Hearing Loss: GJB2 Gene Sequencing

Test Code: OZ  
Turnaround time: 3 weeks  
CPT Codes: 81252 x1

Condition Description

In the United States, approximately 1 in 1000 children are diagnosed with prelingual hearing loss (HL) or deafness. Approximately half of prelingual hearing loss or deafness is attributed to environmental exposures and the remaining half is attributed to genetic causes. Approximately 30% of hereditary hearing loss is estimated to be syndromic (associated with other birth defects) while the remaining 70% is non-syndromic (isolated and not associated with other findings). Non-syndromic deafness is mainly due to recessive genes (75-80%) and over 20 such genes have been identified, but non-syndromic deafness may also be inherited in autosomal dominant, X-linked, or mitochondrial patterns.

Molecular testing can aid in rapid diagnosis of hearing loss. Early diagnosis of hearing defects can provide diagnostic information, facilitate timely intervention, and assist with genetic counseling.

Connexins are transmembrane proteins that form channels that allow rapid transport of small molecules between cells; the proteins connexin 26 and connexin 30 interact to form a channel that functions in the inner ear. The GJB2 gene encodes the connexin 26 protein and is involved in 50% of autosomal recessive hearing loss. The GJB6 gene is located near the GJB2 gene, and encodes the protein connexin 30. Patients with non-syndromic hearing loss have been found to have two mutations in connexin 26, two mutations in connexin 30, or compound heterozygosity for one mutation in connexin 26 and one mutation in connexin 30 [1,2].

This test involves sequencing of the entire coding sequence of the GJB2 gene that encodes the connexin 26 protein.

References:

Genes

GJB2

Indications

This test is indicated for:

- Individuals with clinical findings consistent with non-syndromic hearing loss when mitochondrial etiologies have been ruled out and testing of connexin 30 has resulted in no mutations found or one mutation found.

Methodology

PCR amplification of exons and flanking regions contained in the GJB2 gene is performed on patient genomic DNA. Direct sequencing of amplification products is performed in both the forward and reverse directions using automated fluorescence dideoxy sequencing methods. Patient gene sequences are compared to a normal reference sequence. Sequence variations are then classified as mutations, benign variants unrelated to disease or variations of unknown clinical significance. Variants of unknown clinical significance may require further studies of the patient and/or family members. This assay does not interrogate the promoter region, deep intronic regions, or other regulatory elements. Large deletions are not detected by this analysis.

Detection

Mutations in the promoter region, some mutations in the introns, and other regulatory elements cannot be detected by this analysis. Large deletions and insertions will not be detected by this assay. Single and multiple exon deletions and duplications can be detected by the separate GJB2 and GJB6 deletion/duplication array. It is possible that some patients with a typical presentation may not carry a mutation detected by this analysis. This analysis may detect novel variants of unclear effect, which may require further studies.

Specimen Requirements

Submit only 1 of the following specimen types

* Preferred specimen type: Whole Blood

Type: Whole Blood

Specimen Requirements:

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

Specimen Collection and Shipping: Refrigerate until time of shipment. Ship sample within 5 days of collection at room temperature with overnight delivery.

**Type: Saliva**

Specimen Requirements:

Oragene™ Saliva Collection kit (available through EGL) used according to manufacturer instructions.

Specimen Collection and Shipping: Store sample at room temperature. Ship sample within 5 days of collection at room temperature with overnight delivery.

### Related Tests

- The Hearing Loss Panel (HL) is indicated for patients who have not have previous molecular testing and includes sequencing of the **GJB2** and **GJB6** genes, targeted mutation analysis of the **GJB6** common 342kb deletion, and testing for mitochondrial mutations associated with aminoglycoside sensitivity.
- For patients with mutations not identified by full gene sequencing, a separate Deletion/Duplication Assay is available for connexin 26 and connexin 30 using a targeted CGH array. Refer to the test requisition or contact the laboratory for more information.
- Custom Diagnostic Mutation Analysis (KM) is available to family members if mutations are identified by sequencing.
- Prenatal testing is available to couples who are confirmed carriers of mutations. Please contact the laboratory genetic counselor to discuss appropriate testing prior to collecting a prenatal specimen.
- Mitochondrial Mutation Panel for patients with a history of aminoglycoside sensitivity (QJ)