Limb-Girdle Muscular Dystrophy (LGMD) Type 2L: \textit{ANO5} Gene Sequencing

\textbf{Test Code:} SANO5  
\textbf{Turnaround time:} 6 weeks  
\textbf{CPT Codes:} 81406 x1

\section*{Condition Description}
Limb-girdle muscular dystrophy (LGMD) is a descriptive term applied to a clinically and genetically heterogeneous group of childhood- or adult-onset muscular dystrophies. LGMD is characterized by weakness and wasting restricted to the limb musculature, proximal greater than distal. Most individuals with LGMD show relative sparing of the heart and bulbar muscles, although exceptions occur, depending on the genetic subtype. Onset, progression, and distribution of the weakness and wasting vary considerably among individuals and genetic subtypes. Serum creatine kinase (CK) levels in individuals with LGMD are usually elevated, and muscle biopsy reveals dystrophic changes. Immunohistochemistry (IHC) testing of a muscle biopsy sample can be used to determine the presence or absence of specific proteins, and confirmatory genetic testing is available in some cases. LGMDs are distinct from the much more common X-linked dystrophinopathies, which include Duchenne and Becker muscular dystrophy (DMD/BMD).

Mutations in the \textit{ANO5} gene (11p14.3) (OMIM \#608662) have been shown to cause the autosomal recessive disorders limb-girdle muscular dystrophy type 2L (LGMD 2L) and Miyoshi myopathy type 3 (MMD3), and the autosomal dominant disorder gnathodiaphyseal dysplasia (GDD), a rare skeletal syndrome. LGMD 2L is characterized by late-onset (mean age 35) proximal weakness with prominent asymmetrical quadriceps femoris and biceps brachii atrophy. A milder degree of distal lower limb weakness may be observed and affected individuals usually remain ambulatory for several decades, although they may have difficulty climbing stairs. There is significant interfamilial variability.

MMD3 is a distal muscular dystrophy, particularly of calf muscles. Affected individuals may have calf weakness with or without atrophy, and have difficulty walking on their toes. Later manifestations include asymmetric involvement of the proximal muscles of the lower and upper limb-girdle, with quadriceps atrophy.

Serum creatine kinase levels are elevated in affected individuals (mean 4000-5000 IU). Cardiac and respiratory function is normal. Females appear to be less frequently affected. Muscle biopsy reveal myopathic or dystrophic changes with variation in fiber size, central nuclei, fiber splitting, degeneration of muscle fibers, and an increase in connective tissue. EMG shows myopathic changes.

In the Bolduc study (2010), two mutations in the \textit{ANO5} genes were found in three of ten LGMD 2L families (30%) and in two of two MMD3 families with linkage to the \textit{ANO5} gene region. In the Hicks study (2011), two mutations in the \textit{ANO5} gene were found in 15 of 59 LGMD/MMD affected families without DYSF mutations (25.4%). The Hicks study suggested a minimum prevalence of ANO5 mutations of 0.27/100,000 in the North of England population.


\section*{References}
- Hicks, D. et al. A founder mutation in anoctamin 5 is a major cause of limb girdle muscular dystrophy. \textit{Brain.} 2011; 143:171-182.

\section*{Genes}
\textbf{ANO5}

\section*{Indications}
This test is indicated for:
- Confirmation of a clinical diagnosis of LGMD 2L.
- Carrier testing in adults with a family history of LGMD 2L.

\section*{Methodology}
\textbf{Next Generation Sequencing}: In-solution hybridization of all coding exons is performed on the patient’s genomic DNA. Although some deep intronic regions may also be analyzed, this assay is not meant to interrogate most promoter regions, deep intronic regions, or other regulatory elements, and does not detect single or multi-exon deletions or duplications. Direct sequencing of the captured regions is performed using next generation sequencing. The patient’s gene sequences are then compared to a standard reference sequence. Potentially causative variants and areas of low coverage are Sanger-sequenced. Sequence variations are classified as pathogenic, likely pathogenic, benign, likely benign, or variants of unknown significance. Variants of unknown significance may require further studies of the patient and/or family members.

\section*{Detection}
\textbf{Clinical Sensitivity:} Unknown. Mutations in the promoter region, some mutations in the introns and other regulatory element mutations cannot be detected by this analysis. Large deletions will not be detected by this analysis. Results of molecular analysis should be interpreted in the context of the patient’s biochemical phenotype.

\textbf{Analytical Sensitivity:} \textasciitilde 99%.

\section*{Specimen Requirements}

Disclaimer: This information is confidential and subject to change without notice. It may not be reproduced in whole or part unless authorized in writing by an authorized EGL representative.
Submit only 1 of the following specimen types

Type: DNA, Isolated

Specimen Requirements:
Microtainer
8µg
Isolation using the Perkin Elmer™ Chemagen™ Automated Extraction method or Qiagen™ Puregene kit for DNA extraction is recommended.

Specimen Collection and Shipping:
Refrigerate until time of shipment in 100 ng/µL in TE buffer. Ship sample at room temperature with overnight delivery.

Type: Saliva

Specimen Requirements:
Oragene™ Saliva Collection Kit
Oragene™ Saliva Collection Kit used according to manufacturer instructions. Please contact EGL for a Saliva Collection Kit for patients that cannot provide a blood sample.

Specimen Collection and Shipping:
Please do not refrigerate or freeze saliva sample. Please store and ship at room temperature.

Type: Whole Blood (EDTA)

Specimen Requirements:
EDTA (Purple Top)
Infants and Young Children (2 years of age to 10 years old): 3-5 ml
Older Children & Adults: 5-10 ml
Autopsy: 2-3 ml unclotted cord or cardiac blood

Specimen Collection and Shipping:
Ship sample at room temperature for receipt at EGL within 72 hours of collection. Do not freeze.

Related Tests

- Deletion/duplication analysis of the ANOS1 gene by CGH array is available for those individuals in whom sequence analysis is negative.
- Custom diagnostic mutation analysis (KM) is available to family members if mutations are identified by targeted mutation testing or sequencing analysis.
- Prenatal testing is available only for known familial mutations to individuals who are confirmed carriers of mutations. Please contact the laboratory genetic counselor to discuss appropriate testing prior to collecting a prenatal specimen.