Corporate Medical Policy

Genetic Testing for Duchenne, Becker, Facioscapulohumeral, Limb-Girdle Muscular Dystrophies AHS – M2074

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Description of Procedure or Service

Muscular dystrophies, genetic conditions characterized by progressive muscle atrophy, can be caused by a number of genetic mutations, including mutations to the dystrophin gene on the X chromosome in the cases of Duchenne muscular dystrophy (DMD) and Becker muscular dystrophy (BMD) (Darras, 2018a) or to a contraction of the polymorphic macrosatellite repeat D4Z4 on chromosome 4q35, resulting in facioscapulohumeral muscular dystrophy (FSHD) (Darras, 2018b).

DMD, the more severe of the dystrophin-related muscular dystrophies, typically presents in males as toddlers. Patients rarely survive beyond their thirties due to respiratory insufficiency or cardiomyopathy. Unlike DMD, BMD is less severe with patients presenting symptoms typically in their teens or even adulthood; moreover, patients typically survive beyond thirty years (Darras, 2018a).

In FSHD, an autosomal dominant disorder, the contraction of the macrosatellite repeat D4Z4 results in an inappropriate expression of the DUX4 (double homeobox protein 4) gene, which alters chromatin structure. FSHD has also been linked to DNA hypomethylation. Symptoms include muscle weakness in the face, arms, legs, abdomen, and scapula with a variable age of onset; however, 90% of patients are affected by the age of 20. Disease progression is typically more slow than DMD with a normal or near-normal life span (Darras, 2018b).

The limb-girdle muscular dystrophies (LGMDs) are a group of more than 30 rare hereditary progressive neuromuscular disorders (Murphy & Straub, 2015) characterized by predominantly proximal distribution of weakness in the pelvic and shoulder girdles. LGMDs result from mutations in genes required for normal muscle function and vary in severity, phenotype, pathology, and age of onset (Darras, 2018c).

***Note: This Medical Policy is complex and technical. For questions concerning the technical language and/or specific clinical indications for its use, please consult your physician.

Policy

BCBSNC will provide coverage for genetic testing for Duchenne, Becker, facioscapulohumeral and limb-girdle muscular dystrophies when it is determined the medical criteria or reimbursement guidelines below are met.

Benefits Application

This medical policy relates only to the services or supplies described herein. Please refer to the Member's Benefit Booklet for availability of benefits. Member's benefits may vary according to benefit design; therefore member benefit language should be reviewed before applying the terms of this medical policy.
When Genetic Testing for Duchenne, Becker, Facioscapulohumeral and Limb-Girdle Muscular Dystrophies is covered

1. Genetic testing for DMD gene mutations is considered medically necessary under the following conditions:
   A. In a male with signs and symptoms of a dystrophinopathy in order to confirm the diagnosis and direct treatment.
   B. For at-risk female relatives: (At-risk females are defined as first- and second-degree female relatives and include the proband’s mother, female siblings of the proband, female offspring of the proband, the proband’s maternal grandmother, maternal aunts and their offspring).
      i. To confirm or exclude the need for cardiac surveillance
      ii. For preconception testing to determine the likelihood of an affected offspring in a woman considering a pregnancy

2. Genetic testing for facioscapulohumeral muscular dystrophy is considered medically necessary to confirm a diagnosis in a patient with clinical signs of the disease.

3. Genetic testing for mutations associated with limb-girdle muscular dystrophy (LGMD) to confirm a diagnosis of LGMD is considered medically necessary when signs and symptoms of LGMD are present but a definitive diagnosis cannot be made without genetic testing, and when the results of testing may lead to changes in clinical management that improve outcomes (e.g., confirming or excluding the need for cardiac surveillance) or genetic testing will allow the affected patient to avoid invasive testing, including muscle biopsy.

4. Genetic testing for mutations associated with limb-girdle muscular dystrophy (LGMD) in the reproductive setting is considered medically necessary when:
   A. There is a diagnosis of LGMD in one or both of the parents, AND
   B. Results of testing will allow informed reproductive decision making.

