Mental Retardation with Language Impairment and Autistic Features: FOXP1 Gene Sequencing

Test Code: SFOX1
Turnaround time: 4 weeks
CPT Codes: 81479 x1

Condition Description

Hamdan et al. (2010) identified two patients with de novo mutations in the FOXP1 gene (3p14.1). Mutation of the FOXP1 gene causes autosomal dominant mental retardation with language impairment and autistic features. Common features seen in these patients include global developmental delay with severe language impairment, mild to moderate intellectual disability, autism or autistic features, and internalizing and externalizing behavior problems. The FOXP1 gene and its closest homolog, the FOXP2 gene, may regulate common processes. They are both expressed in overlapping regions of the brain including areas associated with the production and processing of vocalization and language.

For patients with suspected mental retardation with language impairment and autistic features, sequence analysis is recommended as the first step in mutation identification. For patients in whom mutations are not identified by full gene sequencing, deletion/duplication analysis is appropriate.

References:
- OMIM #605515: FOXP1 gene
- OMIM #613670: Mental Retardation with Language Impairment and Autistic Features

Genes

FOXP1

Indications

This test is indicated for:
- Confirmation of a clinical diagnosis of mental retardation with language impairment and autistic features.
- Carrier testing in adults with a family history of mental retardation with language impairment and autistic features.

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

Clinical Sensitivity: Unknown. Mutations in the promoter region, some mutations in the introns and other regulatory element mutations 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

* Preferred specimen type: Whole Blood

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: 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**

- Deletion/duplication analysis of the **FOXP1** gene by CGH array is available for those individuals in whom sequence analysis is negative.
- Sequencing and deletion/duplication analysis of the **FOXP2** gene are available.
- Custom diagnostic mutation analysis (KM) is available to family members if mutations are identified by targeted mutation testing or sequencing analysis.
- Prenatal testing is available only for known familial mutations to individuals who are confirmed carriers of mutations. Please contact the laboratory genetic counselor to discuss appropriate testing prior to collecting a prenatal specimen.