Supplemental Tables

Supplemental Table 1. Mastocytosis Subtypes (Variants)

Cutaneous mastocytosis

- Urticaria pigmentosa / maculopapular cutaneous mastocytosis
- Diffuse cutaneous mastocytosis
- Mastocytoma of skin

Systemic mastocytosis

- Indolent systemic mastocytosis (includes bone marrow mastocytosis)[a]
- Smoldering systemic mastocytosis [a]
- Aggressive systemic mastocytosis [a]
- Mast cell leukemia
- Systemic mastocytosis with an associated myeloid neoplasm

Mast cell sarcoma

a The diagnosis of these variants of systemic mastocytosis require correlation with B and C findings.

Supplemental Table 2. Systemic Mastocytosis: B-findings

1. High mast cell burden, >30% of BM cellularity by mast cell aggregates (assessed on BM biopsy) and serum tryptase >200 ng/mL
2. Cytopenia (not meeting criteria for C findings) or -cytosis. Reactive causes are excluded, and criteria for other myeloid neoplasms are not met.
3. Hepatomegaly without impairment of liver function, or splenomegaly without features of hypersplenism including thrombocytopenia, and/ or lymphadenopathy (>1 cm size) on palpation or imaging

Supplemental Table 3. Mast Cell Leukemia

1. Meets diagnostic criteria for SM
2. BM aspirate shows $\geq$20% atypical immature mast cells[a/b]

[a] Atypical immature mast cells include promastocytes, metachromatic blast-like forms, multinucleated or highly pleomorphic mast cells.

[b] In the presence of a suboptimal aspirate (dry tap), a BM biopsy showing a dense, diffuse mast cell infiltration of atypical immature mast cells is sufficient to support the diagnosis of mast cell leukemia.

Supplemental Table 4. Features of the various clonal cytopenias

Type		**Dysplasia[a]**	**Other features**
Clonal cytopenia of undetermined significance (CCUS)		Absent	No comorbid condition that explains the cytopenia; no MDS-defining genetic abnormality[b]
VEXAS syndrome		Absent[c]	Autoimmune manifestations *UBA1* mutation; no MDS-defining genetic abnormality[b]
Myelodysplastic syndrome		Present, or an MDS-defining genetic abnormality[b]	Classified according to Table 20

[a]Defined as dysplastic cytologic changes in ≥10% of erythroid cells, granulocytic cells, and/or megakaryocytes; absence of dysplasia requires less than these thresholds in all lineages in an adequate bone marrow sample.

[b]MDS-defining genetic abnormalities are *SF3B1* mutation (VAF >10%), multi-hit *TP53* mutation (VAF >10%), or del(5q), del(7q), -7 or complex karyotype detected by karyotype. Additional features may be required in the setting of a germline predisposition condition (see "Diagnosis of Myelodysplastic Syndrome in the Setting of Germline Predisposition" section).

[c]Vacuolation of erythroid and myeloid precursors are not considered to be MDS-defining dysplastic features in the setting of VEXAS.

Supplemental Table 5. Symptoms and signs at diagnosis of JMML.[1]

Pallor	64%	Splenomegaly	97%
Fever	54%	Hepatomegaly	97%
Infection	45%	Lymphadenopathy	76%
Bleeding	46%	Skin rash	36%
Cough	40%	Café au lait spots	12%
Abdominal pain	7%	Xanthoma	7%
Bone pain	< 4%	CNS infiltration*	< 3%
Diarrhea	< 4%		

*myeloid sarcoma, diabetes insipidus, facial palsy.

Supplemental Table 6. Acute myeloid leukemia (AML) with other rare recurring translocations

- AML with t(1;3)(p36.3;q21.3)/*PRDM16*::*RPN1*
- AML with t(3;5)(q25.3;q35.1)/*NPM1*::*MLF1*
- AML with t(8;16)(p11.2;p13.3)/*KAT6A*::*CREBBP*
- AML (megakaryoblastic) with t(1;22)(p13.3;q13.1)/*RBM15*::*MRTF1**
- AML with t(5;11)(q35.2;p15.4/ *NUP98::NSD1**
- AML with t(11;12)(p15.4;p13.3)/*NUP98::KMD5A**
- AML with *NUP98* and other partners*
- AML with t(7;12)(q36.3;p13.2)/*ETV6*::*MNX1**
- AML with t(10;11)(p12.3;q14.2)/*PICALM::MLLT10*
- AML with t(16;21)(p11.2;q22.2)/*FUS::ERG*
- AML with t(16;21)(q24.3;q22.1)/*RUNX1::CBFA2T3*
- AML with inv(16)(p13.3q24.3)/*CBFA2T3::GLIS2**

