

Higher-risk MDS and AML: How new guidelines are changing diagnosis, classification and management

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Presenting symptoms and the diagnostic process for MDS and AML

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Presenting symptoms of MDS and AML

MDS¹

-  Easy bruising
-  Pallor
-  Pale conjunctiva
-  Mucosal bleeding
-  Hypotension
-  Tachycardia
-  Emphysema
-  Heart failure

-  Epistaxis^{1,2}
-  Angina pectoris^{1,2}
-  Petechiae^{1,2}
-  Frequent infections^{1,2}
-  Fatigue^{1,2}
-  Exercise intolerance^{1,2}
-  Headache^{1,2}
-  Major bleeding^{1,2}

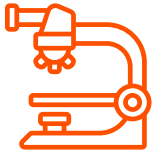
AML²

-  Gingival haemorrhage
-  Fever
-  Hypoxia
-  Adenopathy
-  Organomegaly
-  Dyspnoea
-  Respiratory failure
-  Confusion
-  Seizures
-  Palpitations
-  Menorrhagia
-  Coma visual disturbances
-  Claudication

AML, acute myeloid leukaemia; GI, gastrointestinal; ICC, International Consensus Classification; MDS, myelodysplastic neoplasms (WHO 2022)/myelodysplastic syndromes (ICC 2022); WHO, World Health Organization.

1. Barzi A, Sekeres MA. *Cleve Clin J Med.* 2010;77:37–44; 2. Smith M, et al. *Crit Rev Oncol Hemat.* 2004;50:197–222.

Modes of presentation

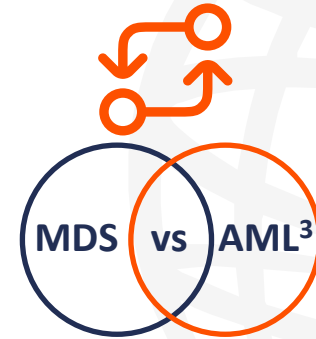


Incidental cytopenia¹

- ICUS²
- CCUS²



Prior cytotoxic therapy³



AML, acute myeloid leukaemia; CCUS, clonal cytopenia of undetermined significance; ICC, International Consensus Classification; ICUS, idiopathic cytopenia of undetermined significance; MDS, myelodysplastic neoplasms (WHO 2022)/myelodysplastic syndromes (ICC 2022); WHO, World Health Organization.

1. Samiev D, et al. *Korean J Fam Med.* 2014;35:111–8; 2. Fenaux P, et al. *Ann Oncol.* 2021;32:142–56; 3. Khoury JD, et al. *Leukemia.* 2022;36:1703–19.

Diagnosing MDS or AML



Laboratory parameters (MDS only)¹

- Ferritin
- Transferrin
- Transferrin saturation
- Reticulocyte counts
- Vitamin B12
- Folate concentrations
- Haptoglobin
- Creatinine levels



Blood counts (MDS only)¹

Blood counts

- Evaluate cytopenia

Cytomorphology

- Dysplastic features



Bone marrow aspiration^{1,2}

Cytomorphology

- Dysplastic features
- Blast counts

Cytogenetics








Molecular studies



Bone marrow biopsy^{1,2}

Cellularity and fibrosis

Categorization of MDS by WHO and ICC

Blast burden	Genetic	WHO 2022 ¹			ICC 2022 ²
 BM blasts <5%  PB blasts <2%	del(5q)	MDS-5q		AML with defining genetic abnormalities*	MDS-del(5q)
	<i>SF3B1</i>	MDS- <i>SF3B1</i>			MDS- <i>SF3B1</i>
	Other	MDS-LB			MDS, NOS Without dysplasia or with SL/ML dysplasia
 BM blasts 5–9%  PB blasts 2–4%		MDS-IB1	MDS-f	MDS-bi <i>TP53</i>	MDS-EB [‡]
 BM blasts 10–19%  PB blasts 5–19%  Auer rods		MDS-IB2			MDS/AML [‡] Unless AML-defining cytogenetic or molecular abnormality*

*AML except *BCR::ABL* and *CEBPA* mut (≥20% blasts required). †PB blasts 2–9%. ‡PB blasts 5–19% and no requirement for auer rods.

AML, acute myeloid leukaemia; BM, bone marrow; ICC, International Consensus Classification; MDS, myelodysplastic neoplasms (WHO 2022)/myelodysplastic syndromes (ICC 2022); MDS-EB, MDS with excess blasts; MDS-f, MDS with fibrosis; MDS-IB, MDS with increased blasts; MDS-LB, MDS with low blasts; MDS-NOS, MDS not otherwise specified; ML, multilineage; PB, peripheral blood; SL, single lineage; WHO, World Health Organization.

