Primary Congenital Glaucoma, *CYP1B1* Sequencing

Indications for Ordering

- Confirm clinical diagnosis of
  - Congenital glaucoma
  - Peters anomaly
  - Axenfeld-Rieger anomaly
  - Other malformations of the anterior chamber of the eye
- Carrier screening for family members of individuals with congenital glaucoma or previously identified *CYP1B1* gene variant(s)
- Prenatal screening for couples with a child with known *CYP1B1* gene variant(s)

Test Description

Polymerase chain reaction and sequencing

Tests to Consider

Glaucoma (Primary Congenital), *CYP1B1* Sequencing 0051476

- Diagnostic testing or carrier screening for primary congenital glaucoma and related disorders

Disease Overview

Prevalence at birth

- 1/5,000-22,000 in Western countries
- More common in certain populations
  - 1/1,250 in Slovakian Romani populations
  - 1/2,500 in Middle Eastern countries
  - 1/3,300 in Andhra Pradesh state in India

Age of onset – infancy

Symptoms

- Ocular symptoms vary in severity – bilateral 70% of the time
  - Photophobia
  - Epiphora
  - Blepharospasm
  - Chronic red or irritated eyes, excessive tearing
  - Reduced visual acuity – eventual blindness
- Signs
  - Globe enlargement/edema
  - Iris and pupillary abnormalities
  - Optic nerve cupping
  - Myopia
  - Corneal opacification
  - Elevated intraocular pressure
  - Thinning of anterior sclera, anomalous deep anterior chamber

Genetics

Gene – *CYP1B1*

Inheritance – autosomal recessive

Test Interpretation

Sensitivity/specificity

- Clinical sensitivity
  - 20-100% for familial cases
  - 10-15% for isolated cases
- Analytical sensitivity/specificity – 99%

Results

- Positive
  - Two variants on opposite chromosomes detected
    - Individual is predicted to be clinically affected
  - One variant detected
    - Individual is at least a carrier
- Negative – no variant detected
  - Does not exclude the possibility of disease or being a carrier of the disease
- Uncertain – variants of unknown significance may be detected

Limitations

- Not identified
  - Large deletions/duplications or deep intronic variants
- Diagnostic errors can occur due to rare sequence variations