* Occurs predominantly in infants and children

Supplemental Table 7. Provisional entities in acute lymphoblastic leukemia/lymphoma (ALL) (See references for reviews and additional references therein) [2-14]

B-ALL					
Subtype	Frequency	Gene expression pattern	Genomics	Immunophenotype	Comment
ETV6::*RUNX1*-like	<5%, mostly children	GEP Clusters with *ETV6*::*RUNX1*	Fusions or CNAs in ETS family genes including *ETV6*, *FUS* and also *IKZF1*; some cases harbor germline LOF *ETV6* mutations	CD27+CD44- or low, like *ETV6*::*RUNX1*	Good prognosis in children, not adults
PAX5 alteration** (PAX5alt)	10% children and adults	Broad GEP cluster near Ph like	Various mutations (esp. compound heterozygosity for R38, R140), intragenic amplifications and non-kinase fusions (*ETV6* most common)		Intermediate prognosis
ZEB2 (p.H1038R) or *IGH::CEBPE*	< 1%	GEP cluster of *ZEB2* H1038R and IGH::*CEBPE* fusion	*ZEB2 (*H1038R) mutation, mostly coexisting with IGH::*CEBPE* or other known gene fusions**,** Frequent *NRAS* mutations (50%), LMO1 upregulation and downregulation of SMAD1 and BMP2		
KMT2A-like	<1%	GEPClusters with *KMT2A*	Some with *HOXA* fusions		
ZNF384-like	<1%	GEP clusters with *ZNF384*or *ZNF362*	unknown	Like *ZNF384*	
T-ALL/LL					
Subtype	Frequency	Partner genes/other rearrangements		Immunophenotype	Comment
HOXA dysregulated	15-25%	*HOXA*::TRB/TRG; *KMT2A*-Rearranged; *PICALM*::*MLLT10*; *SET*::*NUP214*		Immature, some ETP	

SPI1 rearrangement	<5%, children	*STMN1*; *TCF7*; *BCL11B*	CD4-, CD8+/-, DR+	Very poor prognosis
TLX1 rearrangement	5-10% children; near 30% adult	TCR	CD4+, CD8+/-,CD1a+, cortical thymocyte	Good prognosis
TLX3 rearrangement	20-25% children <5% adult	TCR; *BCL11B*; *CDK6*	CD4+, CD8+/-, CD1a+, cortical thymocyte, some ETP or near ETP	Good prognosis; BCL11B overexpression different from ETP group
NKX2 rearrangement	<5% children	*NKX2.1/NKX2.2/NKX2.5*::TCR; *BCL11B*; *CDK6*	CD4+, CD8+	Similar GEP to *TLX1*-R
TAL1-2 rearrangement	30-40% (TAL2 rare)	TRA/D; TRB (*TAL2*); 1p32 deletion (*STIL*); intergenic SNV (super enhancer)	CD3+, late cortical	Poor prognosis
LMO1-2 rearrangement	*LMO1*-R -5% *LMO2*-R 10%	TCR; cryptic deletion; enhancer/promoter mutations	Immature but not-ETP	Form LMO complex with bHLH factors. Extremely high LMO expression.
BHLH, other	<2%	*LYL1*::TRB *OLIG2/BHLHB1*::TCR	Immature but not ETP	Extremely high LMO expression *LYL1*-R shows stem cell-like signature

[a] Not all examples of these entities can be defined by conventional FISH or WTS alone because of intragenic alterations that dysregulate these genes and produce leukemias with an identical gene expression pattern.

WTS; whole transcriptome sequencing; GEP; gene expression profile, LMO; LIM-domain-only, BHLH; basic helix-loop-helix, CNA: copy number alteration

Supplemental Table 8. ICC Myeloid Neoplasm/Acute Leukemia Disease Co-chairs and Work Group Participants.

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