0.9%-4%</td>
</tr>
<tr>
<td>LGMD1C</td>
<td>Caveolin-3</td>
<td>3 class III studies</td>
<td>Not described</td>
<td>1.3%-2.6%</td>
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<tr>
<td>LGMD2A</td>
<td>Calpain-3</td>
<td>2 class I studies</td>
<td>1105 patients with genetic muscle disorders; 68 with LGMD</td>
<td>26.5% of all LGMD cases</td>
</tr>
<tr>
<td></td>
<td></td>
<td>84 patients with unknown MD</td>
<td>46.4%</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>19 class III studies</td>
<td>Not described</td>
<td>6%-57%; most series reporting 18.5%-35%</td>
</tr>
<tr>
<td>LGMD2B</td>
<td>Dysferlin</td>
<td>1 class I study</td>
<td>1105 patients with genetic muscle disorders; 68 with LGMD</td>
<td>5.9% of LGMD cases</td>
</tr>
<tr>
<td></td>
<td></td>
<td>11 class III studies</td>
<td>Not described</td>
<td>0.6%-33% of LGMD</td>
</tr>
<tr>
<td>LGMD2C</td>
<td>γ-sarcoglycan</td>
<td>2 class I studies</td>
<td>1105 patients with genetic muscle disorders; 68 with LGMD</td>
<td>5.9% of all muscle disorder cases</td>
</tr>
<tr>
<td></td>
<td></td>
<td>204 patients with dystrophy on muscle biopsy and normal dystrophin</td>
<td>2%</td>
<td></td>
</tr>
<tr>
<td></td>
<td>α-sarcoglycan</td>
<td>16 class III studies</td>
<td>Not described</td>
<td>1.3%-13.2%</td>
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<tr>
<td></td>
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<td>2 class I studies</td>
<td>1105 patients with genetic muscle disorders; 68 with LGMD</td>
<td>0.07 per 100,000</td>
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<td>204 patients with dystrophy on muscle biopsy and normal dystrophin</td>
<td>3.4%</td>
<td></td>
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<tr>
<td></td>
<td>β-sarcoglycan</td>
<td>14 class III studies</td>
<td>Not described</td>
<td>3.3%-15%</td>
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<td>2 class I studies</td>
<td>1105 patients with genetic muscle disorders; 68 with LGMD</td>
<td>2.9% of all muscle disorder cases</td>
</tr>
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<td></td>
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<td>204 patients with dystrophy on muscle biopsy and normal dystrophin</td>
<td>1%</td>
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<tr>
<td></td>
<td></td>
<td>13 class III studies</td>
<td>Not described</td>
<td>0%-23%</td>
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</table>
The studies included in the AAN and AANEM systematic review on the prevalence of variants in various populations were heterogeneous in terms of patient populations used. Some representative studies are detailed next.

In 2009, Norwood et al reported on the prevalence of genetic variants in a large population of patients with genetic muscle disorders (included in the AAN and AANEM systematic review). The population included 1105 cases with various inherited muscle diseases diagnosed and treated by at a single neuromuscular clinic, which was considered to be the only neuromuscular disorders referral center for northern England. Of the total patient population, 75.7% (n=836) had a confirmed genetic diagnosis. Myotonic dystrophy was the most commonly represented single diagnosis, representing 28.1% of the total sample, while 22.9% had a dystrophinopathy. Sixty-eight patients had a clinical diagnosis of LGMD, of whom 43 (6.15%) had positive genetic testing for a gene associated with LGMD. Of patients with a clinical diagnosis of LGMD, 72.1% had positive genetic testing, most commonly for LGMD2A (26.5%; 95% confidence interval [CI], 16.0% to 37.0%).

Variable Gene Expression
For some LGMD subtypes, there is variable expressivity for a given gene variant, which has been characterized in several retrospective analyses of the clinical features of patients with a specific gene.
variant. Maggi et al (2014) conducted a retrospective cohort analysis to characterize the clinical phenotypes of myopathic patients (n=78) and nonmyopathic patients with LMNA variants (n=78). Of the 78 myopathic patients, 37 (47%) had an LGMD phenotype (LGMD1B), 18 (23%) had congenital MD, 17 (22%) had autosomal dominant Emery-Dreifuss MD, and 6 (8%) had an atypical myopathy. Of the myopathic patients, 54 (69.2%) had cardiac involvement and 41 (52.6%) received an implantable cardioverter defibrillator (ICD). Among 30 family members without myopathy but with LMNA variants, 20 (66.7%) had cardiac involvement, and 35% underwent ICD placement. Among all patients, frameshift variants were associated with a higher risk of heart involvement.

