MAYO CLINIC LABORATORIES

Test Definition: P190M

BCR::ABL1, p190, mRNA Detection, Reverse Transcription PCR, Quantitative, Monitoring Assay, Bone Marrow

Overview

Useful For

Detection of e1/a2 *BCR::ABL1* (p190) fusion at diagnosis of acute myeloid leukemia (ALL) and *BCR::ABL1* (p210) negative chronic myeloid leukemia (CML) using bone marrow specimens

Monitoring response to therapy in patients with known e1/a2 *BCR::ABL1* (p190) fusion forms in childhood ALL, adult ALL, and rare CML cases

Method Name

Quantitative Reverse Transcription Polymerase Chain Reaction (RT-PCR)

NY State Available

No

Specimen

Specimen Type

Bone Marrow

Necessary Information

The following information is required:

1. Pertinent clinical history including if the patient has a diagnosis of chronic myeloid leukemia or other *BCR::ABL1*-positive neoplasm
2. Date of collection

Specimen Required

Container/Tube: Lavender top (EDTA)

Specimen Volume: 4 mL

Collection Instructions:

1. Invert several times to mix bone marrow.
2. Send bone marrow specimen in original tube. **Do not aliquot**.

Specimen Minimum Volume

1 mL

Reject Due To

Gross	Reject

hemolysis	
Moderately to severely clotted	Reject

Specimen Stability Information

Specimen Type	Temperature	Time	Special Container
Bone Marrow	Refrigerated (preferred)	72 hours	
	Ambient	72 hours	

Clinical & Interpretive

Clinical Information

Messenger RNA (mRNA) transcribed from *BCR::ABL1* (fusion of the breakpoint cluster region gene [*BCR*] at chromosome 22q11 to the Abelson gene [*ABL1*] at chromosome 9q34) is detected in all patients with chronic myeloid leukemia (CML) and a subset of patients with both acute lymphoblastic leukemia (ALL) and acute myeloid leukemia. Although breakpoints in the *BCR* and *ABL1* genes may occur in a variety of locations, splicing of the primary RNA transcripts result in only 8 fusion site variants (e1/a2, e6/a2, e13/a2, e14/a2, e19/a2, and e1/a3, e13/a3, e14/a3), which incorporate the entire sequence of the exons on both sides of the fusion site. The e1/a2 and e1/a3 fusion forms produce a 190-kDa protein designated p190. This BCR::ABL1 protein form is found in approximately 75% of patients with childhood ALL and approximately 50% of patients with adult ALL, with the majority arising from e1/a2 mRNA. The p190 is also the predominant fusion form in a small subset of patients with CML, although the vast majority of CML cases contain the p210 protein, typically from e13/a2 or e14/a2 mRNA fusions. Other fusion forms are very rare.

Quantitative reverse-transcription polymerase chain reaction is the most sensitive method for monitoring *BCR::ABL1* levels during treatment. This test detects mRNA coding for the most common p190 fusion form (e1/a2).

Reference Values

An interpretive report will be provided

Interpretation

The interpretive report includes an overview of the findings.

Cautions

This test detects only the e1/a2 *BCR::ABL1* (p190) fusion form. Other fusion forms are not detected by this assay, including those containing the *BCR* e13 and e14 exons, which code for the p210 protein commonly found in chronic myeloid leukemia, and the rare e1/a3 (p190) fusion form.

The precision of this assay at very low *BCR::ABL1* levels is less reliable, such that interassay variation can be more variable. If the results are being used to make major therapeutic decisions, significant changes during monitoring should be verified with a subsequent specimen.

Results of this assay cannot be directly compared with results generated from other polymerase chain reaction (PCR) assays, including identical assays performed in other laboratories. Monitoring should be performed using the same method and laboratory for each subsequent specimen.