5. Genetic testing for mutations associated with LGMD is considered medically necessary in an asymptomatic individual to determine future risk of disease when both the following criteria (A & B) are met:
   A. The individual has:
      i. A close relative (i.e., first- or second-degree relative) with a known mutation consistent with LGMD; OR
      ii. A close relative (i.e., first- or second-degree relative) diagnosed with LGMD whose genetic status is unavailable.
   B. Results of testing will lead to changes in clinical management (e.g., confirming or excluding the need for cardiac surveillance.)
When Genetic Testing for Duchenne, Becker, Facioscapulohumeral and Limb-Girdle Muscular Dystrophies is not covered

1. Genetic testing for DMD gene mutations is considered investigational in all other situations.

2. Genetic testing for facioscapulohumeral muscular dystrophy is considered investigational for all other indications.

3. Genetic testing for mutations associated with LGMD is considered investigational in all other situations.

Policy Guidelines

Background

Duchenne and Becker Muscular Dystrophies

Dystrophinopathies, such as DMD and BMD, are due to mutations in the dystrophin gene, DMD, located on the X-chromosome inherited in a recessive pattern. All hemizygous males will exhibit the characteristic phenotype whereas females heterozygous for a pathogenic mutation may exhibit a range of clinical manifestations. Dystrophinopathies are classified as either DMD or BMD if primarily skeletal muscles are affected; however, if primarily cardiac muscle is affected, then it is characterized as DMD-associated dilated cardiomyopathy (DCM) (Darras, Urion, & Ghosh, 2018).

DMD, the more severe phenotype of the skeletal muscle dystrophinopathies, typically presents in males before the age of five with progressive, symmetric muscle weakness usually with calf hypertrophy. Affected males are usually wheelchair-dependent before their teens, and the individual rarely survives beyond their thirties due to respiratory complications and heart failure. BMD is often less severe and manifests later in affected individuals with most individuals remaining ambulatory into adulthood. Some patients have been reported to remain ambulatory as late as their 60s. Even though skeletal muscle deterioration progresses more slowly in BMD, affected individuals do have a shortened life expectancy, typically due to cardiomyopathy, with a mean age of death in the mid-40s (Darras et al., 2018).

DMD or BMD should be suspected in males presenting with the clinical symptoms of a dystrophinopathy who have elevated serum creatine phosphokinase (CK) levels. Males with DMD or BMD have elevated serum CK concentrations (>10-times of normal and >5-times of normal, respectively) since the dystrophic muscle fibers release CK. CK levels in patients with advanced disease progression can have a decrease in serum CK due to the loss of dystrophic muscle fibers. Even hemizygous female carriers can exhibit elevated serum CK levels (2-10 times of normal) (Darras et al., 2018).

Clinical Validity and Utility of DMD/BMD Genetic Testing

A recent Chinese study (H. Wang et al., 2017) of 146 at-risk pregnancies in 131 DMD families report a 99% mutation detection rate using “a prenatal diagnosis algorithm for dystrophinopathies that combines multiplex ligation-dependent probe amplification (MLPA), quantitative PCR, sequencing and linkage analyses.” Their data also show that 51.1% of the probands had de novo exon deletions. Recombination of the DMD gene occurred in 9 of the 146 pregnancies. The authors conclude, “The present results demonstrate the importance of considering maternal germline mosaicism in the genetic assessment. Prenatal diagnosis should be suggested to the parent with a DMD proband whether carrier testing found the causative mutation in the mother’s blood or not (H. Wang et al., 2017).” The reported accuracy rate of this multiplex/quantitative PCR-based method is considerably higher than the reported accuracy rate (>70%) of a real-time PCRA assay of the DMD gene (Zhang et al., 2013).
Genetic Testing for Duchenne, Becker, Facioscapulohumeral, Limb-Girdle Muscular Dystrophies AHS – M2074

MLPA-based genetic testing of dystrophinopathies has been reported in many studies with varying degrees of sensitivity. A large study of 1053 Chinese DMD/BMD patients using MLPA testing reported identifying 70.56% of the probands (Yang et al., 2013) whereas a smaller study of 121 individuals (both male and female) reports confirmation of only 63% of patients and symptomatic females (Luce et al., 2016). A third study of using an algorithm of mPCR and MLPA on 150 male patients reported a 75% confirmation rate (Murugan, Chandramohan, & Lakshmi, 2010). Another study using MLPA concluded, “The reading-frame rule held in 90% to 94% of children, which is consistent with reports from other parts of the world. However, testing by MLPA is a limitation, and advanced sequencing methods including analysis of the structure of mutant dystrophin is needed for more-accurate assessments of the genotype-phenotype correlation (Vengalil et al., 2017).”

