Pulmonary Arterial Hypertension

Pulmonary arterial hypertension (PAH) is caused by widespread occlusion or destruction of the smallest pulmonary arteries, leading to increased blood flow resistance, right ventricular hypertrophy, and heart failure. Genetic testing is most appropriate when no obvious etiology for pulmonary hypertension is found or if a family history of PAH exists.

DISEASE OVERVIEW

Symptoms
- Shortness of breath
- Fatigue
- Syncope
- Chest pain
- Palpitations
- Edema

Epidemiology
Incidence – 1-2/million

Inheritance
- Autosomal dominant – ACVRL1, BMPR2, CAV1, ENG, KCNA5, KCNK3, and SMAD9
- Autosomal recessive – EIF2AK4

TEST DESCRIPTION

See Genes Tested table for genes included in the panel.

Clinical Sensitivity
- 75-80% for familial cases (Austin, 2017; Garcia-Rivas, 2017)
- ~25% for simplex cases (Austin, 2017; Garcia-Rivas 2017)

Limitations
- A negative result does not exclude a heritable form of pulmonary arterial hypertension.
- Diagnostic errors can occur due to rare sequence variations.
- Interpretation of this test result may be impacted if the individual has had an allogeneic stem cell transplantation.
- The following will not be evaluated:
  - Variants outside the coding regions and intron-exon boundaries of the targeted genes
  - Regulatory region variants and deep intronic variants
  - Breakpoints of large deletions/duplications
  - Deletions/duplications in KCNA5
  - Noncoding transcripts
- The following may not be detected:
  - Deletions/duplications/insertions of any size by massively parallel sequencing
  - Deletions/duplications less than 1kb in the targeted genes by array
  - Some variants due to technical limitations in the presence of pseudogenes, repetitive, or homologous regions
  - Low-level somatic variants

TESTS TO CONSIDER

Pulmonary Arterial Hypertension (PAH) Panel, Sequencing and Deletion/Duplication 2009345
Method: Massively Parallel Sequencing/Exonic Oligonucleotide-based CGH Microarray
Preferred test to confirm a diagnosis of PAH, especially in those with a family history of PAH

Pulmonary Arterial Hypertension (BMPR2) Sequencing and Deletion/Duplication 2003405
Method: Polymerase Chain Reaction/Sequencing/Multiplex Ligation-dependent Probe Amplification
Acceptable test for individuals with clinical symptoms of PAH

Pulmonary Arterial Hypertension (BMPR2) Sequencing 2009410
Method: Polymerase Chain Reaction/Sequencing
Alternate test for individuals with clinical symptoms of PAH

EIF2AK4-Associated Disorders (EIF2AK4) Sequencing 2010696
Method: Polymerase Chain Reaction/Sequencing
Preferred test to confirm diagnosis or assess carrier status for an EIF2AK4-associated disorder such as pulmonary capillary hemangiomatosis (PCH) and pulmonary veno-occlusive disease (PVOD)

Familial Mutation, Targeted Sequencing 2001961
Method: Polymerase Chain Reaction/Sequencing
- Recommended test if there is a known familial sequence variant previously identified in a family member.
- A copy of the family member’s lab report documenting the known familial variant is required.
- Single exon deletions/duplications in the following exons:
  
  - **EIF2AK4** (NM_001013703) 2, 5, 29, 34, 35

**Analytical Sensitivity**

For massively parallel sequencing:

<table>
<thead>
<tr>
<th>Variant Class</th>
<th>Analytical Sensitivity (PPA) Estimate</th>
<th>Analytical Sensitivity (PPA) 95% Credibility Region</th>
</tr>
</thead>
<tbody>
<tr>
<td>SNVs</td>
<td>99.2%</td>
<td>96.9-99.4%</td>
</tr>
<tr>
<td>Deletions 1-10 bp</td>
<td>93.8%</td>
<td>84.3-98.2%</td>
</tr>
<tr>
<td>Deletions 11-44 bp</td>
<td>100%</td>
<td>87.8-100%</td>
</tr>
<tr>
<td>Insertions 1-10 bp</td>
<td>94.8%</td>
<td>86.8-98.5%</td>
</tr>
<tr>
<td>Insertions 11-23 bp</td>
<td>100%</td>
<td>62.1-100%</td>
</tr>
</tbody>
</table>

*Genes included on this test are a subset of a larger methods-based validation from which the PPA values are derived. bp, base pairs; PPA, positive percent agreement; SNVs, single nucleotide variants

**Genes Tested**

<table>
<thead>
<tr>
<th>Gene</th>
<th>MIM Number</th>
<th>Disorder</th>
<th>PAH Attributable to Gene</th>
</tr>
</thead>
<tbody>
<tr>
<td>ACVRL1</td>
<td>601284</td>
<td>HHT type 2</td>
<td>1%</td>
</tr>
<tr>
<td>BMP2</td>
<td>600799</td>
<td>BMP2-related PAH; PAH1; PVOD type 1</td>
<td>≤75% of familial cases; ≤25% of simplex cases</td>
</tr>
<tr>
<td>CAV1</td>
<td>601047</td>
<td>PAH3</td>
<td>≤1%</td>
</tr>
<tr>
<td>EIF2AK4</td>
<td>609280</td>
<td>PVOD2</td>
<td>&gt;10%</td>
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<tr>
<td>ENG</td>
<td>131195</td>
<td>HHT type 1</td>
<td>≤1%</td>
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<tr>
<td>KCNA5</td>
<td>176267</td>
<td>Familial atrial fibrillation-7</td>
<td>Unknown</td>
</tr>
<tr>
<td>KCNK3</td>
<td>603220</td>
<td>PAH4</td>
<td>≤1-3%</td>
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<tr>
<td>SMAD9</td>
<td>603295</td>
<td>PAH2</td>
<td>Unknown</td>
</tr>
</tbody>
</table>

HHT, hereditary hemorrhagic telangiectasia; PAH, pulmonary arterial hypertension; PCH, pulmonary capillary hemangiomatosis; PVOD, pulmonary veno-occlusive disease

**REFERENCES**