Sarkozy et al (2013) evaluated the prevalence of ANO5 variants and associated clinical features among 205 patients without a genetic diagnosis but with a clinical suspicion of ANO5 variant (or LGMD2L), who were evaluated at a single European center. A clinical suspicion of the ANO5 variant (anoctaminopathy) could have been based on clinical examination, muscle assessment, and clinical evaluations including CK analysis, EMG, muscle MRI, and/or muscle biopsy. ANO5 gene sequence variants were identified in 90 (44%) unrelated individuals and 5 affected relatives. Sixty-one percent of variants were a c.191dupA variant, which is a founder variant found in most British and German LGMD2L patients. Age of onset was variable, ranging from teens to late 70s, with lower-limb predominance of symptoms. Three individuals with ANO5 variants had very mild clinical disease, and 1 patient was asymptomatic, but no specific genotype-phenotype correlations were demonstrated.

**Panel Testing**

Ghosh et al (2012) described the yield of a LGMD panel, which included testing for genes associated with lamin A/C (LGMD1B), caveolin-3 (LGMD1C), calpain-3 (LGMD2A), dysferlin (LGMD2B), the sarcoglycans (LGMD2C-2F), and Fukutin-related protein (LGMD2I), among 27 patients with a clinical suspicion of LGMD seen at a single center. Ten (37%) patients had positive testing, most commonly for LGMD2A (n=4). The testing yield was higher among children (3/6 [50%] patients tested), although the sample was very small.

**LGMD Patients With Muscle Biopsy Results**

A smaller number of studies have evaluated the yield of genetic variant testing for LGMD in patients suspected of having a particular LGMD subtype on the basis of muscle biopsy.

In 2009, Fanin et al evaluated the yield of molecular diagnostics among 550 cases with specific LGMD-related phenotypes, including severe childhood-onset LGMD, adult-onset LGMD, distoproximal myopathy, and asymptomatic hyper-CK-emia, who had undergone muscle biopsy with multiple protein screening. Prior to muscle biopsy, testing of all patients had excluded recent physical exercise or toxic or endocrinologic causes of myopathy. Dystrophinopathy was also excluded in all cases. Muscle biopsy samples underwent a systematic evaluation of calpain-3 (for LGMD2A), dysferlin (for LGMD2B), and α-sarcoglycan (for LGMD2D) by immunoblotting and of caveolin-3 (for LGMD1C) by immunohistochemistry. Calpain-3 autolytic activity was also evaluated using a functional in vitro assay. Genetic testing of DYSF, CAPN3, sarcoglycans, FKRP, and LMNA was conducted single-strand conformational polymorphism or denaturing high-performance liquid chromatography analysis, which are older methods of gene variant analysis. Of the 550 cases with muscle biopsies, 122 had childhood-onset LGMD, 186 had adult-onset LGMD, 38 had distoproximal myopathy, and 204 had asymptomatic hyper-CK-emia. In the entire cohort, a molecular
Genetic Testing for Limb-Girdle Muscular Dystrophies

Policy # 00489
Original Effective Date: 01/22/2016
Current Effective Date: 07/19/2017

diagnosis (positive genetic testing) was made in 234 (42.5%) cases, most commonly a calpain-3 variant, consistent with LGMD2A. Excluding patients with asymptomatic hyper-CK-emia, a molecular diagnosis was made in 205 cases (59.2% of 346 with a LGMD phenotype). Patients with childhood-onset LGMD were more likely to have a molecular diagnosis (94/122 [77.0%]). Of the 226 patients with a protein abnormality on muscle biopsy, 193 (85.4%) had a genetic diagnosis.

