Lynch Syndrome: \textit{MLH1}, \textit{MSH2}, and \textit{MSH6} Gene Sequencing Panel

\textbf{Test Code: UI}
\textbf{Turnaround time:} 4 weeks
\textbf{CPT Codes:} 81292 x1, 81295 x1, 81298 x1

\section*{Condition Description}

Lynch syndrome, caused by a germline mutation in a mismatch repair gene or associated with tumors exhibiting MSI, is characterized by an increased risk of colon cancer and other cancers (e.g., of the endometrium, ovary, stomach, small intestine, hepatobiliary tract, upper urinary tract, brain, skin). Individuals with Lynch syndrome have an approximately 80% lifetime risk for colon cancer. The average age of colorectal cancer diagnosis is 61 years. Women with Lynch syndrome have a 20%-60% lifetime risk of endometrial cancer. The average age of diagnosis of endometrial cancer is age 46-62 years. Among women with Lynch syndrome who develop both colon cancer and endometrial cancer, approximately 50% present first with endometrial cancer. In Lynch syndrome, the mean age of diagnosis of gastric cancer is age 56 years, with intestinal-type adenocarcinoma being the most commonly reported pathology. Lynch syndrome-associated ovarian cancers have a mean age of diagnosis of 42.5 years; approximately 30% are diagnosed before age 40 years.

The diagnosis of Lynch syndrome can be made on the basis of the Amsterdam Clinical Criteria or by molecular genetic testing for germline mutations in one of several mismatch repair (MMR) genes. The Amsterdam Criteria, first established in 1990 for research purposes, were later modified to include the other Lynch syndrome-related cancers for clinical diagnostic purposes. The Amsterdam Criteria are 1) Three or more family members, one of whom is a first-degree relative of the other two, with a confirmed diagnosis of colorectal cancer 2) Two successive affected generations 3) One or more colorectal cancers diagnosed before age 50 years. The modified Amsterdam Criteria replace "colorectal cancer" with "any Lynch syndrome-related cancers." The sensitivity and specificity of the Amsterdam Criteria for identifying a mutation in the mismatch repair genes \textit{MSH2} and \textit{MLH1} have been reported to be 61% and 67%, respectively. The sensitivity is increased to 78% using the modified Amsterdam Criteria. However, broadening the criteria decreases the specificity.

Lynch syndrome is known to be associated with mutations in four genes involved in the mismatch repair pathway (\textit{MLH1}, \textit{MSH2}, \textit{MSH6}, and \textit{PMS2}). Germline mutations in \textit{MLH1} and \textit{MSH2} account for approximately 90% of detected mutations in families with Lynch syndrome. Mutations in \textit{MSH6} have been reported in approximately 7%-10% of families with Lynch syndrome. Mutations in \textit{PMS2} account for fewer than 5% of mutations in families with Lynch syndrome. Up to 39% of families with mutations in an Lynch syndrome gene do not meet the Amsterdam Criteria. Therefore, families found to have a deleterious mutation in an Lynch syndrome gene should be considered to have Lynch syndrome regardless of the extent of the family history. At least 20% of mutations in \textit{MSH2} and 5% of mutations in \textit{MLH1} are large deletions or genetic rearrangements.

Lynch syndrome is inherited in an autosomal dominant manner. The majority of individuals diagnosed with Lynch syndrome have inherited the condition from a parent. However, because of incomplete penetrance, variable age of cancer development, cancer risk reduction as a result of screening or prophylactic surgery, or early death, not all individuals with a Lynch syndrome gene mutation have a parent who had cancer.

\textbf{Click here} for the GeneTests summary on this condition.


\section*{Genes}

\textit{MLH1}, \textit{MSH2}, \textit{MSH6}

\section*{Indications}

This test is indicated for:

- Confirmation of a clinical diagnosis of Lynch syndrome
- Individuals at-risk for Lynch syndrome due to family history

\section*{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.

\section*{Detection}

Next Generation Sequencing: Clinical Sensitivity: Unknown. Pathogenic variants in the promoter region, some pathogenic variants in the introns and other regulatory element mutations cannot be detected by this analysis. Large deletions/duplications will not be detected by this analysis. Results of molecular analysis should be interpreted in the context of the patient's clinical/biochemical phenotype. Analytical Sensitivity: ~99%.

\section*{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 (Children (>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, if appropriate. 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 EGL Genetics, please submit a copy of the sequencing report with the test requisition.

**Related Tests**

- Deletion/duplication analysis of the Lynch syndrome genes *MLH1, MSH2,* and *MSH6* by CGH array is available for those individuals in whom sequence analysis is negative.
- Sequencing of all four Lynch syndrome genes is also available individually.
- Custom diagnostic mutation analysis (KM) is available to family members if mutations are identified by targeted mutation testing or sequencing analysis.
- Prenatal testing is available for individuals who are confirmed carriers of mutations. Please contact the laboratory genetic counselor to discuss appropriate testing prior to collecting a prenatal specimen.