1. Khoury JD, et al. *Leukemia*. 2022;36:1703–19; 2. Arber DA, et al. *Blood*. 2022;140:1200–28.

WHO 2022 classification of AML¹

Myeloid neoplasm post-cytotoxic therapy¹

- Acute promyelocytic leukaemia with *PML::RARA* fusion
- AML with *DEK::NUP214* fusion
- AML with *MECOM* rearrangement
- AML with *RUNX1::RUNX1T1* fusion
- AML with *RBM15::MRTFA* fusion
- AML with *NUP98* rearrangement
- AML with *CBFB::MYH11* fusion
- AML with *BCR::ABL1* fusion
- AML with *NPM1* mutation
- AML with *KMT2A* rearrangement
- AML with *CEBPA* mutation

AML with defining genetic abnormalities¹

Defining cytogenetic abnormalities

- Complex karyotype (≥ 3 abnormalities)
- 12p del or loss of 12p due to unbalanced translocation
- 5q del or loss of 5q due to unbalanced translocation
- Monosomy 13 or 13q del
- Monosomy 7, 7q del or loss of 7q due to unbalanced translocation
- 17p del or loss of 17p due to unbalanced translocation
- 11q del
- Isochromosome 17q
- Idic(X)(q13)

Defining somatic mutations

<i>ASXL1</i>	<i>SRSF2</i>
<i>BCOR</i>	<i>STAG2</i>
<i>EZH2</i>	<i>U2AF1</i>
<i>SF3B1</i>	<i>ZRSR2</i>

AML, myelodysplasia-related¹

AML with other defined genetic alterations²

- AML with *RUNX1T3(CBFA2T3)::GLIS2* fusion
- AML with *KAT6A::CREBBP* fusion
- AML with *MNX1::ETV6* fusion
- AML with *FUS::ERG* fusion
- AML with *NPM1::MLF* fusion

AML defined by differentiation¹

- AML with minimal differentiation
- Acute basophilic leukaemia
- Acute erythroid leukaemia*
- AML without maturation
- Acute myelomonocytic leukaemia
- Acute megakaryoblastic leukaemia
- AML with maturation
- Acute monocytic leukaemia

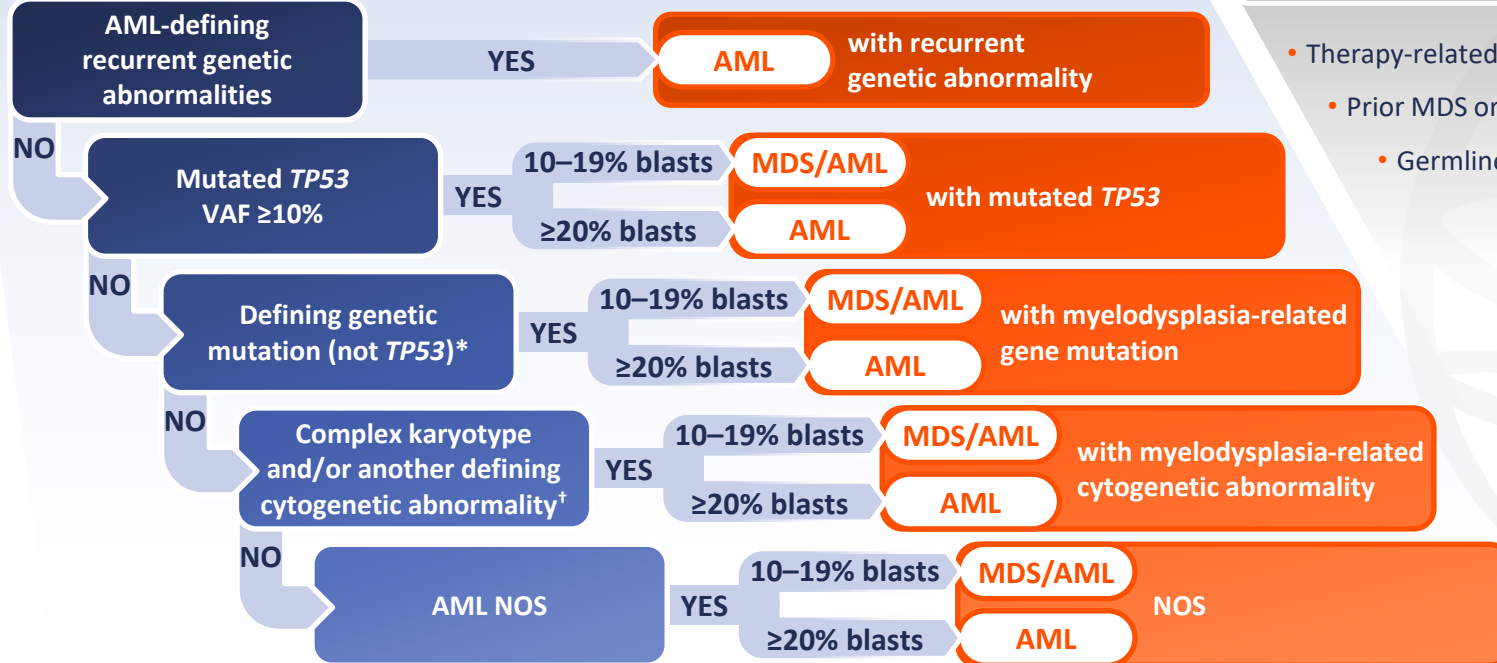
*Previously pure erythroid leukaemia. AML, acute myeloid leukaemia; WHO, World Health Organization.

