Mucopolysaccharidosis Type III: **SGSH, GNS, HGSNAT, and NAGLU** Gene Sequencing Panel

**Condition Description**

Mucopolysaccharidosis type III (MPS III, Sanfilippo syndrome), is a member of a group of inherited metabolic disorders collectively termed mucopolysaccharidoses (MPS's). The MPS's are caused by a deficiency of lysosomal enzymes required for the degradation of mucopolysaccharides or glycosaminoglycans (GAGs) within the lysosome [1]. When functioning normally, the lysosomal enzymes break down these GAGs, however when the enzyme is deficient, the GAGs build up in the lysosomes causing damage to the body's tissues. The MPS's share a chronic progressive course with multisystem involvement and characteristic physical features such as coarse facies, hypertelorism, and coarse hair. The MPS patients are also characterized by developmental regression, hepatosplenomegaly and characteristic laboratory and radiographic abnormalities.

Clinical features of MPS III are similar to other MPS's and include hyperactivity, aggressiveness, and developmental delays in childhood. Mental abilities decline as the disease progresses. Involvement of other organ systems tends to be mild and dysmorphic features are more subtle than those observed in other type of mucopolysaccharidosis [1].

MPS III is caused by a deficiency of any of four lysosomal membrane enzymes, which leads to impaired degradation of heparan sulfate. The forms of MPS III are clinically indistinguishable each other and are caused by mutations in distinct genes. All four forms of MPS III result in buildup of the same GAG, heparan sulfate.

- MPS IIIA is caused by deficiency of the enzyme heparan N-sulfatase, encoded by the gene **SGSH**.
- MPS IIIB is caused by deficiency of the enzyme alpha-N-acetylgalcosaminidase, encoded by the gene **NAGLU**.
- MPS IIIC is caused by deficiency of the enzyme N-acetylglucosaminide N-acetyltransferase (N-acetyltransferase), encoded by the gene **HGSNAT**.
- MPS IIID is caused by deficiency of the enzyme N-acetylglucosamine 6-sulfatase (N-acetyltransferase), encoded by the gene **GNS**.

Diagnostic sequencing analysis of the panel of genes associated with MPS III is available for patients with a clinical diagnosis who have not had a fibroblast enzyme study to identify the specific subtype (FQ). For patients with mutations not identified by full gene sequencing, a separate deletion/duplication assay is available using a targeted CGH array (HV). For questions about testing for MPS III, call EGL Genetics at (470) 378-2200. 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**

**GNS, HGSNAT, NAGLU, SGSH**

**Indications**

This test is indicated for:
- Confirmation of a clinical diagnosis of MPS III when enzyme activity studies have not been obtained to identify the specific subtype.
- Carrier testing in adults with a family history of MPS III

**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**

MPS IIIA: Clinical Sensitivity: 46/46 mutations identified in 23 patients, 4 mutations in 2 Chinese patients were identified.
MPS IIIB: Clinical Sensitivity: 34/36 mutations identified in 18 patients, 36/36 mutations identified in 18 Greek families, 13/14 mutations identified in 7 Japanese families.
MPS IIIC: Clinical Sensitivity: 51/60 mutations identified in 30 patients, 22/24 mutations identified in 12 patients.
MPS IIID: Clinical Sensitivity: 2/2 mutations identified in 1 patient, 1 mutation and an 8.7kb deletion in 1 patient, 2/2 mutations identified in 1 patient.
Analytical Sensitivity: >99%

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

Prevalence: The estimated prevalence of all lysosomal storage disorders is 2-5 per 100,000. The prevalence of MPS III is not specifically known, but is likely to be rare and vary by ethnicity.

**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.

**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**

- Mucopolysaccharide screen (urine GAG) (GA)
- Gene sequencing for a specific MPS III gene when enzyme activity studies have identified the subtype.
- Known mutation analysis (Custom Diagnostics) is available to test family members if mutations are identified by sequencing
- For comprehensive testing a deletion/duplication assay is available separately. This test is indicated for individuals where mutations are not identified by sequence analysis.
- 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.