Facioscapulohumeral Muscular Dystrophy

Facioscapulohumeral muscular dystrophy (FSHD), an autosomal dominant genetic disorder, is caused by a deletion of the macrosatellite repeat regions D4Z4 of the DUX4 gene in the subtelomeric region of chromosome 4q. In healthy individuals, the DUX4 gene is epigenetically silenced in somatic tissues; however, contraction of the D4Z4 repeats allows for inefficient chromatin silencing due to abnormal chromatin structure, resulting in inappropriate somatic expression. Unaffected individuals have a variable number of D4Z4 repeats, ranging from 11 to more than 100, whereas FSHD1 patients have only 1 – 10 repeats on one of the copies of chromosome 4. The DUX4 protein is usually only expressed in the germline as a DNA-binding protein with presumed transcription factor activity. Its toxicity in somatic cells is unknown. Two forms of FSHD have been classified—FSHD1, the major form due to a major contraction of the D4Z4 macrosatellite repeat sequences, and FSHD2, a minor form with a normal number of D4Z4 repeats but abnormal D4Z4 chromatin structure. FSHD2 patients have a disease status that cannot be confirmed by using the standard molecular diagnostic testing used in FSHD1 patients (van der Maarel, Tawil, & Tapscott, 2011). 85% of patients with FSHD2 have mutations in the SMCHD1 gene on chromosome 18, which encodes for a chromatin modifier believed to be involved in maintaining the D4Z4 chromatin structure (R. J. Lemmers et al., 2012).

FSHD patients exhibit a progressive muscular dystrophy with variability of affected muscles between patients. Generally, muscles of the face, arms, legs, shoulders, and abdomen can be affected. Serum-based diagnostic testing for FSHD has been elusive. A cross-sectional study by Petek and colleagues, using high-throughput proteomics, show that the levels of creatine kinase MM and MB isofoms, carbonic anhydrase III, and troponin I type 2 were elevated at least 1.5-fold in affected individuals and correlated with the severity and state of disease (Petek et al., 2016). Because of the variability of FSHD, genetic testing is still “the preferred diagnostic choice” (Lemmers, O’Shea, Padberg, Lunt, & van der Maarel, 2012).

Methylation of the D4Z4 regions also plays a role in disease expression and progression (Haynes, Bomsztyk, & Miller, 2018; Mul et al., 2018; van der Maarel et al., 2011). A study by Mul and colleagues researched the clinical variability of FSHD1 patients for possible linkage between the severity of disease, the repeat array size of D4Z4, and D4Z4 methylation. Unsurprisingly, unaffected gene carriers had both a higher number of array repeats and a higher methylation levels. One interesting result is that the location of the affected body region did show a correlation between disease severity and DNA modification. “The D4Z4 repeat array size and D4Z4 methylation contribute to variability in disease severity and penetrance, but other disease modifying factors must be involved as well. The larger effect of the D4Z4 repeat array on facial muscle involvement suggests that these muscles are more sensitive to the influence of the FSHD1 locus itself, whereas leg muscle involvement seems highly dependent on modifying factors (Mul et al., 2018).”

