

Gamma Globin (HBG1 and HBG2) Sequencing

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Fetal hemoglobin (Hb F) is the predominant hemoglobin in the fetus and is comprised of two alpha globin chains and two gamma chains. A-gamma is expressed from the *HBG1* gene and G-gamma is expressed from the *HBG2* gene. Promoter variants in either *HBG1* or *HBG2* can result in nondeletional hereditary persistence of fetal hemoglobin (HPFH), a clinically benign condition but can ameliorate disease severity in sickle cell disease and thalassemia. The majority of genetic variants in the gamma genes are clinically benign; however, rare variants that result in qualitative defects may produce a clinical phenotype in neonates. Unstable variants may result in hemolytic anemia/hyperbilirubinemia, high- or low-oxygen affinity variants may present as erythrocytosis or cyanosis, and M-hemoglobin variants typically resolve after 6 months of age due to the gamma- to beta-globin switch.

Disease Overview

Expression of variant gamma proteins is related to the overall expression of Hb F and will vary over time.

Clinical symptoms related to gamma chain variants commonly resolve after the first 6 months of life, given the normal switch from fetal hemoglobin expression to adult hemoglobin expression that occurs at that time.

Clinical presentations in neonates include:

- Hemolytic anemia/hyperbilirubinemia
- Erythrocytosis
- Cyanosis
- Methemoglobinemia

HPFH may occur in adults:

- A clinically benign disorder characterized by elevated Hb F into adulthood
- · When coinherited with sickle cell disease or beta thalassemia, HPFH may ameliorate disease severity

Genetics

Genes

HBG1 (A-gamma) and HBG2 (G-gamma)

Inheritance

Autosomal dominant

Variants

Over 100 gamma globin variants have been described, many of which are clinically benign.

- Qualitative defects:
 - Unstable variants may result in hemolytic anemia/hyperbilirubinemia
 - High- or low-oxygen affinity variants may result in erythrocytosis or cyanosis, respectively
 - M hemoglobin variants may cause methemoglobinemia

Featured ARUP Testing

Gamma Globin (HBG1 and HBG2) Sequencing 3001957

Method: Polymerase Chain Reaction/Sequencing

- Use to assess for gamma globin gene variants resulting in neonatal hemolytic anemia, cyanosis, or methemoglobinemia in symptomatic infants when other etiologies have been excluded
- Use to assess for nondeletional HPFH in individuals with elevated fetal hemoglobin
- Characterizes abnormal hemoglobins identified by
 electrophoresis suspected to represent gamma
 chain variants

- Quantitative defects
 - Promoter region variants may be associated with non-deletional HPFH, a clinically benign condition
 - Polymorphisms may influence expression of the gamma genes

Test Interpretation

Sensitivity/Specificity

- Clinical sensitivity: Unknown
 - Gamma globin variants are a rare cause of neonatal hemolytic anemia, cyanosis, erythrocytosis, or methemoglobinemia
- Analytic sensitivity/specificity: >99%

Test Methodology

• Long-range polymerase chain reaction (PCR) followed by nested PCR and bidirectional sequencing of all coding regions, intron/exon boundaries, proximal promoter, and 5' proximal promoters of the *HBG1* and *HBG2* genes

Results

- No pathogenic variants detected
 - Reduces the likelihood of a gamma globinopathy or nondeletional gamma HPFH
- Pathogenic variant detected
 - Consistent with a diagnosis of a gamma globinopathy or nondeletional gamma HPFH
 - Clinical manifestations are variable and dependent on the effect of the identified variant on protein function/expression and on the age of the patient
 - Correlation with hematologic parameters and hemoglobin electrophoresis results is strongly recommended
- · Gamma globin gene sequencing may identify variants of unknown clinical significance

Limitations

- Diagnostic errors can occur due to rare sequence variations or repeat element insertions
- · Large deletions/duplications, distal regulatory region variants, deep intronic variants, and hybrid gene events will not be detected

Additional Resources

Manca L, Masala B. Disorders of the synthesis of human fetal hemoglobin. IUBMB Life. 2008;60(2):94-111.

Patrinos GP, Giardine B, Riemer C, et al. Improvements in the HbVar database of human hemoglobin variants and thalassemia mutations for population and sequence variation studies. *Nucleic Acids Res*. 2004;32(Database issue):D537-D541.

Related Information

Unstable Hemoglobinopathies

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