Metachromatic Leukodystrophy: ARSA Gene Deletion/Duplication

Test Code: LI
Turnaround time: 2 weeks
CPT Codes: 81228 x1

Condition Description

Metachromatic leukodystrophy (MLD) is an autosomal recessive lysosomal storage disorder caused by an insufficiency of the enzyme arylsulfatase A. Patients with decreased arylsulfatase A activity have elevated urinary sulfatides and metachromatic sulfatide containing lipid deposits in their brain and nervous tissue. Development is normal until the onset of symptoms, which include progressive loss of motor function, neurological deterioration, behavioral changes, seizures, and MRI changes. The age of onset varies between forms and ranges from early childhood (late infantile MLD, approximately 50-60% of cases), to childhood (juvenile MLD, approximately 20-30% of cases), to adulthood (adult MLD, approximately 15-20% of cases). The age of onset is usually similar within a family, though exceptions have been reported.

All three forms of MLD are caused by mutations in the ARSA gene. Mutations that result in no enzyme activity are called I alleles while mutations that result in some residual enzyme activity are called A alleles. Pseudodeficiency mutations, called Pd alleles, which result in lower enzyme activity but are not disease-causing have been described. Diagnostic sequencing analysis of the ARSA gene coding region is available for patients with metachromatic leukodystrophy and their at-risk relatives on a clinical basis.

For questions about testing for MLD, call EGL Genetics at (470) 378-2200 or (855) 831-7447. For further clinical information about lysosomal storage diseases, including management and treatment, call the Emory Lysosomal Storage Disease Center at (404) 778-8565 or (800) 200-1524.

References:

Genes

ARSA

Indications

- Confirmation of a clinical diagnosis of metachromatic leukodystrophy.
- Prenatal testing for known familial mutation.
- Assessment of carrier status in high risk family members known mutation analysis.

Methodology

DNA isolated from peripheral blood is hybridized to a CGH array to detect deletions and duplications. The targeted CGH array has overlapping probes which cover the entire genomic region.

Detection

Detection is limited to duplications and deletions. Array CGH will not detect point mutations or intronic mutations. Results of molecular analysis must be interpreted in the context of the patient's clinical and/or biochemical phenotype.

Specimen Requirements

Submit only 1 of the following specimen types

Type: Whole Blood (EDTA)

Specimen Requirements:
EDTA (Purple Top)
Infants and Young Children (2 years of age to 10 years old): 3-5 ml
Older Children & Adults: 5-10 ml
Autopsy: 2-3 ml unclotted cord or cardiac blood

Specimen Collection and Shipping:
Ship sample at room temperature for receipt at EGL within 72 hours of collection. Do not freeze.

Type: DNA, Isolated

Specimen Requirements:
Microtainer

3µg

Isolation using the Perkin Elmer™Chemagen™ Automated Extraction method or Qiagen™ Puregene kit for DNA extraction is recommended.

Specimen Collection and Shipping:
Refrigerate until time of shipment in 100 ng/µL in TE buffer. Ship sample at room temperature with overnight delivery.

Special Instructions

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

Related Tests

- Arylsulfatase A Enzyme Assay is available for diagnosis.
- Lysosomal Enzyme Screening Panel is available to assess for 13 lysosomal storage diseases.
- Mutation Analysis for Pseudodeficiency Allele may be available upon request.
- Known Mutation Analysis (KM) is available to test family members.
- Prenatal testing is available for known familial mutations only. Please call the Laboratory Genetic Counselor for specific requirements for prenatal testing before collecting a fetal sample.