



History

Treatment for pediatric ALL is a success story of modern oncology

- 1950s: fatal
- Today: ~90% survival for children
 - While overall survival has improved, ALL is still one of the leading causes of cancer deaths in children

Adult survival has also improved

~40-50% survival for adults (age dependent)

• AYA patients benefit from pediatric-inspired regimens

Progress through improved understanding of ALL biology

Advances in diagnosis, prognosis and therapy









Classification of acute leukemias is increasingly complex

- French-American-British classification of 1976
 - Morphology
- Cytochemistry
- WHO classifications of 2001 and 2008
 - Morphology
 - Clinical features
 - Immunophenotype
- Genetics
- 2016 revision of WHO classification
- Includes substantial new genetic knowledge





Transcriptional landscape of B cell precursor acute lymphoblastic leukemia based on an international study of 1,223 cases

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Li JF, et al. Proc Natl Acad Sci U S A. 2018 Dec 11;115(50):E11711-E11720. 1223 cases; 14 subtypes

PAX5-driven subtypes of B-progenitor acute lymphoblastic leukemia

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G1 (MEF2D fusions)

G5 (ZNF384 fusions)

G7 (Hyperdiploidy)

Subgroup

G2 (TCF3-PBX1)

G6 (BCR-ABL1/Ph-like)

G8 (KMT2A fusions)

G3 (ETV6-RUNX1/-like) G4 (DUX4 fusions)

Recently described ALL rearrangements

DUX4 rearranged

• Often IGH-DUX4 rearrangement

- Loss of ERG function, either via deletion or expression of dominant negative isoform
- Patients seem to do well with standard therapy despite frequent IKZF1 deletions

MEF2D rearranged

ZNF384 rearranged

Two PAX5-related groups:

- PAX5 p.Pro80Arg, typically with loss-of-function of the other allele
- PAX5-altered, with rearrangements, other sequence mutations, or focal intragenic amplifications

BCR-ABL1-like

Multiple subcategories

MYC/BCL2/BCL6 rearranged

NUTM1 rearranged

Prognosis

Fusion identification can be used for risk-adapted therapy in ALL





BCR-ABL1-like (Ph-like) B-ALL

•Defined by expression pattern similar to BCR-ABL1 rearranged B-ALL, but without BCR-ABL1 rearrangement

• Originally described in 2009

•Approximately 15% childhood B-ALL overall, with increasing incidence by age

• From 10% (standard risk children) to ~20% (adolescents) to ~25% (young adults)

•Approximately 20% of adult B-ALL

BCR-ABL1-like B-ALL: biology

Activation of kinase signaling pathways via many different alterations

ABL1-class rearrangements

- ~15-20% BCR-ABL1-like
- Rearrangements of ABL1, ABL2, CSF1R, PDGFRB ("ABL1-class")
- Diverse partners with common result of kinase signaling activation

CRLF2 rearrangements leading to CRLF2 overexpression

- ~50% of BCR-ABL1-like
- Cytokine receptor-like factor 2 located in pseudo-autosomal region of the X and Y chromosomes
- Rearrangement with IGH (chromosome 14) or P2RY8 (Xp22/Yp11)
- Many of these cases also have activating alterations in the JAK/STAT pathway, particularly JAK2 point mutations

Activating rearrangements of JAK2 or EPOR

- ~10-15% BCR-ABL1-like
- Diverse partners with common result of signaling pathway activation



