MYL3 – Associated Hypertrophic Cardiomyopathy

MYL3 – Associated Hypertrophic Cardiomyopathy (HCM) is characterized by left ventricular hypertrophy in the absence of predisposing cardiac conditions. While there are more than 18 genes associated with autosomal dominant HCM, MYL3 mutations are thought to comprise 1% of all cases (1). The MYL3 gene codes for the protein myosin essential light chain (also known as alkali light chain), which plays a role in stabilizing the long alpha-helical neck of the myosin head (2). The MYL3 gene contains 7 exons and is located on chromosome 3p21.31.

Homozygous mutations in the MYL3 gene have been associated with restrictive physiology in one consanguineous family with early-onset hypertrophy (3). Approximately 50-65% of individuals with a known or suspected diagnosis of familial HCM have a mutation in one of a number of genes encoding components of the sarcomere and cytoskeleton.

Indication

MYL3 gene testing is utilized to confirm a diagnosis of HCM in patients with clinically evident disease. Genetic testing allows for early identification and diagnosis of individuals at greatest risk prior to the expression of typical clinical manifestations. If a mutation is identified in an asymptomatic individual, regular and routine outpatient follow up is indicated. If clinically unaffected members of a family with an identified mutation for HCM are found not to carry that mutation, they can be definitely diagnosed as unaffected and reassured that neither they nor their children will be at higher risk compared to the general population to develop symptoms related to HCM. A negative test result in an individual with a known familial mutation also eliminates the need for routine follow up.
Methodology:

All 6 coding exons of the MYL3 gene, as well as the exon/intron boundaries and portion of untranslated regions of the gene are amplified by PCR. Genomic DNA sequences from both forward and reverse directions are obtained by automatic fluorescent detection using an ABI PRISM® 3730 DNA Analyzer. Sequence variants different from National Center for Biotechnology Information GeneBank reference are further evaluated for genetic significance. If a mutation is identified, a known familial mutation analysis will be available for additional family members.

Sensitivity & Accuracy:

Greater than 98.5% of the mutations in exons 1-6 of MYL3 are detectable by sequence based methods. Sequencing does not detect deletions or duplications.

References:


Specimen:

Peripheral blood in EDTA tube
Adult: 5-10mL
Child: 3-5mL
Infant: 1-3mL
For other specimen types, please contact Amy Shikany at 513-803-3317

Turnaround Time:

Full Mutation Analysis 2-4 weeks
Known Mutation Analysis 1-2 weeks

CPT Codes:

Full Gene Sequencing  81405
Additional Family Members  81403