

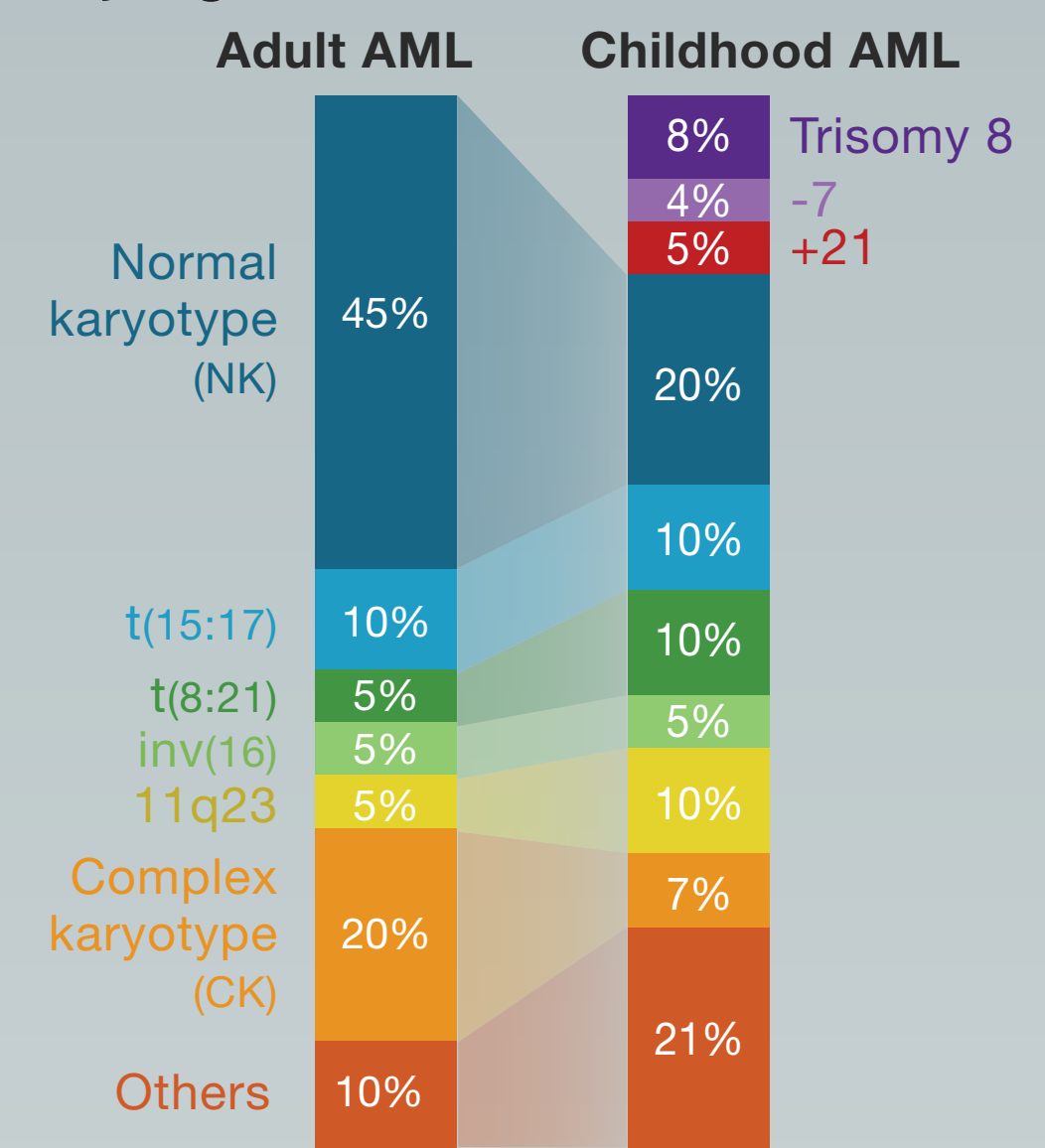
SnapShot: Acute Myeloid Leukemia

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Clinical Features and Risk Stratification of AML

Prognostic category	Favorable risk (5 yr OS: 45%-80%)		Intermediate risk (5 yr OS: 20%-40%)		Adverse risk (5 yr OS: 5%-20%)	
	40%-45% of AML cases		25%-35% of AML cases		25%-30% of AML cases	
	Aberration	Frequency (%)	Aberration	Frequency (%)	Aberration	Frequency (%)
Favorable risk	t(15:17)	7-12	NK with <i>FLT3</i> -ITD	15-20	11q23	3-5
	t(8:21)	5-8	NK with <i>NPM</i> ^{WT} & no <i>FLT3</i> -ITD	10-17	inv(3)/t(3;3)/ <i>EVI-1</i>	~1
	inv(16)	5-8	t(9:11)	2-3	t(6;9)/ <i>DEK-NUP214</i>	~1
	NK with <i>NPM</i> ^{mut} & no <i>FLT3</i> -ITD	18-25	Other cytogenetic abnormalities not included elsewhere	5-8	-7/7q-	3-5
	NK with biallelic <i>CEBPA</i> ^{mut}	6-12			-5/5q-	2-3
Intermediate risk					17p deletions	~2
					CK	10-12
Adverse risk						
Current therapies	Standard induction cytotoxic therapy ("3+7"), followed by postremission therapy with high dose cytarabine ATRA as a differentiating agent with anthracycline based chemotherapy in t(15;17)		Standard induction cytotoxic therapy ("3+7"), followed by postremission consolidation Allogeneic HSCT should be considered as main modality of consolidation, especially in patients with <i>FLT3</i> -ITD		Standard induction cytotoxic therapy ("3+7"), although dismal outcome with chemotherapy alone Allogeneic HSCT should be offered in clinical remission 1 Consider use of investigational and novel agents	

