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FLT3 Mutation Detection

FLT3 mutations have been identified in hematologic neoplasms, particularly in 20-30% of acute myeloid leukemia (AML). *FLT3* internal tandem duplication (ITD) mutations have been associated with an unfavorable outcome. FLT3 tyrosine kinase domain mutations affecting codon D835 are also common (7%) but have a less-clear prognostic significance. Early mutation identification may provide better prognostication and aid in the determination of the most effective therapeutic regimen.

INDICATIONS FOR ORDERING

- Refine classification and determine prognosis in patients with AML.
- Determine FLT3 mutational status in relapsed AML.
- Aid in selection of appropriate chemotherapy regimen.
- Not intended for minimal residual disease monitoring.

DISEASE OVERVIEW

Treatment Issues

- 50% of cases are cytogenetically normal AML (CN-AML) and are considered to be intermediate risk.
- Mortality varies significantly among patients within the intermediate risk group.
- Mutational testing may help in AML prognostication.
  - Presence of mutations may alter therapeutic decisions.

GENETICS

Structure/Function

FLT3

- ITDs on exon 14/15; D835 mutation on exon 20
- Tyrosine kinase receptor regulates cell survival and maturation.

RELATED INFORMATION

Acute Myeloid Leukemia - AML

Tumor Markers

TESTS TO CONSIDER

Initial Prognostication in AML

FLT3 ITD and TKD Mutation Detection 3001161
Method: Polymerase Chain Reaction

Genomic DNA is extracted and amplified in multiplex with primers targeting *FLT3* mutations in AML

- *FLT3* mutation detection by polymerase chain reaction (PCR) amplification of exon 14 ITDs and D835
- PCR products are *EcoRV*-digested and analyzed by capillary electrophoresis
- ITDs are reported with a signal ratio and D835 variants as Detected or Not Detected

Myeloid Malignancies Mutation Panel by Next Generation Sequencing 2011117
Method: Massively Parallel Sequencing

NPM1 Mutation Detection by RT-PCR, Quantitative 3000066
Method: Quantitative Reverse-Transcription Polymerase Chain Reaction

CEBPA Mutation Detection 2004247
Method: Polymerase Chain Reaction/Sequencing

IDH1 and IDH2 Mutation Analysis, exon 4 2006444
Method: Polymerase Chain Reaction/Sequencing

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