Fragile X: FMR1 Gene Sequencing

Test Code: SFMR1
Turnaround time: 4 weeks
CPT Codes: 81479 x1

Condition Description

Expansion of a CGG triplet repeat leading to DNA methylation and silencing of the FMR1 gene is the most frequent cause of fragile X syndrome. However, other mutations within the FMR1 gene have also been identified that cause fragile X syndrome. These include deletions, point mutations that disrupt RNA splicing and a missense mutation. EGL Genetics offers full gene sequencing to detect mutations other than CGG expansion as a cause of fragile X syndrome.

Sequencing of the FMR1 gene will only be done if the patient first tests negative for expansion of the CGG tract and FMR1 DNA methylation. The FMR1 gene consists of 17 exons. These coding exons, as well as the immediate flanking regions, are PCR amplified and sequenced in both forward and reverse strands. In addition, the entire FMR1 promoter, including the four known transcription factor binding sites and the transcription initiation site, are assessed by DNA sequencing. This analysis will therefore detect coding sequence changes, splice donor and acceptor site mutations and changes in the promoter sequence. In addition, both small and large deletions will be detected in males. Small deletions will also be detected in females, although larger deletions of the entire gene potentially could escape detection.

It is important to note that testing for expansion of the CGG tract and FMR1 DNA methylation alone does not rule out a diagnosis of fragile X syndrome or involvement of FMR1 in the patient's phenotype. Specialized consultation is available with Dr. Stephen Warren, an authority on FMR1, on the interpretation of missense mutations.

For patients with mutations not identified by full gene sequencing, a separate deletion/duplication assay is available using a targeted CGH array KQ.


Reference:
- GeneReviews Clinical Summary

Genes
FMR1

Indications

This test is indicated for:
- Confirmation of a clinical diagnosis of fragile X syndrome who have tested negative by CGG repeat analysis.
- Carrier testing in adults with a family history of fragile X syndrome who have tested negative by CGG repeat analysis.

Methodology

Sequencing of the FMR1 gene will only be done if the patient first tests negative for expansion of the CGG tract and FMR1 DNA methylation. The FMR1 gene consists of 17 exons. These coding exons, as well as the immediate flanking regions, are PCR amplified and sequenced in both forward and reverse strands. In addition, the entire FMR1 promoter, including the four known transcription factor binding sites and the transcription initiation site, are assessed by DNA sequencing.

Detection

This test uses sequence analysis of the coding region of the FMR1 gene which is estimated to identify 90-95% of mutations. Mutations in the promoter region, some mutations in the introns, and other regulatory elements cannot be detected by this analysis. Large deletion and insertion mutations will not be detected by this assay. 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) tube:
- Infants (2 years): 3-5 ml
- Older Children & Adults: 5-10 ml
Type: Saliva

Specimen Requirements:

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

Related Tests

- For Fragile X testing, CGG repeat analysis is the recommended first tier test. Sequencing and deletion/duplication analysis are also available and should follow CGG repeat analysis.