Cytogenetic Aberrations in AML



Molecular Mechanisms, Recurrent Gene Mutations, and Emerging Targeted Therapies in AML

t(15:17), PML-RAR α

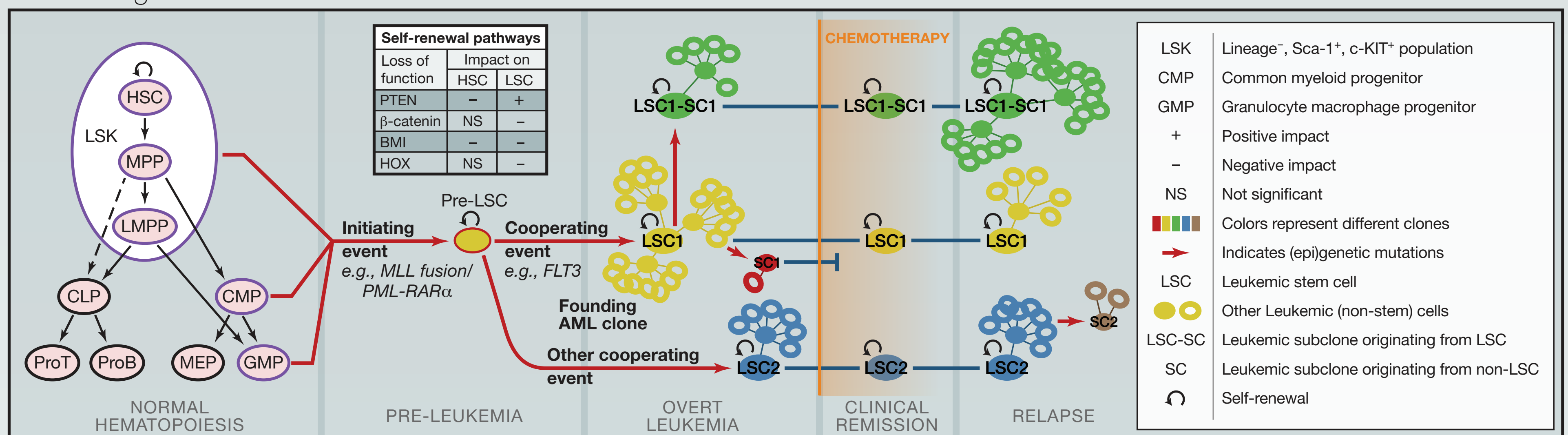
11q23, MLL fusion

t(8:21), AML1-ETO; inv(16), CBF-MYH11

t(8:21), AML1-ETO

Gene	Frequency (in NK-AML) and comments
Signalling	
<i>FLT3</i> -ITD	20%-25% (28%-35%); High blast count; Poor prognosis especially in cases with high mutant to WT allelic ratio
<i>FLT3</i> -TKD	5%-7% (10%-14%); Prognostic impact remains controversial
<i>NRAS</i>	10% (9%-14%); Enriched in CBF AML; Prognosis unknown
<i>C-KIT</i>	<5% (<5%); 25-30% in CBF leukaemia
<i>PTEN</i>	<2% (2%); Prognosis unknown
Transcription factors (TF)	
<i>NPM1</i>	25%-30% (40%-65%); M4 blast morphology lacks CD34 expression; Hox gene upregulation; Favorable prognosis in the presence of <i>FLT3</i> ^{WT} ; Female preponderance
<i>CEBPA</i>	5%-10% (10-19%); Favorable prognosis if biallelic mutation
<i>RUNX1</i>	5%-13% (6-25%); Enriched in trisomy 13 and FAB M0; Poor prognosis
<i>WT1</i>	10% (10%-13%); Associated with M0 FAB type; Poor prognosis
<i>TP53</i>	2%-4% (<2%); Predominantly in CK-AML; Very poor prognosis
Epigenetic modifiers	
<i>DNMT3A</i>	20%-25% (32%-35%); Heterozygous R882 mutations account for 40%-60% of mutations; Poor prognosis in NK-AML
<i>IDH1/IDH2</i>	12%-22% (25%-30%); Mutant <i>IDH1</i> & 2 are mutually exclusive; <i>IDH1</i> mutations enriched in patients with <i>NPM1</i> ^{mut} ; <i>IDH1</i> is localized in cytoplasm and peroxisomes
<i>TET2</i>	7%-15% (15%-23%); Mutually exclusive to <i>IDH1/2</i> mutations; More prevalent in secondary AML especially MPN
<i>ASXL1</i>	3% (3%-5%); Poor prognosis
<i>EZH2</i>	<2% (<1%); Enriched in MDS/MPN; Prognosis unknown
<i>MLL-PTD</i>	<2% (2%-5%); Enriched in trisomy 11
Overexpressed	
<i>EVI-1</i>	Deregulated in inv(3)(q21q26); Poor prognosis
<i>MN1</i>	Poor response to chemotherapy; Correlated with <i>NPM1</i> ^{WT} and high BAALC expression
<i>BAALC</i>	High expression in NK and +8; Poor prognosis
<i>ERG</i>	Poor prognosis in CK and NK AML
<i>miR-181</i>	Increased in FAB M1/M2, <i>CEBPA</i> ^{mut} ; Favorable prognosis

Cell of Origin and Clonal Evolution Model of Leukemic Stem Cells



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