In an earlier, smaller study, Guglieri et al (2008) reported on results from molecular diagnostic testing for a series of 181 patients (155 families) with clinical signs of LGMD and muscle biopsy with dystrophic features. The genetic testing yield varied by muscle biopsy protein (Western blotting and immunohistochemistry) findings: among 72 subjects with calpain-3 deficiency on protein testing, the variant detection rate was 61%, compared with 93.5% of the 31 subjects with dysferlin deficiency, 87% (for any sarcoglycan gene variant) of the 32 subjects with sarcoglycan deficiency, and 100% of the 52 subjects with caveolin-3 deficiency. The frequency of LGMD subtypes was as follows: LGMD1C (caveolin-3) 1.3%; LGMD2A (calpain-3) 28.4%; LGMD2B (dysferlin) 18.7%; LGMD2C (γ-sarcoglycan) 4.5%; LGMD2D (α-sarcoglycan) 8.4%; LGMD2E (β-sarcoglycan) 4.5%; LGMD2F (δ-sarcoglycan) 0.7%; LGMD2I (Fukutin-related protein) 6.4%; and undetermined 27.1%.

In another small study, Fanin et al (2009) reported on rates of sarcoglycan gene variants among 18 subjects with MD and α-sarcoglycan deficiency assessed using immunohistochemistry and immunoblotting of muscle biopsy samples. Pathogenic variants in 1 gene involved in the sarcoglycan complex were identified in 13 patients.

Krahn et al (2009) evaluated the testing yield for DYSF variants in a cohort of 134 patients who had a clinical phenotype consistent with LGMD2B, loss or strong reduction of dysferlin protein expression on muscle biopsy Western blot and/or immunohistochemistry, or both. DYSF variants known to be associated with myopathy were detected in 89 (66%) patients. Bartoli et al (2014) reported on results of whole exome sequencing in a follow up analysis of 37 patients who had negative targeted DYSF variant testing. In 5 (13.5%) cases, molecular diagnosis could be made directly by identification of compound heterozygous or homozygous variants previously associated with LGMD on whole exome sequencing, including 2 CAPN3 variants, 1 ANO5 variant, 1 GNE variant, and 1 DYSF variant, with 1 additional case requiring additional Sanger sequencing for complete identification.

Section Summary: Clinical Validity

Estimates of the genetic testing yield for variants associated with LGMD vary by the variants included and the characteristics of the patient populations tested. The true clinical sensitivity and specificity of genetic testing for LGMD variants in general cannot be determined, because there is no criterion standard test for diagnosing LGMD. Studies have reported genetic testing yields ranging from 37% to greater than 70% in patients with clinically suspected LGMD. The criterion standard for diagnosing a LGMD subtype is the genetic test. The specificity of a positive LGMD genetic test result in predicting the clinical phenotype of LGMD is not well-defined. However, there is some evidence to support a finding that some variants associated with LGMD predict the presence of cardiac complications.
Clinical Utility

Clinical utility is how the results of a diagnostic test will be used to change management of a patient and whether these changes in management lead to clinically important improvements in health outcomes.

The clinical utility of testing for variants associated with LGMD for an index case (a patient with clinically suspected LGMD) includes:

- Confirming the diagnosis of LGMD and initiating and directing treatment of the disease, including evaluation by a cardiologist with cardiac testing, respiratory function testing and monitoring, and prevention of secondary complications (e.g., through immunizations, physical therapy or bracing, fracture risk reduction).
- Avoidance of treatments that might be initiated for other neuromuscular disorders not known to be efficacious for LGMD, such as glucocorticoids for suspected dystrophinopathy or immunosuppressants for suspected myositis.
- Potential discontinuation of routine cardiac and respiratory surveillance in patients who have an identified variant not known to be associated with cardiac or respiratory dysfunction.
- Potential avoidance of invasive testing (e.g., muscle biopsy).
- Reproductive planning.

The clinical utility of testing for variants associated with LGMD for an at-risk family member (i.e., first- or second-degree relative of a proband) includes:

- Confirming or excluding the need for cardiac surveillance.
- Reproductive planning in individuals considering offspring who would alter reproductive decision making based on test results.

