Mowat-Wilson Syndrome: ZEB2 Gene Sequencing

Condition Description

Mowat-Wilson syndrome (MWS) is a clinically recognizable syndrome characterized by intellectual disability, dysmorphic features, and multiple congenital anomalies. All patients are reported with moderate to severe intellectual disability. Distinct facial features evolve with age. In young children the facial features are characterized by:

- prominent chin
- deep-set eyes
- broad nasal bridge
- open mouth with a full lower lip
- hypertelorism
- broad eyebrows
- posteriorly rotated ears with uplifted earlobes and a central depression

In older children, the chin becomes more prominent, the face elongates and the nasal tip becomes more prominent extending below the ala nasi. Individuals often have a smiling expression. Nearly all individuals have microcephaly and seizures. Many individuals have hypotonia with delayed motor milestones. Speech may be absent or delayed. Hirschsprung disease is present in ~60% of patients. Other reported congenital anomalies include heart defects (~45%), genitourinary anomalies, and agenesis of the corpus callosum [1, 2].

De novo deletion or mutation of the ZEB2 gene located at 2q22 is associated with MWS. In a series of 47 patients with MWS and an identified mutation in ZEB2, 39 (83%) had a mutation identifiable by gene sequencing and 8 (17%) had a chromosome deletion or rearrangement detectable by deletion/duplication array analysis [3]. A small number of patients with a clinical diagnosis of MWS but no identified mutation in ZEB2 have been reported [2]. ZEB2 encodes the transcriptional corepressor, Smad Interacting Protein 1 (SIP1). It is suggested that haploinsufficiency of this gene leads to a gene dosage effect early in development. All reported cases are sporadic, and recurrence risk in families is thought to be low, however, parental mosaicism and germline mosaicism have been reported [4]. For patients with mutations not identified by full gene sequencing, a separate deletion/duplication assay is available.

References:

Genes

ZEB2, ZFHX1B

Indications

This test is indicated for:

- Patients with clinical features indicative of MWS.

Methodology

The 9 coding exons and immediate flanking regions of the ZEB2 gene are amplified by PCR and sequenced in both forward and reverse directions. The patient's gene sequences are then compared to a normal reference sequence. Sequence variants are classified as previously described mutations, novel mutations, or variants of unknown significance. This analysis may detect novel variants of unclear effect, which require further studies.

Detection

This sequencing assay will detect over 95% of sequence variants in the coding region and splice junctions. Mutations in the promoter region, some mutations in the introns or other regulatory elements, large deletions, 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.

Results of molecular analysis must be interpreted in the context of the patient's clinical and/or biochemical phenotype.

Reference Range

Gene sequencing is a qualitative assay.

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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.

Special Instructions

Please submit copies of diagnostic biochemical test results along with the sample. Contact the laboratory if further information is needed. Sequence analysis is required before deletion/duplication analysis by targeted CGH array. If sequencing is performed outside of Emory Genetics Laboratory, please submit a copy of the sequencing report with the test requisition.

Related Tests

- Chromosomal microarray analysis is indicated for patients with intellectual disability or congenital anomalies.
- Deletion/Duplication Assay is available separately for individuals where mutations are not identified by sequence analysis. Refer to the test requisition or contact the laboratory for more information.
- Known Mutation Analysis (KM) is available to family members if mutations are identified by sequencing.
- Prenatal testing is available to individuals with a previous child with Mowat-Wilson syndrome when the mutation in the child has been identified. Please contact the laboratory genetic counselor to discuss appropriate testing prior to collecting a prenatal specimen.