

Acute Lymphocytic Leukemia (ALL) Panel by FISH, Adult

Indications for Ordering

Risk stratification and therapeutic management in adults with newly diagnosed ALL

Test Description

Fluorescence in situ hybridization

- FISH probes detect
 - *BCR/ABL1* t(9;22)
 - *MLL* 11q23 rearrangement (partner not determined)
 - t(1;19) translocation
 - IGH rearrangement (partner not determined)
 - *MYC* rearrangement (partner not determined)
- Each probe can be run as part of the panel or individually
- Bone marrow (BM) cells on unstimulated cultures either from direct harvest or 24-hour culture

Tests to Consider

Typical testing strategy

At diagnosis, minimum ALL workup includes BM aspirate for

- Morphology
- Immunophenotyping
- Cytogenetics
- ALL panel by FISH
 - Adjunct to conventional cytogenetics (CC)
 - Option for detecting prognostically important rearrangements

Primary test

[Acute Lymphocytic Leukemia \(ALL\) Panel by FISH, Adult 2002647](#)

- Recommended FISH panel for adults with newly diagnosed ALL

Related tests

[Leukemia/Lymphoma Phenotyping by Flow Cytometry 2008003](#)

- Aids in diagnosis of hematopoietic neoplasms

[Chromosome Analysis, Bone Marrow 2002292](#)

- Diagnosis, prognosis, and monitoring of ALL

[Chromosome Analysis, Bone Marrow with Reflex to Genomic Microarray 2007130](#)

- Diagnosis, prognosis, and monitoring of ALL
- If chromosome analysis is “normal” or “no growth,” then genomic microarray testing will be added

[Cytogenomic SNP Microarray – Oncology 2006325](#)

- Preferred test for fresh specimens at time of diagnosis for detecting prognostically important genomic abnormalities in leukemias/lymphomas and solid tumors involving
 - Loss/gain of DNA
 - Loss of heterozygosity (LOH)
 - Monitor disease progression and response to therapy

[Chromosome FISH, Interphase 2002298](#)

- Specific FISH probes must be requested and include
 - *MYC*
 - *BCR-ABL1*
 - *MLL*
 - *IGH*
 - *TCF3 (E2A)*

[BCR-ABL1, Qualitative with Reflex to BCR-ABL1 Quantitative 2005010](#)

- Recommended when submitting initial diagnostic sample for chronic myelogenous leukemia (CML) or Ph+ ALL (no previous *BCR-ABL1* testing)
- If qualitative test is positive, the appropriate corresponding quantitative test is performed

Disease Overview

Incidence – 1.6/100,000 individuals per year

- Most common leukemia in childhood

Treatment issues

- Treatment protocols are stratified by the presence of t(9;22) (ie, Philadelphia chromosome status) and age
- Cytogenetic studies are very important for prognostication

Prognosis	Good	Poor
Age	Younger age <ul style="list-style-type: none"> • Especially <25 years when treated with a pediatric protocol 	Older age <ul style="list-style-type: none"> • Individuals >60 years have a particularly poor prognosis High WBC <ul style="list-style-type: none"> • >30 x 10⁹/L for B-cell ALL • >100 x 10⁹/L for T-cell ALL
Mutations		t(9;22) positive <ul style="list-style-type: none"> • Most frequent chromosomal abnormality <i>MLL</i> rearrangements t(8;14) Complex karyotype (>5 chromosomal abnormalities) Low hypodiploidy/near triploidy

Genetics

Genes – *BCR-ABL*, *MLL*, *E2A*, *IGH*, *MYC*

Structure/function

- *BCR-ABL1* t(9;22)
 - Results in chimeric constitutively active tyrosine kinase
 - Present in 25% of adult ALL
- *MLL* t(v;11q23)
 - Results in disruption of regulation of Hox gene expression
 - Present in 10% of adult ALL
- *TCF3(E2A)-PBX1* t(1;19)
 - Chimeric E2A-PBX1 protein interacts with major HOX proteins
 - Present in 3% of adult ALL
- *c-MYC* t(8;14), t(2;8), t(8;22)
 - Results in *MYC* overexpression with subsequent dysregulation of proliferation, differentiation, and cell death lymphoid transcriptional programs
 - Present in 4% of adult ALL
 - There are multiple potential partners of *IGH* rearrangements in ALL

Test Interpretation

Results

- Normal – no evidence of *BCR/ABL1* t(9;22), *MLL* rearrangement, *TCF3 (E2A)* translocation, *IGH* or *MYC* rearrangement
- Abnormal – one of the above rearrangements or translocations detected

Limitations

- Panel detects only the specific aberrations targeted by the probes
- Chromosome alterations outside the regions complementary to these FISH probes will not be detected