1. Khoury JD, et al. *Leukemia*. 2022;36:1703–19; 2. Li W. In: Li W (ed). *Leukemia*. Brisbane, Australia: Exon Publications, 2022;1–21.

Hierarchical classification of AML: ICC

≥10% myeloid blasts or blast equivalents in the bone marrow or blood

Diagnostic qualifiers appended to any diagnosis

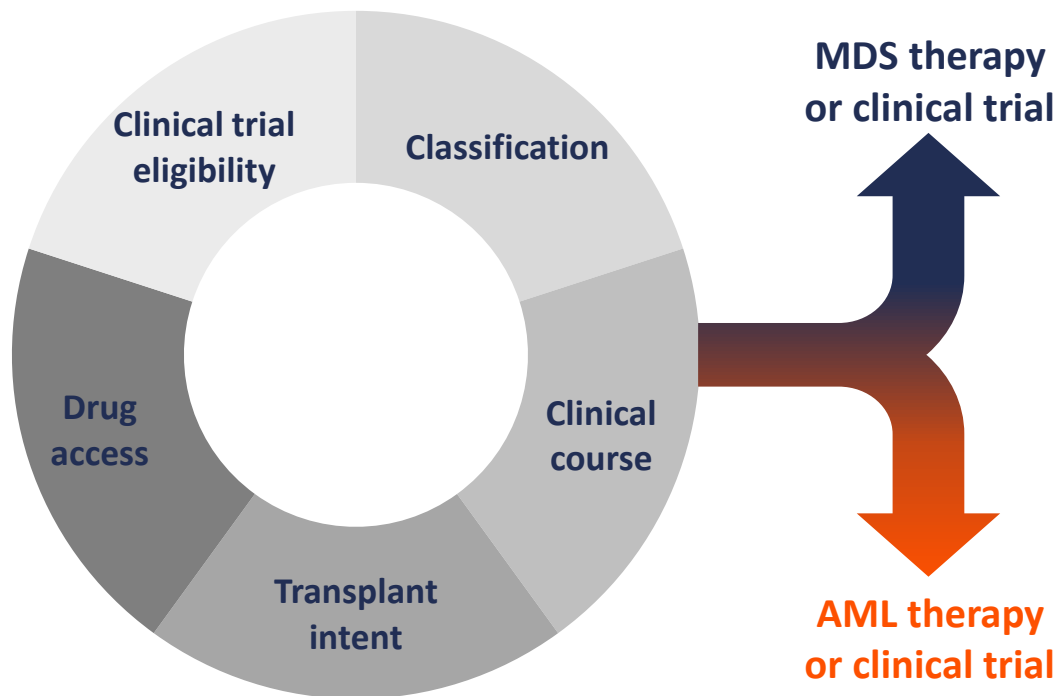


- Therapy-related
- Prior MDS or MDS/MPN
- Germline predisposition

*ASXL1, BCOR, EZH2, RUNX1, SF3B1, SRSF2, STAG2, U2AF1 and/or ZRSR2. †del(5q)/t(5q)/add(5q), -7/del(7q), +8, del(12p)/t(12p)/(add(12p), i(17q), -17/add(17p)/del(17p), del(20q) or idic(X)(q13). AML, acute myeloid leukaemia; ICC, International Consensus Classification; MDS, myelodysplastic neoplasms (WHO 2022)/myelodysplastic syndromes (ICC 2022); MPN, myeloproliferative neoplasms; NOS, not otherwise specified; VAF, variant allele frequency; WHO, World Health Organization.

