LPL - LPL-ROHINI (NATIONAL REFERENCE LAB)
SECTOR - 18, BLOCK -E ROHINI
DELHI 110085

Name	:	**DUMMY--Z535**				**Collected**	: **16/4/2018 7:01:00AM**
						Received	: **16/4/2018 2:20:00PM**
Lab No.	:	**LPLT12428**	**Age: 15 Years**	**Gender:**	**Male**	**Reported**	: **23/6/2018 4:02:54PM**
A/c Status	:	**P**	**Ref By :**	**----------**		**Report Status**	:

Test Name	Results	Units	Bio. Ref. Interval
PML-RARA GENE REARRANGEMENT, PCR QUALITATIVE (Real Time PCR)			
PML - RARA Type bcr 1			
PML - RARA Type bcr 2			
PML - RARA Type bcr 3			

Note

1. Sensitivity of the assay is 0.01% when copies of ABL detected is 100,000
2. Limit of detection is 10 copies of PML-RARA fusion gene transcripts per PCR
3. This is an in-house developed assay designed as per EAC (Europe Against Cancer) protocol
4. This test detects 3 types of translocations - bcr 1, bcr 2 & bcr 3
5. Test conducted on Whole blood / Bone Marrow

Comments

Acute Promyelocytic Leukemia (APL) is characterized by a unique reciprocal chromosomal translocation t(15;17) (q22;q11-12) and its underlying fusion gene PML / RARA rearrangement. The fusion is seen between Promyleocytic (PML) gene on chromosome 15 and RARA gene on chromosome 17. Based on PML breakpoint location, the PML RARA transcripts subtype bcr 1 & bcr 2 (Long transcript type) and bcr 3 (Short transcript type) may be formed.

Uses

- For diagnostic identification of PML RARA in cases of Acute Promyelocytic Leukemia
- To assess molecular resistance & predict response to treatments containing ATRA and / or ATO

Test Name	Results	Units	Bio. Ref. Interval
AML ETO GENE REARRANGEMENT t(8;21) (q22;q22);(RUNX1;RUNX1T1), PCR, QUALITATIVE (Real Time PCR)			

Note

1. Sensitivity of the assay is 0.01% when copies of ABL detected is 100,000
2. Limit of detection is 10 copies of 8;21 fusion gene transcripts per PCR
3. This is an in-house developed assay designed as per EAC (Europe Against Cancer) protocol

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Test Name	Results	Units	Bio. Ref. Interval

4. Test conducted on Whole blood / Bone Marrow

Comments

Cytogenetic aberrations play a central role in the classification of AML. These aberrations are detected in 50-70% cases of AML by using standard techniques. The AML1(CBFA2, RUNX1)-ETO (MTG8) gene fusion results from the t(8;21)(q22;q22), which is the commonest chromosomal rearrangement associated with AML, being detected in approximately 8% of AML cases in children and young adults. Most t(8;21) positive AML's are de novo leukemias - vast majority being M2 FAB subtype. This translocation creates chimeric genes encoding fusion proteins that interfere with the function of CBFα and block the maturation of myeloid cells.

Uses

- For diagnostic identification of AML having morphological, imuunophenotypic or clinical features strongly suggestive of translocation 8;21
- For prognostic evaluation - Presence of this translocation is associated with a favorable prognosis

INV 16 (p13q22) / t(16;16)(p13;q22), GENE REARRANGEMENT, PCR , QUALITATIVE
(Real Time PCR)

Note

1. Sensitivity of the assay is 0.01% when copies of ABL detected is 100,000
2. Limit of detection is 10 copies of Inv(16)(p13q22) / t(16;16)(p13;q22) with the CBFB-MYH11 fusion gene transcript per PCR
3. This is an in-house developed assay designed as per EAC (Europe Against Cancer) protocol
4. This tests detects A, D, and E transcripts but does not distinguish between them
5. Test conducted on Whole blood / Bone Marrow

Comments

Cytogenetic aberrations play a central role in the classification of AML. These aberrations are detected in 50-70% cases of AML by using standard techniques. Pericentric inversion of chromosome 16, inv(16)(p13q22), is found in about 4% of cytogenetically abnormal AML cases. Inv(16) or the rarer t(16;16)(p13;q22) creates chimeric genes encoding fusion genes that interfere with the function of CBFα and block the maturation of myeloid cells. Around 10 different CBFB-MYH11 FG transcripts have been reported. More than 85% of positive patients have the type A transcript; type D and E transcripts each represent nearly 5%, whereas all other types occur sporadically.

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Test Name	Results	Units	Bio. Ref. Interval

Uses

- For diagnostic identification of AML having morphological, imuunophenotypic or clinical features strongly suggestive of M4eo FAB subtype
- For prognostic evaluation - Presence of this translocation is associated with a favorable prognosis

Dr.Atul Thatai
PhD (Biotechnology)
HOD Molecular Diagnostics - NRL

Dr. Anil Arora
MD (Pathology)
HOD Hemat & Imm - NRL

Result/s to follow:
AML CHARACTERIZATION by PCR

IMPORTANT INSTRUCTIONS

*Test results released pertain to the specimen submitted.*All test results are dependent on the quality of the sample received by the Laboratory. *Laboratory investigations are only a tool to facilitate in arriving at a diagnosis and should be clinically correlated by the Referring Physician .*Sample repeats are accepted on request of Referring Physician within 7 days post reporting.*Report delivery may be delayed due to unforeseen circumstances. Inconvenience is regretted.*Certain tests may require further testing at additional cost for derivation of exact value. Kindly submit request within 72 hours post reporting.*Test results may show interlaboratory variations.*The Courts/Forum at Delhi shall have exclusive jurisdiction in all disputes/claims concerning the test(s) & or results of test(s).*Test results are not valid for medico legal purposes. *Contact customer care Tel No. +91-11-39885050 for all queries related to test results.