MUTYH-Associated Polyposis: MUTYH Common Mutation Panel

Test Code: TW
Turnaround time: 3 weeks
CPT Codes: 81401 x1

Condition Description

MUTYH-Associated Polyposis (MAP) results from mutations in the MUTYH gene. MAP is an autosomal recessive disorder characterized by the development of multiple adenomatous polyps in the colon, stomach, or duodenum, and an increased risk for cancer. This accounts for a proportion of patients with a clinical diagnosis of familial adenomatous polyposis (FAP) or attenuated FAP (AFAP) who do not have a detectable APC gene mutation. Studies from multiple FAP registries suggest that approximately 7-17% of patients with the FAP or AFAP phenotype carry biallelic mutations in the MUTYH gene. In these individuals, the polyp burden ranges from only a few to the hundreds typical of classic FAP.

The MUTYH gene (1p34.3-1p32.1), also referred to as the MYH gene, has 16 exons and is involved in DNA mismatch repair. Although this condition is newly described, some studies have found that 1% of Caucasians will carry one of two common mutations, p.Y179C (previously reported as p.Y165C or p.Y176C) and p.G396D (previously reported as p.G382D or p.G393D), in MUTYH. Prevalence of MUTYH mutations in other ethnic groups is currently unknown.

Testing of the MUTYH gene is recommended in individuals with a suspected clinical diagnosis of FAP or AFAP in whom no APC gene mutation was identified. Testing can confirm the presence of mutations in a proband, identify at-risk or carrier individuals among the proband’s relatives, and provide prenatal diagnosis in families with known mutations.

For Caucasian patients with suspected MAP, a common mutation panel is available to test for the two common mutations found in that population. For non-Caucasian patients with suspected MAP, or Caucasian patients with suspected MAP in whom common mutation analysis did not identify two mutations, sequence analysis is recommended as the first or next step in mutation identification. For patients in whom mutations are not identified by full gene sequencing, deletion/duplication analysis is appropriate.

For Caucasian patients with suspected MAP, a common mutation panel is available to test for the two common mutations found in that population. For non-Caucasian patients with suspected MAP, or Caucasian patients with suspected MAP in whom common mutation analysis did not identify two mutations, sequence analysis is recommended as the first or next step in mutation identification. For patients in whom mutations are not identified by full gene sequencing, deletion/duplication analysis is appropriate.

Please click here for the National Cancer Institute summary on this condition.

References:
http://www.cancer.net/patient/Cancer+Types/MYH-Associated+Polyposis
http://www.mtsinai.on.ca/familialgicancer/Diseases/MAP/default.htm


Genes

MUTYH

Indications

This test is indicated for:

- Caucasian individuals with a clinical diagnosis of polyposis who do not have a detectable APC mutation.
- Caucasian individuals at-risk for MAP due to family history
- Carrier testing in Caucasian adults with a family history of MAP.

Methodology

Presence/absence of the p.Y179C and p.G396D mutations are detected by PCR amplification and sequencing of the resulting fragments.

Detection

All p.Y179C or p.G396D mutant alleles will be detected by this assay. Some studies have found that 1% of Caucasians will carry one of these two common mutations in MUTYH. Prevalence of MUTYH mutations in other ethnic groups is currently unknown.

Results of molecular analysis should be interpreted in the context of the patient's clinical presentation and family history.

Specimen Requirements

Submit only 1 of the following specimen types

* Preferred specimen type: Whole Blood

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.
Type: Whole Blood

Specimen Requirements:

In EDTA (purple top) or ACD (yellow 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

Please submit copies of pedigree or other family history information along with the sample. 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 Emory Genetics Laboratory, please submit a copy of the sequencing report with the test requisition form.

Related Tests

- **MUTYH-Associated Polyposis**: MUTYH Gene Sequencing (QV) is available for non-Caucasian individuals and for Caucasian individuals in whom common mutation testing does not identify two mutations.
- **MUTYH-Associated Polyposis**: MUTYH Gene Deletion/Duplication (QW) is available for those individuals in whom sequence analysis is negative.
- **Familial Adenomatous Polyposis**: APC Gene Sequencing (TV) and Familial Adenomatous Polyposis: APC Gene Deletion/Duplication (QP) are available for APC-associated polyposis conditions, and may be indicated for individuals with a clinical diagnosis of polyposis who do not have a detectable MYH mutation.
- **Known Mutation Analysis (KM)** is available to family members if mutations are identified by sequencing.
- Prenatal testing is available to couples who are confirmed carriers of mutations. Please contact the laboratory genetic counselor to discuss appropriate testing prior to collecting a prenatal specimen.