Döhner H, et al. *Blood*. 2022;140:1345–77.

MDS vs AML: Treatment considerations¹⁻³



AML, acute myeloid leukaemia; ICC, International Consensus Classification; MDS, myelodysplastic neoplasms (WHO 2022)/myelodysplastic syndromes (ICC 2022); WHO, World Health Organization.

1. Fenaux P, et al. *Ann Oncol.* 2021;32:142–56; 2. Heuser M, et al. *Ann Oncol.* 2020;31:697–712; 3. Döhner H, et al. *Blood.* 2022;140:1345–77.

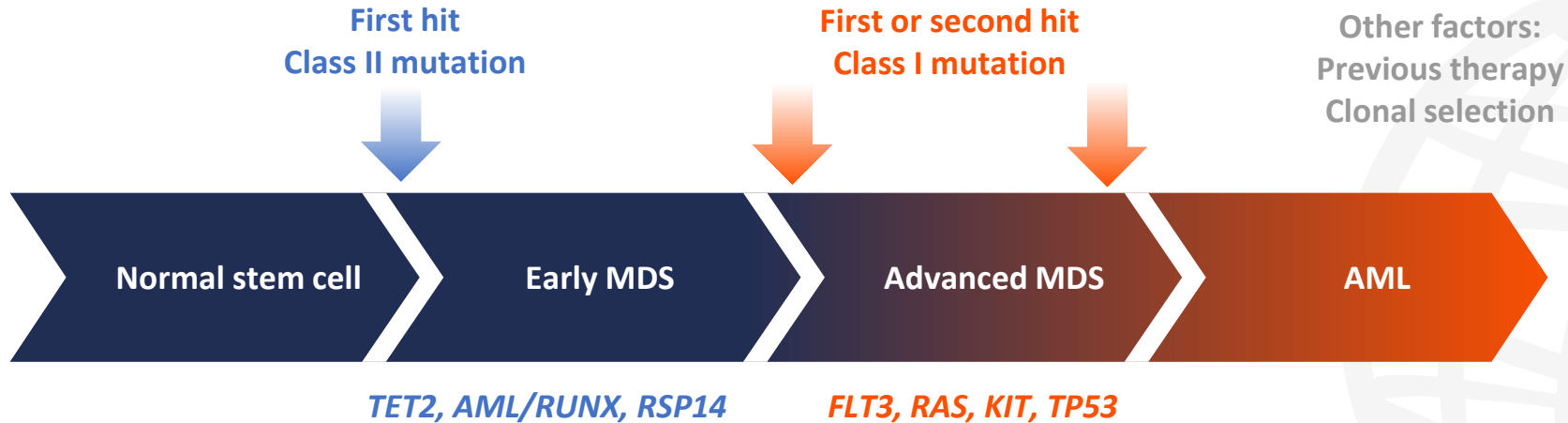
Pathophysiology of MDS and AML and how it relates to disease classification

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Model of progression from MDS to AML¹



MDS²

- Cytopenia
- Inefficient haematopoiesis
- Dysplasia in one or more myeloid cell lineages
- Increased risk of development of AML

AML³

- Clonal expansion of myeloid blasts in the bone marrow, peripheral blood or other tissues

AML, acute myeloid leukaemia; MDS, myelodysplastic neoplasms (WHO 2022)/myelodysplastic syndromes (ICC 2022).

1. Porwit A, Saft L. *J Hematop.* 2011;4:69–79; 2. Visconte V, et al. *Blood Res.* 2014;49:216–27; 3. He GL, et al. *Cancer Cell Int.* 2014;14:111.

WHO and ICC classification comparison

WHO¹

MDS = myelodysplastic neoplasms

MDS with defining genetic abnormalities

- MDS with low blasts and isolated 5q deletion
- MDS with low blasts and *SF3B1* mutation
- MDS with biallelic *TP53* inactivation

MDS, morphologically defined

- MDS with low blasts (MDS-LB)
- MDS, hypoplastic (MDS-h)
- MDS with increased blasts (MDS-IB)
 - MDS-IB1
 - MDS-IB2
 - MDS with fibrosis (MDS-f)

ICC²

MDS = myelodysplastic syndromes

- MDS with del(5q)
- MDS with mutated *SF3B1*
- MDS with mutated *TP53*
- MDS, not otherwise specified (MDS, NOS)
 - MDS, NOS without dysplasia
 - MDS, NOS with single lineage dysplasia
 - MDS, NOS with multilineage dysplasia
- MDS with excess blasts (MDS-EB)
 - MDS/AML
 - MDS/AML with mutated *TP53*
 - MDS/AML with myelodysplasia-related gene mutations
 - MDS/AML with myelodysplasia-related cytogenetic abnormalities
 - MDS/AML, not otherwise specified

