Pulmonary Hypertension: Sequencing Panel

Test Code: MM098
Turnaround time: 6 weeks
CPT Codes: 81405 x1, 81406 x1

Condition Description

Pulmonary hypertension (PH) is increased pulmonary pressure in the absence of common causes such as lung, heart, or thromboembolic chronic diseases. It is thought that both genetic and environmental factors that alter vascular structure and function contribute to the pathogenesis of PH.

Familial cases of PH are usually inherited in an autosomal dominant manner. With the identification of pathogenic variants in genes known to cause PH, what was previously thought to be idiopathic PH is now known to be genetic. A pathogenic variant in the \textit{BMPR2} gene causes ~70% of hereditary cases of pulmonary arterial hypertension (PAH) and in 10-40% of idiopathic PAH. Other genes with pathogenic variants implicated in PH include: \textit{CAV1}, \textit{GDF2}, \textit{RASA1}, \textit{SMAD4}, and \textit{SMAD9}.

Heterozygous pathogenic variants in the \textit{ENG} and \textit{ACVRL1} (previously known as \textit{ALK1}) genes cause hereditary hemorrhagic telangiectasia (HHT). HHT is an autosomal dominant vascular disorder characterized by acquired cutaneous telangiectasias and arteriovenous malformations that can lead to the development of PAH.

References:

- OMIM

Genes

\textit{ACVRL1}, \textit{BMPR2}, \textit{CAV1}, \textit{ENG}, \textit{GDF2}, \textit{RASA1}, \textit{SMAD4}, \textit{SMAD9}

Indications

This test is indicated for:

- Confirmation of a clinical diagnosis of pulmonary hypertension.
- Carrier testing in adults with a family history of pulmonary hypertension.

Methodology

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.

Detection

Next Generation Sequencing: Clinical Sensitivity: A pathogenic variant in the \textit{BMPR2} gene can be identified in ~70% of hereditary cases of pulmonary arterial hypertension and in 10-40% of idiopathic PAH. The clinical sensitivity for \textit{ENG}, \textit{ACVRL1}, and \textit{CAV1} is unknown. Pathogenic variants in the promoter region, some pathogenic variants in the introns and other regulatory element pathogenic variants 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 clinical and/or biochemical phenotype.

Analytical Sensitivity: ~99%.

Specimen Requirements

Submit only 1 of the following specimen types

Type: Whole Blood

Specimen Requirements:

- In EDTA (purple top) tube:
  - Infants (2 years): 3-5 ml
  - Older Children & Adults: 5-10 ml

Specimen Collection and Shipping: Ship sample at room temperature with overnight delivery.
Type: Isolated DNA

Specimen Requirements:

In microtainer: 60 ug

Isolation using the Qiagen™ Puregene kit for DNA extraction is recommended.

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

Related Tests

- Comprehensive cardiomyopathy panel
- Pulmonary Hypertension: Deletion/Duplication Panel