Clinical Validity and Utility of FSHD Genetic Testing

The data on the clinical validity and utility of FSHD genetic testing is limited. The American Academy of Neurology and the American Association of Neuromuscular & Electrodiagnostic
Genetic Testing for Duchenne, Becker, Facioscapulohumeral, Limb-Girdle Muscular Dystrophies AHS – M2074

Medicine released their joint guidelines stating the following: “Our systematic review identified 9 Class III studies from specialty clinics that, together, demonstrate that the finding of a D4Z4 contraction on chromosome 4q35 likely has a sensitivity of 93% and a specificity of 98% for diagnosis of clinically defined FSHD (Tawil et al., 2015).” A 2010 study of more than 800 individuals, however, question the criteria for the molecular diagnosis of FSHD. They found that 3% of asymptomatic, healthy individuals actually had a reduced number of D4Z4 repeats, varying 4 to 8 units, on chromosome 4 and that almost one-half of probands had a normal copy number of D4Z4 repeats. “Our results suggest that the genetic basis of FSHD, which is remarkably heterogeneous, should be revisited, because this has important implications for genetic counseling and prenatal diagnosis of at-risk families (Scionti et al., 2012).”

**Limb-Girdle Muscular Dystrophies**

Generally, limb-girdle muscular dystrophies (LGMDs) are uncommon disorders with estimated prevalence ranging from 0.07 per 100,000 to 0.43 per 100,000. The most common LGMD, Becker muscular dystrophy, has an estimated prevalence of 2.38–7.29 per 100,000 (Narayanaswami et al., 2014).

The LGMDs vary widely in their genetics and clinical features ranging from mild forms allowing patients to maintain a fairly normal life to severe deterioration of proximal limb muscles with significant physical weakness and shortened life-span (Monies et al., 2016). Thirty-one loci have been identified so far, eight autosomal dominant and 23 autosomal recessive. The dominant forms (LGMD1) are: LGMD1A (myotilin), LGMD1B (lamin A/C), LGMD1C (caveolin 3), LGMD1D (DNAJB6), LGMD1E (desmin), LGMD1F (transportin 3), LGMD1G (HNRPDL), LGMD1H (chr. 3). The autosomal recessive forms (LGMD2) are: LGMD2A (calpain 3), LGMD2B (dysferlin), LGMD2C (γ sarcoglycan), LGMD2D (α sarcoglycan), LGMD2E (β sarcoglycan), LGMD2F (δ sarcoglycan), LGMD2G (telethonin), LGMD2H (TRIM32), LGMD2I (FKRP), LGMD2J (titin), LGMD2K (POMT1), LGMD2L (anoctamin 5), LGMD2M (fukutin), LGMD2N (POMT2), LGMD2O (POMTnG1), LGMD2P (dystroglycan), LGMD2Q (plectin), LGMD2R (desmin), LGMD2S (TRAPPC11), LGMD2T (GMPPB), LGMD2U (ISPD), LGMD2V (Glucosidase, alpha), LGMD2W (PINCH2)(Nigro & Savarese, 2014).

**Clinical Validity and Utility of LGMD Genetic Testing**

Based on published literature, the clinical validity of genetic testing for LGMD is difficult to ascertain. The yield of genetic testing in patients with signs and symptoms of LGMD varies depending on the mutation and population characteristics. There are some studies that conclude that the clinical validity is reasonably high (Fanin et al., 2009; F. Norwood, de Visser, Eymard, Lochmuller, & Bushby, 2007). According to Norwood et al (2011), “DNA analysis directed to provide confirmation of mutation in the affected gene(s) is the gold standard of diagnosis, and necessary to be able to offer carrier or presymptomatic testing to other family members”.

Monies et al (2016) screened fifty random genetically unstudied families with LGMD with a gene panel incorporating 759 OMIM gene associated with neurological disorders. They found that “Our panel identified the mutation in 76 % of families (38/50; 11 novel). Thirty-four families had mutations in LGMD-related genes with four others having variants not typically associated with LGMD. The majority of cases had recessive inheritance with homoallelic pathogenic variants (97.4 %, 37/38), as expected considering the high rate of consanguinity in the study population.” The authors concluded that the “neurological panel achieved a high clinical sensitivity (76 %) and is an effective first-line laboratory test in patients with LGMD and other myopathies. This sensitive, cost-effective, and rapid assay significantly assists clinical practice especially in these phenotypically and genetically heterogeneous disorders. Moreover, the application of the American College of Medical Genetics (ACMG) and Association for Molecular Pathology (AMP) guidelines applied in the classification of variant pathogenicity provides a clear interpretation for physicians on the relevance of such findings (Monies et al., 2016).”
Genetic Testing for Duchenne, Becker, Facioscapulohumeral, Limb-Girdle Muscular Dystrophies AHS – M2074