The results of this assay cannot be directly compared with *BCR::ABL1* results obtained using fluorescence in situ hybridization (FISH) technology. FISH measures DNA alleles and this PCR-based assay measures messenger RNA (mRNA) transcripts. Because a single DNA allele can produce many mRNA transcripts, the values are not directly comparable.

Blood is the specimen of choice for monitoring. While most patients show similar *BCR::ABL1* levels in blood and bone marrow collected at the same time, some patients have a consistent difference in the levels in blood and bone marrow such that altering specimen types during monitoring can lead to confusion.

Assay precision does not appear to be significantly affected by specimen transport or moderate delays in processing. However, in specimens with very low levels of *BCR::ABL1*, these conditions may cause sufficient RNA degradation to produce false-negative results. Thus, specimens should be shipped as quickly as possible. Ambient specimens received greater than 3 days after specimen collection and refrigerated specimens received greater than 5 days after specimen collection are unacceptable.

Clinical Reference

1. Hughes TP, Kaeda J, Branford S, et al. Frequency of major molecular responses to imatinib or interferon alfa plus cytarabine in newly diagnosed chronic myeloid leukemia. N Engl J Med. 2003;349(15):1423-1432
2. Radich JP, Gooley T, Bryant E, et al. The significance of *BCR*/*ABL* molecular detection in chronic myeloid leukemia patients "late," 18 months or more after transplantation. Blood. 2001;98(6):1701-1707
3. Olavarria E, Kanfer E, Szydlo R, et al. Early detection of *BCR-ABL* transcripts by quantitative reverse transcriptase-polymerase chain reaction predicts outcome after allogeneic stem cell transplant for chronic myeloid leukemia. Blood. 2001;97(6):1560-1565
4. Tefferi A. The classic myeloproliferative neoplasms: Chronic myelogenous leukemia, polycythemia vera, essential thrombocythemia, and primary myelofibrosis. In: Valle DL, Antonarakis S, Ballabio A, Beaudet AL, Mitchell GA, eds. The Online Metabolic and Molecular Bases of Inherited Disease. McGraw-Hill; 2019. Accessed November 27, 2024. Available at https://ommbid.mhmedical.com/content.aspx?sectionid=225078035&bookid=2709

Performance

Method Description

The assay is performed using an automated platform, GeneXpert (Cepheid). Bone marrow specimen is processed and added to an individual sample cartridge and loaded onto the GeneXpert machine. All subsequent reactions are performed within the cartridge and the results are processed and calculated by the instrument. Within the cartridge, RNA is extracted and converted to complementary DNA (cDNA). Quantitative, reverse transcription polymerase chain reaction (PCR) is performed with a nested PCR reaction containing primers designed to amplify cDNA from the e1a2 fusion products. A fragment of ABL1 cDNA is also amplified as a control for RNA degradation and for normalization of

BCR::ABL1 results.(Unpublished Mayo method)

PDF Report
Supplemental

Day(s) Performed
Monday through Friday

Report Available
2 to 4 days

Specimen Retention Time
2 weeks

Performing Laboratory Location
Mayo Clinic Jacksonville Clinical Lab

Fees & Codes

Fees
- Authorized users can sign in to Test Prices for detailed fee information.
- Clients without access to Test Prices can contact Customer Service 24 hours a day, seven days a week.
- Prospective clients should contact their account representative. For assistance, contact Customer Service.

Test Classification
This test was developed and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. It has not been cleared or approved by the US Food and Drug Administration.

CPT Code Information
81207

LOINC® Information

Test ID	Test Order Name	Order LOINC® Value
P190M	BCR/ABL1, p190, Quant, Monitor, BM	49795-8

Result ID	Test Result Name	Result LOINC® Value
618880	Interpretation	69047-9
622946	Signing Pathologist	19139-5
623196	Indication for Testing	42349-1
623197	Specimen	31208-2

623275	Source	31208-2
623198	Sample ID	80398-1
623199	Result	82939-0
623200	Method Summary	85069-3
623201	Disclaimer	62364-5