Management of Cardiac Complications

Similar to Duchenne and Becker MDs, patients with LGMD are at higher risk of cardiac abnormalities, including dilated cardiomyopathy (DCM) and various arrhythmias. Specific LGMD subtypes are more likely to be associated with cardiac disorders. Potential device-based therapies for patients at risk of arrhythmias include cardiac pacing and implantation of an ICD. Guidelines from the American College of Cardiology, American Heart Association, and Heart Rhythm Society on the use of device-based therapy of cardiac rhythm abnormalities published in 2008 recommended that indications for a permanent pacemaker address the presence of MD. These guidelines have recommended considering implantation of a permanent pacemaker for patients with LGMD with any degree of atrioventricular (AV) block (class IIb recommendation; level of evidence: B), or bifascicular block or any fascicular block (class IIb recommendation; level of evidence: C), with or without symptoms, because there may be unpredictable progression of AV conduction disease.

Certain LGMD subtypes are more strongly associated with cardiac disorders than others. LGMD types 2C through 2F and 2I are associated with a primary DCM, with conduction disorders occurring as a secondary phenomenon. Other LGMD subtypes are recognized not to have associations with cardiomyopathy or conduction disorders. In these cases, recommendations from AAN and AANEM have indicated that routine cardiac surveillance in asymptomatic individuals is not required.
Genetic Testing for Limb-Girdle Muscular Dystrophies

Policy # 00489
Original Effective Date: 01/22/2016
Current Effective Date: 07/19/2017

There is clinical utility for identifying a specific LGMD gene variant for patients presenting with signs and symptoms of LGMD to allow discontinuation of cardiac surveillance in patients found to have a variant not associated with cardiac disorders.

On the other hand, there may be clinical utility for testing of asymptomatic family members of a proband with an identified LGMD variant to determine cardiovascular risk. Patients with LMNA variants, regardless of whether they have an LGMD1B phenotype, are at risk for cardiac arrhythmias. Similarly, FKTN variants can be associated with DCM, with or without the presence of myopathy. Murakami et al (2006) reported a cases series of 6 patients from 4 families with compound heterozygous FKTN variants who presented with DCM and no or minimal myopathic symptoms.

**Section Summary: Clinical Utility**
In patients with clinically suspected LGMD, genetic testing is primarily to confirm a diagnosis, but may also have a prognostic role given the clinical variability across LGMD subtypes. For asymptomatic but at-risk family members, testing may also confirm a diagnosis or allow prediction of symptoms. No direct evidence exists on the impact of testing on outcomes. However, a chain of evidence suggests that the establishment of a specific genetic diagnosis has the potential to change clinical management.

**TARGETED TESTING OF ASYMPTOMATIC RELATIVES OF AN INDIVIDUAL WITH LGMD AND A FAMILIAL VARIANT**

**Clinical Context and Test Purpose**
The purpose of genetic testing of asymptomatic first- and second-degree relatives of an individual with LGMD and a known familial variant is to determine carrier or genetic status to confirm or exclude the need for cardiac surveillance and inform the reproductive planning process.

The question addressed in this evidence review is: In individuals with suspected LGMD, does use of the genetic testing result lead to reductions in unnecessary cardiac surveillance and lead changes in reproductive planning?

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

**Patients**
The relevant population of interest includes asymptomatic first- and second-degree relatives of a patient with LGMD and a known familial variant.

**Interventions**
The relevant intervention of interest is targeted familial variant testing.

**Comparators**
The relevant comparator of interest is standard diagnostic workup without genetic testing.
Outcomes
The general outcomes of interest include overall survival, test accuracy and validity, changes in reproductive decision making, change in disease status, and morbid events.

The potential beneficial outcomes of primary interest would be confirming or excluding the need for cardiac surveillance based on LGMD subtype and changes in reproductive planning.

Setting
The time frame for outcome measures varies from short-term changes in the development of symptoms, disease status, or changes in cardiac function to long-term improvements in outcomes or to changes in reproductive decision making.

In asymptomatic individuals, evaluation may occur in pediatrics, primary care, or neurology due to the variability in clinical presentation and age of onset. Genetic testing is used to confirm a genetic status of a known familial variant. If the known familial variant is detected, referral to cardiology is important to initiate cardiac surveillance if the specific LGMD subtype is associated with the development of cardiac symptoms. Referral for genetic counseling is important for explanation of genetic disease, heritability, genetic risk, test performance, and possible outcomes.

Analytic Validity
See the discussion of analytic validity in the Testing Individuals With Signs or Symptoms of LGMD section above.

Clinical Validity
See the discussion of clinical validity in the Testing Individuals With Signs or Symptoms of LGMD section above.