Harris et al (2017) performed whole exome sequencing (WES) on 104 patients with LGMD in which standard gene testing had not yet yielded a diagnosis, and 91 patients using sequential gene by gene testing. They found that “Patients selected for WES had undergone more extensive prior testing than those undergoing standard genetic testing and on average had had 8 genes screened already. In this extensively investigated cohort WES identified the genetic diagnosis in 28 families (28/75, 37%), including the identification of the novel gene ZAK and two unpublished genes. WES of a single affected individual with sporadic disease yielded a diagnosis in 13/38 (34%) of cases. In comparison, conventional gene by gene testing provided a genetic diagnosis in 28/84 (33%) families.” The authors concluded that “WES was able to overcome many limitations of standard testing and achieved a higher rate of diagnosis than standard testing even in this cohort of extensively investigated patients. Earlier application of WES is therefore likely to yield an even higher diagnostic rate. We obtained a high diagnosis rate in simplex cases and therefore such individuals should be included in exome or genome sequencing projects. Disease due to somatic mosaicism may be increasingly recognized due to the increased sensitivity of next generation sequencing techniques to detect low level mosaicism (Harris et al., 2017).” A similar study by Reddy and colleagues reported 40% of the LGMD families tested “had novel and previously reported pathogenic mutations, primarily in LGMD genes, and also in genes for Duchenne muscular dystrophy, facioscapulohumeral muscular dystrophy, congenital myopathy, myofibrillar myopathy, inclusion body myopathy and Pompe disease (Reddy et al., 2017).”

Applicable Federal Regulations
No U.S. Food and Drug Administration (FDA)-cleared genotyping tests were found. Thus, genotyping is offered as a laboratory-developed test. These laboratory-developed tests (LDTs) are regulated by the Centers for Medicare and Medicaid (CMS) as high-complexity tests under the Clinical Laboratory Improvement Amendments of 1988 (CLIA ’88). As an LDT, the U. S. Food and Drug Administration has not approved or cleared this test; however, FDA clearance or approval is not currently required for clinical use.

Guidelines and Recommendations

Best Practice Guidelines on molecular diagnostics in Duchenne/Becker muscular dystrophies Workshop report (Abbs et al., 2010)

The international workshop comprised of scientists from Europe, the US, India, and Australia was organized and sponsored by the European Neuro-Muscular Centre, the European Molecular Genetics Quality Network, TREAT-NMD, and Euro-Gentest. The flow chart for the diagnostic work-up of a dystrophinopathy they recommend is shown below in Figure 1 (Abbs et al., 2010).
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Genetic Testing for Duchenne, Becker, Facioscapulohumeral, Limb-Girdle Muscular Dystrophies AHS – M2074

Recommendations for testing are: If there is a clinical suspicion of a dystrophinopathy, first screen for deletions and duplications. If no deletion or duplication is detected, but the clinical diagnosis is verified, screening for point mutations should be performed (Abbs et al., 2010).

The DMD Care Considerations Working Group (Bushby et al., 2010)

The CDC selected 84 clinicians to comprise the DMD Care Considerations Working Group to develop recommendations regarding all aspects of DMD care, including the diagnosis and genetic testing of muscular dystrophy. They state the following: “Testing for a DMD mutation in a blood sample is always necessary even if DMD is first confirmed by the absence of dystrophin protein expression on muscle biopsy. The results of genetic testing provide the clinical information required for genetic counselling, prenatal diagnosis, and consideration for future mutation-specific therapies... If analysis by one or more of these techniques leads to the identification and full characterisation of a dystrophin mutation, then no further testing is required. If deletion/ duplication testing is negative, then dystrophin gene sequencing should be done to look for point mutations or small deletions/insertions. Full characterisation of the mutation (deletion endpoints or exact position of any point mutation) is required to allow correlation of the predicted effect of the mutation on the reading frame of the gene, which is the major determinant of the phenotypic variability seen in dystrophinopathy, as well as to determine eligibility for the mutation-specific treatments currently in trials (Bushby et al., 2010).”