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BCK	-ABL	.1-11Ke E	Fusion partners	
	ADI 1	I Ni	identified to date, if	CENDO ETVO EOVELLONINA NUESS
	ADLI	imaunib/dasatinib	13	SEPO SNX1 SNX2 SPTNA1 ZMIZ1
r	ABL2	Imatinib/dasatinib	3	PAG1. BCSD1. ZC3HAV1
	CSF1R	Imatinib/dasatinib	3	MEF2D. SSBP2. TBL1XR1
class fusions	PDGFRA	Imatinib/dasatinib	1	FIP1L1
	PDGFRB	Imatinib/dasatinib	8	ATF7IP, EBF1, ETV6, SNX29, SSBP2, TNIP1, ZEB2, ZMYND8
	LYN	Imatinib/dasatinib	2	GATAD2A, NCOR1
ì	CRLF2	JAK2 inhibitor	3	CSF2RA, IGH, P2RY8
AK/STAT	JAK2	JAK2 inhibitor	21	ATF7IP, BCR, EBF1, ETV6, GOLGA5, HMBOX1, OFD1, PAX5, PCM1, PPFIBP1, RFX3, SMU1, SNX29, SSBP2, STRN3, TERF2, TPR, USP25, ZBTB46, ZNF274, ZNF340
ating fabiono	EPOR	JAK2 inhibitor	4	IGH, IGK, LAIR1, THADA
	TSLP	JAK2 inhibitor	1	IQGAP2
	TYK2	TYK2 inhibitor	3	MYB, SMARCA4, ZNF340
	IL2RB	JAK1/JAK3 inhibitor	1	MYH9
	NTRK3	TRK inhibitor	1	ETV6
	PTK2B	FAK inhibitor	3	KDM6A, STAG2, TMEM2
	FGFR1	Ponatinib	1	BCR
	FLT3	FLT3 inhibitor	1	ZMYM2
	DGKH		1	ZFAND3
	BLNK		1	DNTT













Common genetic findings in T-ALL

- Rearrangements between T cell receptor loci and various partner genes are most common
- Alterations in *NOTCH1* and/or *FBXW7*, both of which result in *NOTCH1* pathway activation
- Deletions of CDKN2A/B
- JAK-STAT, PI3K-AKT, RAS-MAPK pathway activation

Recurrent T-ALL rearrangements

Rearrangements resulting in deregulated expression of a target gene			Rearrangements resulting in chimeric fusions		
Target gene	п	Rearrangement partner (number of cases)	Gene	п	Partner gene
TLX1	17	TRB (7), TRA (5), TLX1-upstream (4), LINC00502-TLX1 (1) BCL 11B-TLX3 (8), CDK6-TLX3 (2), TRB (1)	MLLT10	15	PICALM (9), DDX3X (2), KMT2A (1), FAM171A1 (1), NAP111 (1), CAPS2 (1)
TAL	50	TLX3-CASC15 (1), TLX3-TARBP1 (1) STI((50), TRX(5), DHY0, TAL1(1), CNIDAT, TAL1(1)	KMT2A	12	MLLT1 (7), ELL (1), MLLT10 (1), AFDN (1), MLLT6 (1),
TALI	00	TALI-TARP (1)	ABL1	7	NUP214 (4), SLC9A3R1 (1), ETV6 (1), MBNL1 (1)
TAL2	6	1RB (6)	NUP98	5	RAP1GDS1 (2), CCDC28A (1), LNP1 (1), PSIP1 (1)
LMOI	3		TFG	3	ADGRG7 (3)
LMU2	13	TRA (6), TRB (5), CSTF3-LMO2 (1), FOXJ3-LMO2 (1)	JAK2	2	PCM1 (1), CD99 (1)
LYLI	1	TRB (1)	ETV6	2	ABL1 (1), CTNNB1 (1)
NKX2-1	9	TRA (6), NKX2-1–BCL11B (1), CDK6–NKX2-1 (1), NKX2-1–DIO2 (1)	ZC3HAV1	2	ABL2 (1), AKAP11 (1)
HOXA	7	TRB (4), HOXA insertion (1), LINC01260–HOXA (1), POLR2E–HOXA (1)	LMAN2	2	NSDI (1), PAPOLA (1)
МҮВ	11	TRB (2), SLC12A9-MYB (1), MYB-PLAGL1 (1), MYB-BDP1 (1), MYB-CHMP1A (1)			
		An11-WTD (S)			
					Liu Y et al, Nat Genet. 2017 Aug;49(8):1211-121

Fusion detection strategies

Diversity of underlying genetic alterations makes detection complex!

Expression analysis

- Can identify category as a whole, but not specific alteration
- Possible screening tool
- Children's Oncology Group (COG) uses a low density array (LDA) for *BCR-ABL1*-like screening
- Targeted fusion analysis
- Multiplex FISH
- Multiplex RT-PCR
- Targeted RNA sequencing panels

Comprehensive analysis

- Whole transcriptome sequencing
- Whole genome sequencing

Increasing role for molecular testing