Clinical Utility
Genetic testing of asymptomatic individuals with a first- or second-degree relation with LGMD may have clinical utility in:

- Confirming or excluding the need for cardiac surveillance based on the presence or absence of a known familial variant.
- Informing the reproductive decision-making process for preimplantation testing and/or prenatal (in utero) testing when a known familial variant is present in a parent. Preimplantation testing is addressed elsewhere.

GENETIC TESTING IN ASYMPTOMATIC RELATIVES OF AN INDIVIDUAL WITH LGMD AND UNKNOWN GENETIC STATUS
Clinical Context and Test Purpose
The purpose of genetic testing of asymptomatic first- and second-degree relatives of individuals with LGMD whose genetic status is unknown is to determine carrier or genetic status to confirm or exclude the need for cardiac surveillance and inform the reproductive planning process.
The question addressed in this evidence review is: In individuals with suspected LGMD, does use of the genetic testing result lead to reductions in unnecessary cardiac surveillance and to changes in reproductive planning?

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

**Patients**
The relevant population of interest includes asymptomatic first- and second-degree relatives of a patient with LGMD whose genetic status is unknown.

**Interventions**
The relevant intervention of interest is genetic testing for genes associated with LGMD.

**Comparators**
The relevant comparator of interest is standard diagnostic workup without genetic testing.

**Outcomes**
The general outcomes of interest include overall survival, test accuracy and validity, changes in reproductive decision making, change in disease status, and morbid events. The potential beneficial outcomes of primary interest would be confirming or excluding the need for cardiac surveillance based on LGMD subtype and changes in reproductive planning.

**Setting**
The time frame for outcome measures varies from short-term changes in development of symptoms, disease status, or changes in cardiac function to long-term improvements in outcomes or to changes in reproductive decision making.

**Setting**
In asymptomatic individuals, evaluation may occur in pediatric, primary care, or neurology departments due to the variability in clinical presentation and age of onset. Genetic testing is used to confirm the genetic status of a pathogenic variant in a LGMD-associated gene. If the pathogenic variant in a LGMD-associated gene is detected, referral to cardiology is important to initiate cardiac surveillance if the specific LGMD subtype is associated with the development of cardiac symptoms. Referral for genetic counseling is important for explanation of genetic disease, heritability, genetic risk, test performance, and possible outcomes.

**Analytic Validity**
See the discussion of analytic validity in the Testing Individuals With Signs or Symptoms of LGMD section above.

**Clinical Validity**
See the discussion of clinical validity in the Testing Individuals With Signs or Symptoms of LGMD section above.
Clinical Utility
Genetic testing of asymptomatic individuals with first- and second-degree relations with LGMD whose genetic status in unknown may have clinical utility in:

- Confirming or excluding the need for cardiac surveillance based on the presence or absence of a pathogenic variant in a LGMD-associated gene.
- Informing the reproductive decision-making process for preimplantation testing and/or prenatal (in utero) testing when a pathogenic variant in a LGMD-associated gene is present in a parent. Preimplantation testing is addressed elsewhere.

SUMMARY OF EVIDENCE
For individuals who have signs or symptoms of LGMD who receive genetic testing for LGMD-associated genes, the evidence includes systematic reviews, case series, and genotype-phenotype correlations evaluating the clinical validity and yield of genetic testing. Relevant outcomes are overall survival, test accuracy and validity, changes in reproductive decision making, change in disease status, and morbid events. The analytic validity of genetic testing for LGMD-associated genes is likely to be high. The true clinical sensitivity and specificity of genetic testing for LGMD in general cannot be determined. While the yield of genetic testing in patients with clinically suspected LGMD varies by population characteristics (ie, patients with only clinical symptoms vs patients with biopsy findings suggestive of LGMD), the available body of evidence suggests that testing yield is reasonably high. Genetic testing is generally considered the criterion standard for diagnosis of a specific LGMD subtype. For patients with clinically suspected LGMD, there is clinical utility in genetic testing to confirm a diagnosis of LGMD and direct treatment and monitoring on the basis of a specific genetic diagnosis (including discontinuation of routine cardiac and/or respiratory surveillance if a specific genetic diagnosis not associated with these complications can be made), to avoid therapies not known to be efficacious for LGMD, potentially to avoid invasive testing, and to allow reproductive planning. The evidence is sufficient to determine that the technology results in a meaningful improvement in the net health outcome.

