XLMR Snyder-Robinson Type: SMS Gene Sequencing

Test Code: SSMSX  
Turnaround time: 6 weeks  
CPT Codes: 81479 x1

Condition Description

Intellectual disability (ID) is a nonprogressive cognitive impairment affecting 1-3% of the Western population. It is estimated that up to 50% of moderate-severe cases have genetic causes and approximately 10% are due to X-linked intellectual disability disorders (XLID). XLID can be syndromic or nonsyndromic and is observed in all ethnic groups. More than 100 XLID syndromes have been described in the literature to date. Fragile X is the most common XLID syndrome (~1 in 4000 males) while others can be quite rare with only a few patients reported in the literature. Males can have moderate to severe intellectual disability depending on the syndrome, and carrier females can also be affected, but typically have milder clinical symptoms.

Cason et al. (2003) identified a splice site mutation in the SMS gene (Xp22.1) in a family with Snyder-Robinson XLMR syndrome. Affected males with Snyder-Robinson XLMR syndrome have mild to moderate ID. Additionally, they present with unsteady gait, hypotonia, decreased muscle mass, speech abnormalities, and movement disorders consistent with cerebellar circuitry/red nucleus dysfunction. Carrier females are clinically unaffected.

References:
- Cason et al. (2003), Eu J Hum Genet, 11;937-944.
- OMIM #300105: SMS gene
- OMIM #309583: Snyder-Robinson XLMR Syndrome

Genes

SMS

Indications

This test is indicated for:
- Confirmation of a clinical diagnosis of XLMR Snyder-Robinson Type.
- Carrier testing in adults with a family history of XLMR Snyder-Robinson Type.

Methodology

PCR amplification of 11 exons contained in the SMS gene is performed on the patient's genomic DNA. Direct sequencing of amplification products is performed in both forward and reverse directions, using automated fluorescence dideoxy sequencing methods. The patient's gene sequences are then compared to a normal reference sequence. Sequence variations are 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, and does not detect large deletions.

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) 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

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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 SMS gene by CGH array is available for those individuals in whom sequence analysis is negative.
- 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.
- X-Linked Intellectual Disability panels are available for 30, 60, and 90 genes.