Hypertrophic Cardiomyopathy (HCM) is relatively common, with a prevalence of 1 in 500 adults (1). HCM is a primary disorder of heart muscle characterized by left ventricular hypertrophy. The most classic finding in HCM is asymmetric septal hypertrophy, with or without left ventricular outflow tract obstruction. The disease demonstrates extensive clinical variability with regard to age of onset, severity and progression of disease. HCM can affect infants and children although it is more typically identified in adolescence or adulthood (1,2). The MYH7 gene contains 38 exons and is located at chromosome 14q12. Up to 30% of individuals with a clinical diagnosis of HCM have MYH7 mutations (1-3). MYH7 mutations are inherited in an autosomal dominant manner. The majority of individuals inherit the MYH7 from a parent, although, de novo mutations do occur.

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 (1). Compound heterozygous mutations have been reported in MYH7 and other genes associated with HCM (1,2). Mutations in the MYH7 gene have been primarily associated with HCM, but can also be associated with other types of heart muscle disease including dilated cardiomyopathy, restrictive cardiomyopathy and left-ventricular non-compaction (1).

**Indication**

MYH7 testing is utilized to confirm a diagnosis of HCM in patients with clinically evident disease. Genetic testing also 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 38 exons of the **MYH7** gene, as well as the exon/intron boundaries and a 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 GenBank references 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 exon 1-38 of **MYH7** are detectable by sequence based methods. Sequencing does not detect deletions or duplications. Mutations in **MYH7** account for up to 30% of cases of idiopathic hypertrophic cardiomyopathy.

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 4-6 weeks
Known Mutation Analysis 1-2 weeks

CPT Codes:

Full Gene Sequencing 81407
Additional Family Members 81403