For individuals who are asymptomatic with a first- or second-degree relative with LGMD with a known familial variant who receive targeted familial variant testing, the evidence is limited. Relevant outcomes are overall survival, test accuracy and validity, changes in reproductive decision making, change in disease status, and morbid events. Published data on the analytic and clinical validity for testing for a known familial variant are lacking, but the validity is expected to be high. Direct evidence on the clinical utility of LGMD-associated familial variant testing in asymptomatic relatives is lacking. However, the chain of evidence is strong, because determination of carrier status for a LGMD familial variant necessitates or eliminates the need for routine cardiac surveillance and can indicate the likelihood of an affected offspring in women considering children. The evidence is sufficient to determine that the technology results in a meaningful improvement in the net health outcome.

For individuals who are asymptomatic with a first- or second-degree relative with LGMD whose genetic status is unknown who receive genetic testing for LGMD-associated genes, the evidence is limited. Relevant outcomes are overall survival, test accuracy and validity, changes in reproductive decision making, change in disease status, and morbid events. Published data for the analytic and clinical validity of testing for a known familial variant are lacking, but the validity is expected to be high. Direct evidence on the
clinical utility of genetic testing for LGMD-associated genes in asymptomatic relatives is lacking. However, the chain of evidence is strong, because determination of carrier status for a LGMD pathogenic variant necessitates or eliminates the need for routine cardiac surveillance and can indicate the likelihood of an affected offspring in women considering children. The evidence is sufficient to determine that the technology results in a meaningful improvement in the net health outcome.

References
 genetic testing for limb-girdle muscular dystrophies

Policy # 00489
Original Effective Date: 01/22/2016
Current Effective Date: 07/19/2017


Policy History
Original Effective Date: 01/22/2016
Current Effective Date: 07/19/2017
01/07/2016 Medical Policy Committee review
01/22/2016 Medical Policy Implementation Committee approval. New Policy.
01/01/2017 Coding update: Removing ICD-9 Diagnosis Codes
07/06/2017 Medical Policy Committee review
07/19/2017 Medical Policy Implementation Committee approval. The policy is revised with updated genetics nomenclature. “Mutations” changed to “variants” in policy statements. Removed coverage statement with criteria for genetic testing in the reproductive setting. Coverage statements updated to separate “targeted familial variant testing” and “genetic testing of LGMD-associated genes” in asymptomatic individuals. Added a “Note” in two places to the coverage to include the most common genes associated with LGMD. Policy title changed to “Genetic Testing for Limb-Girdle Muscular Dystrophies”, so that “Genetic” replaces “Mutation”.

Next Scheduled Review Date: 07/2018
Genetic Testing for Limb-Girdle Muscular Dystrophies

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<tr>
<td>CPT</td>
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*Investigational – A medical treatment, procedure, drug, device, or biological product is Investigational if the effectiveness has not been clearly tested and it has not been incorporated into standard medical practice. Any determination we make that a medical treatment, procedure, drug, device, or biological product is Investigational will be based on a consideration of the following:
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B. Whether the medical treatment, procedure, drug, device, or biological product requires further studies or clinical trials to determine its maximum tolerated dose, toxicity, safety, effectiveness, or effectiveness as compared with the standard means of treatment or diagnosis, must improve health outcomes, according to the consensus of opinion among experts as shown by reliable evidence, including:
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   2. Credible scientific evidence published in peer-reviewed medical literature generally recognized by the relevant medical community; or
   3. Reference to federal regulations.

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A. In accordance with nationally accepted standards of medical practice;
B. Clinically appropriate, in terms of type, frequency, extent, level of care, site and duration, and considered effective for the patient's illness, injury or disease; and
C. Not primarily for the personal comfort or convenience of the patient, physician or other health care provider, and not more costly than an alternative service or sequence of services at least as likely to produce equivalent therapeutic or diagnostic results as to the diagnosis or treatment of that patient's illness, injury or disease.

For these purposes, “nationally accepted standards of medical practice” means standards that are based on credible scientific evidence published in peer-reviewed medical literature generally recognized by the relevant medical community, Physician Specialty Society recommendations and the views of Physicians practicing in relevant clinical areas and any other relevant factors.

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