Spinal Muscular Atrophy: \textit{SMN1} Common Deletion Testing

\textbf{Test Code:} SM  
\textbf{Turnaround time:} 2 weeks  
\textbf{CPT Codes:} 81400 x1

\section*{Condition Description}

Spinal muscular atrophy (SMA) is the second most common lethal, autosomal recessive disorder in Caucasians. SMA is characterized by anterior horn cell degeneration which causes a symmetrical muscle weakness and wasting. Three types of SMA are described:

- Type I (Werdnig-Hoffman disease): most severe form of SMA with an onset of symptoms before 6 months of age; affected individuals usually die by 2 years of age.
- Type II (intermediate form): intermediate in severity between Types I and III, with an onset of symptoms between 6 and 18 months of age; death occurs after 2 years of age.
- Type III (Wohlfart-Kugelberg-Welander disease): mildest form of childhood onset SMA, with symptoms beginning between 18 months and 17 years of age; affected individuals survive into adulthood.

All three SMA types are linked to chromosome 5q11.2-q13.3. A telomeric gene, known as the \textit{survival motor neuron (SMN1)} gene, was found to be deleted in about 98% of patients. Point mutations are also known in this gene.

\textit{SMN1} is deleted in about 95% of individuals with SMA. This assay tests for the common \textit{SMN1} deletion only; other pathogenic variants will not be detected. Note that approximately 5-8% of individuals that are carriers of SMA carry two copies of \textit{SMN1} on one chromosome with a deletion on the second chromosome, and will not be detected with this assay. This assay will not report \textit{SMN2} copy number.

Please \textbf{click here} for the GeneReviews clinical summary on this condition.

Visit \url{www.ThinkGenetic.com} for patient-friendly information on spinal muscular atrophy.

\subsection*{Genes}

\textit{SMN1}

\subsection*{Indications}

\subsection*{Methodology}

\textit{SMN1} gene deletions were quantified by multiplex ligation polymerase chain reaction amplification (MLPA) of exons 7 and 8. Gene dosage ratios of \textit{SMN1} are calculated relative to the average of 16 reference loci and are expressed as gene dosage, and/or copy number, according to the SALSA protocol available from MRC Holland. Two copies of the \textit{SMN1} genes most often indicate normal (not affected) status and one copy of a deletion of this region most likely indicates carrier status.

\subsection*{Detection}

Deletions of the \textit{SMN1} gene are found in approximately 95% of individuals with SMA. This carrier assay tests for the common \textit{SMN1} deletion only; other pathogenic variants will not be detected. Approximately 5-8% of carrier individuals will have a normal \textit{SMN1} copy number of two, but both copies will be on the same chromosome (in cis) with a deletion on the second chromosome. This assay will not detect these carrier individuals. \textit{SMN2} copy number is not assessed.

\subsection*{Reference Range}

Qualitative assay.

\subsection*{Specimen Requirements}

\textbf{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.

\subsection*{Special Instructions}

Disclaimer: This information is confidential and subject to change without notice. It may not be reproduced in whole or part unless authorized in writing by an authorized EGL representative.
Diagnostic testing only. No prenatal or carrier testing available.

Related Tests

- Congenital Hypotonia Panel