American Academy of Neurology/American Association of Neuromuscular and Electrodiagnostic Medicine (Kang et al., 2015; Narayanaswami et al., 2014)

The Guideline Development Subcommittee of the American Academy of Neurology and the Practice Issues Review Panel of the American Association of Neuromuscular and Electrodiagnostic Medicine published recommendations that “Targeted genetic testing often identifies causative mutations in the classic CMD subtypes... Genetic diagnoses are beneficial to the patient, as they often enable
Genetic Testing for Duchenne, Becker, Facioscapulohumeral, Limb-Girdle Muscular Dystrophies AHS – M2074

physicians to provide more accurate prognoses and facilitate genetic counseling and family-planning discussions, and may enable patients to become more aware of future clinical trials for which they may be eligible”. "When available and feasible, physicians might order targeted genetic testing for specific CMD subtypes that have well-characterized molecular causes” and “In individuals with CMD who either do not have a mutation identified in one of the commonly associated genes or have a phenotype whose genetic origins have not been well characterized, physicians might order whole-exome or whole-genome sequencing when those technologies become more accessible and affordable for routine clinical use” (Kang et al., 2015).

In 2014, the American Academy of Neurology and the Practices Issues review Panel of the American Association of Neuromuscular and Electrodiagnostic Medicine issued evidenced-based guidelines for the diagnosis and treatment of limb-girdle and distal dystrophies, which makes the following recommendations (Narayanaswami et al., 2014):

For the diagnosis of LGMD:

- For patients with suspected muscular dystrophy, clinicians should use a clinical approach to guide genetic diagnosis based on the clinical phenotype, including the pattern of muscle involvement, inheritance pattern, age at onset and associated manifestations (e.g., early contractures, cardiac or respiratory involvement) (Level B recommendation).
- In patients with suspected muscular dystrophy in whom initial clinically directed genetic testing does not provide a diagnosis, clinicians may obtain genetic consultation or perform parallel sequencing of targeted exomes, whole-exome sequencing, whole genome screening, or next-generation sequencing to identify the genetic abnormality (Level C recommendation).

The AAN Guidelines state: “Diagnosis assists in defining the long-term prognosis, since some dystrophies are more rapidly progressive, involve the cardiorespiratory systems more frequently, or are associated with other disorders. The identification of these dystrophies through genetic testing will not only inform long-term prognosis but will also assist in directing care more efficiently (e.g., more frequent cardiorespiratory monitoring and prophylactic treatments such as pacer/defibrillator placement for those disorders known to be associated with cardiac involvement). Precise identification of the disorder also eliminates the need for repeated testing for an acquired, treatable disorder such as an inflammatory myopathy, because some dystrophies have inflammation on muscle biopsy, making diagnosis difficult on the basis of routine biopsy findings. In addition, the temptation to try immunosuppressive agents repeatedly, looking for a therapeutic response, is not unusual when there is no diagnosis and the patient is worsening. This exposes patients to potentially serious side effects of immunosuppressive medications. Patients on immunosuppressants need regular monitoring, adding logistical difficulties to a population that may have significantly impaired mobility. Health care costs are increased by repeated investigations, immunosuppressive treatments, and laboratory monitoring. Although establishing a genetic diagnosis is expensive on the front end, the costs of continued investigation for other causes and the risks and expenses associated with empiric trials of immunosuppressants make a strong case for establishing a genetic diagnosis, which often provides patients a sense of closure. Establishing a genetic diagnosis is crucial for genetic counseling to inform decision-making about having children and for screening of offspring. Treatment of cardiomyopathy, arrhythmias, and ventilatory failure prolongs life and improves quality of life in patients with other neuromuscular diseases (Narayanaswami et al., 2014).”

