Spinal Muscular Atrophy Testing via SMN1/SMN2 Copy Number Analysis

Background

Spinal muscular atrophy (SMA) (OMIM# 253300, 253550, 253400, 271150) is an autosomal recessive neuromuscular disorder, with an incidence of approximately 1 in 10,000 births. The condition has variable severity and age of onset, and has been categorized into clinical types 0-IV. SMA I accounts for 60% of all SMA and has onset of symptoms in infancy. At the most severe end of the spectrum, SMA 0 correlates with prenatal onset of muscular weakness and neonatal respiratory failure, while SMA IV has the mildest presentation and correlates with adult onset of muscle symptoms.

In all types, the genetic cause maps to an inverted duplication on chromosome 5q13.2. (Melki 1990) The complexity of the 5q13 region increases the likelihood of errors during DNA replication, resulting in a relatively high risk of deletions, gene conversions, and new mutations. The survival motor neuron genes, SMN1 and SMN2, are two highly homologous genes located in this region. (Lefebvre 1995, Bürglen 1996) One difference between these genes affects protein coding, with alternative splicing of exon 7 in SMN2 that results in decreased production of the full length, functional SMN protein compared to SMN1. Therefore, SMN1 accounts for the majority of SMN production, and mutations in SMN1 are the cause of the SMA phenotype.

Ninety-five percent of patients with SMA have homozygous deletions of the SMN1 gene [noted as 0+0]. Of the remaining 5%, most are heterozygous for a deletion of SMN1 on one chromosome and a small pathogenic, or disease-causing, variant in the SMN1 copy on the other chromosome (0+1) (Wirth 2000).

SMN1 copy number varies among healthy individuals [1+1 or 2+1]. SMA carriers generally have one copy of SMN1, while the other copy is deleted [1+0]. However, some individuals have two, or even three, copies of SMN1 on the same chromosome. Individuals with two or three copies of SMN1 may therefore also be carriers if all copies are on the same allele [2+0 or 3+0]. Two-copy SMN1 alleles are relatively common, with variability among ethnic groups ranging from about 3.6% in Caucasians up to 27.5% in African-Americans. (Sugarman 2012)

Clinical Indications

Carrier Screening: Both the American College of Medical Genetics and Genomics and the American College of Obstetricians and Gynecologists now recommend that SMA carrier screening be offered to all women/couples who are planning a pregnancy or currently pregnant. (Prior 2008, Rink 2017) In individuals with a family history of SMA, it is best to obtain genetic test reports from family members.

<table>
<thead>
<tr>
<th>Ethnicity</th>
<th>Carrier Rate</th>
<th>Detection Rate (%)</th>
<th>Reduced Risk with 2 SMN1 Copies</th>
<th>Reduced Risk with 3 SMN1 Copies</th>
</tr>
</thead>
<tbody>
<tr>
<td>Caucasian</td>
<td>1:47</td>
<td>94.8</td>
<td>1:834</td>
<td>1:5600</td>
</tr>
<tr>
<td>Asian Indian</td>
<td>1:52</td>
<td>90.2</td>
<td>1:443</td>
<td>1:5400</td>
</tr>
<tr>
<td>Asian</td>
<td>1:59</td>
<td>93.3</td>
<td>1:806</td>
<td>1:5600</td>
</tr>
<tr>
<td>Ashkenazi Jewish</td>
<td>1:67</td>
<td>90.5</td>
<td>1:611</td>
<td>1:5400</td>
</tr>
<tr>
<td>Hispanic</td>
<td>1:68</td>
<td>90.0</td>
<td>1:579</td>
<td>1:5400</td>
</tr>
<tr>
<td>African-American</td>
<td>1:72</td>
<td>70.5</td>
<td>1:130</td>
<td>1:4200</td>
</tr>
</tbody>
</table>

Table adapted from Sugarman et al. 2012
Cleveland Clinic Laboratories

Diagnostic Confirmation: SMN1 gene dosage analysis will confirm diagnosis for around 95% of patients with SMA, those with homozygous deletions of SMN1 [0+0]. In patients with one copy of SMN1 in whom there is a high suspicion of SMA, SMN1 sequencing should be considered to look for a small variant or deletion.

Because the SMN2 gene produces a small amount of SMN protein, increased copy number of this gene is inversely correlated with SMA disease severity. Variation in the number of SMN2 copies is in large part responsible for the variation seen among different types of SMA. However, since other factors also influence severity, definitive genotype-phenotype predictions cannot be made based solely on SMN2 copy number. (Prior 2011)

Methodology

DNA from the patient’s blood specimen is tested by multiplex ligation-dependent probe amplification (MLPA) to detect nucleotides that differ between the highly similar genes, SMN1 and SMN2. The MLPA assay detects SMN1 copy number (by detecting dosage at exon 7), with analytic sensitivity of >99% and clinical sensitivity of 95% for SMA patients. Sensitivity for carrier screening depends on patient ethnicity, as seen in the Table. Analytical and clinical specificity is >99% for use in both diagnostic testing and carrier screening. The test also detects SMN2 copy number (also by detecting exon 7 dosage), which influences severity of disease in affected patients but does not impact carrier status. (Prior 2011)

Limitations

This laboratory developed test does not detect single sequence variants or small deletions/duplications within SMN1. In individuals found to have two copies of SMN1, the test cannot determine whether those copies are on the same [2+0] or opposite [1+1] chromosomes. This impacts the sensitivity of carrier screening. In the case of a two-copy allele, the individual is a “silent carrier” and has a risk of passing on an allele that is deleted for SMN1. A further limitation of reproductive risk assessment is the high rate of de novo SMN1 mutations; 2% of SMA patients have new mutations that were not inherited. (Wirth 1997)

Interpretation

Thorough interpretation of results is dependent on the indication for testing and relies on good communication of clinical information from the ordering provider. In healthy individuals without a family history of SMA, detection of two SMN1 copies reduces (but does not eliminate) the risk of being a carrier, though sensitivity of detection using dosage analysis is lower among some ethnicities. Detection of 3 SMN1 copies further reduces the carrier risk. SMN2 copy number is not relevant for carrier status.

Among patients with clinical presentations suggestive of SMA, detection of zero SMN1 copies confirms the diagnosis. In symptomatic patients with one SMN1 copy, SMN1 gene sequencing should be considered to identify the small percentage of patients with heterozygous sequence variants or small deletions. Symptomatic patients with two SMN1 copies are unlikely to have SMA, though very rare cases of homozygous sequence variants have been reported.

References


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**Test Overview**

<table>
<thead>
<tr>
<th>Test Name</th>
<th>Spinal Muscular Atrophy Carrier Screening and Diagnostic Assay</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mnemonic</td>
<td>SMA12</td>
</tr>
<tr>
<td>Methodology</td>
<td>Multiplex Ligation-dependent Probe Amplification (MLPA)</td>
</tr>
<tr>
<td>Specimen Requirements</td>
<td>4 mL peripheral blood, EDTA (lavender) transported and stored ambient up to 24 hours. Due to difficulties associated with newborn and infant draws, smaller volumes may be submitted (minimum of 0.5mL is required).</td>
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<tr>
<td>CPT Codes</td>
<td>81401, G0452</td>
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</table>

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