American Academy of Neurology (Tawil et al., 2015) reaffirmed in 2018 (AAN, 2018)

The American Academy of Neurology published evidence-based guidelines which found that “the finding of a D4Z4 contraction on chromosome 4q35 likely has a sensitivity of 93% and a specificity of 98% for diagnosis of clinically defined FSHD.” They recommend, “Clinicians should obtain genetic confirmation of FSHD1 in patients with atypical presentations and no first-degree relatives with genetic confirmation of the disease [Level B].” Concerning the use of genetics as a predictor of severity in FSHD, they recommend, “Large D4Z4 deletion sizes (contracted D4Z4 allele of 10–20 kb)
Genetic Testing for Duchenne, Becker, Facioscapulohumeral, Limb-Girdle Muscular Dystrophies AHS – M2074

should alert the clinician that the patient is more likely to develop more significant disability and at an earlier age. Patients with large deletions are also more likely to develop symptomatic extramuscular manifestations [Level B] (Tawil et al., 2015)."

International Standard of Care Committee for Congenital Muscular Dystrophy (C. H. Wang et al., 2010)

As a part of the guidelines concerning newly diagnosed patients, they recommend, “if a genetic diagnosis is known, the recurrence risk and impact on future family planning should be discussed. Even if the exact genetic defect is not known, recurrence risk can sometimes be discussed using a common genetic model that is often associated with the diagnosis (C. H. Wang et al., 2010).”

171st European Neuromuscular Centre International Workshop on Standards of Care and Management of Facioscapulohumeral Muscular Dystrophy (FSHD) (R. J. L. F. Lemmers et al., 2012)

In a report from the 171st European Neuromuscular Centre International Workshop Standards of Care and Management of FSHD held in January 2010, it is stated that “when a physician concludes facioscapulohumeral syndrome based on clinical findings, the odds are in favor of FSHD, and genetic testing is the preferred diagnostic choice (R. J. L. F. Lemmers et al., 2012)”.

Billing/Coding/Physician Documentation Information

This policy may apply to the following codes. Inclusion of a code in this section does not guarantee that it will be reimbursed. For further information on reimbursement guidelines, please see Administrative Policies on the Blue Cross Blue Shield of North Carolina web site at www.bcbsnc.com. They are listed in the Category Search on the Medical Policy search page.

*Applicable service codes: 81161, 81400, 81404, 81405, 81406, 81408, 81479*

BCBSNC may request medical records for determination of medical necessity. When medical records are requested, letters of support and/or explanation are often useful, but are not sufficient documentation unless all specific information needed to make a medical necessity determination is included.

Scientific Background and Reference Sources


Genetic Testing for Duchenne, Becker, Facioscapulohumeral, Limb-Girdle Muscular Dystrophies AHS – M2074


Genetic Testing for Duchenne, Becker, Facioscapulohumeral, Limb-Girdle Muscular Dystrophies AHS – M2074


Genetic Testing for Duchenne, Becker, Facioscapulohumeral, Limb-Girdle Muscular Dystrophies AHS – M2074


Policy Implementation/Update Information

1/1/2019  New policy developed. BCBSNC will provide coverage for genetic testing for facioscapulohumeral muscular dystrophy when it is determined to be medically necessary because criteria and guidelines are met. Medical Director review 1/1/2019. Policy noticed 1/1/2019 for effective date 4/1/2019. (jd)

For policy titled: Genetic Testing for Duchenne Becker, Facioscapulohumeral, Limb-Girdle Muscular Dystrophies

4/16/2019  The following policies have been combined to create a single policy concerning the genetic testing for muscular dystrophies: Genetic Testing for Duchenne and Becker Muscular Dystrophy, Genetic Testing for Facioscapulohumeral Muscular Dystrophies AHS – M2076, Mutation Testing for Limb-Girdle Muscular Dystrophies AHS – M2128. These 3 separate policies are archived. Description section, policy guidelines sections updated with language and criteria indications to reflect the combined policies. When Covered and When Not Covered sections revised to include criteria indications from the three original policies; no change to policy intent. Billing/Coding section and referenced updated. Medical Director review 4/2019. (jd)

10/29/19  Wording in the Policy, When Covered, and/or Not Covered section(s) changed from Medical Necessity to Reimbursement language, where needed. (hb)

2/11/20  Annual review by Avalon 4th Quarter 2019 CAB. No revisions and no change to policy intent. Medical Director review 12/2019. (jd)

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