Validation of MDS guideline updates (1/3)

Retrospective, single-centred cohort study of patients with MDS

Validation of WHO 2022 guidelines



Jan 2018 → Dec 2021



N=118

WHO 2022 classification	% lower-risk patients	Median OS
Genetically defined <ul style="list-style-type: none">MDS-<i>SF3B1</i>MDS-<i>biTP53</i>	91 (IPSS-R/IPSS-M) 14 (IPSS-R/IPSS-M)	7.0 years 0.8 years
Morphologically defined <ul style="list-style-type: none">MDS-LBMDS-IB1MDS-IB2	71 (IPSS-R/IPSS-M) 21 (IPSS-R); 16 (IPSS-M) 0 (IPSS-R); 7 (IPSS-M)	NR NR 1.5 years



- Differing mutational features were prominently associated with both morphologically and genetically defined subgroups
- OS differed between the defined subgroups

Validation of MDS guideline updates (2/3)

Patients with newly diagnosed MDS based on WHO 2016 criteria



Reclassified according to WHO 2022 guidelines

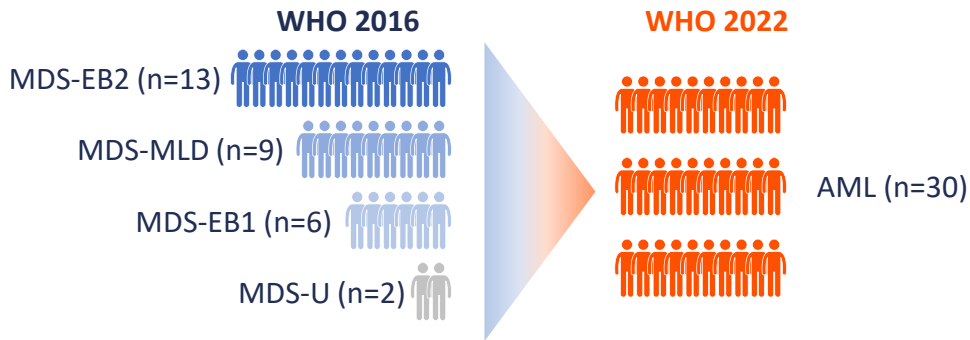


N=852



Aug 2016 → Sep 2021

30 subjects with *NPM1* mutation were reclassified as AML

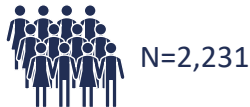


WHO 2022 classification	Median OS
MDS-5q	24 months
MDS- <i>SF3B1</i>	58 months
MDS-bi <i>TP53</i>	10 months
MDS-LB	Unreached
MDS-h	Unreached
MDS-IB1	24 months
MDS-IB2	26 months
MDS-f	15 months

AML, acute myeloid leukaemia; MDS, myelodysplastic neoplasms; MDS-bi*TP53*, MDS with biallelic *TP53* inactivation; MDS-EB, myelodysplastic syndromes with excess blasts; MDS-f, MDS with fibrosis; MDS-h, MDS, hypoplastic; MDS-IB, MDS with increased blasts; MDS-LB, MDS with low blasts; MDS-MLD, myelodysplastic syndromes with multilineage dysplasia; MDS-*SF3B1*, MDS with low blasts and *SF3B1* mutation; MDS-U, myelodysplastic syndromes, unclassifiable; OS, overall survival; WHO, World Health Organization. Zhang Y, et al. *Blood*. 2022;140(Suppl. 1):1343–5.

Validation of MDS guideline updates (3/3)

Retrospective, single-centred
cohort study of patients with MDS



Reclassified by WHO 2022 and
ICC 2022 proposed criteria

WHO 2022

- MDS-IB1 and MDS-IB2 had similar mOS ($p=0.726$)

WHO 2022 and ICC 2022

- MDS with mutated *SF3B1* had best mOS across all subtypes
- Categories for MDS-m*TP53* had worst survival of all subtypes

ICC 2022

- MDS-MLD had significantly worse mOS compared with MDS-SLD (49.6 months vs 79.4 months; $p<0.001$)

ICC, International Consensus Classification; MDS, myelodysplastic neoplasms (WHO 2022)/myelodysplastic syndromes (ICC 2022); MDS-IB, MDS with increased blasts; MDS-MLD, myelodysplastic syndromes with multilineage dysplasia; MDS-m*TP53*, MDS with mutated *TP53*; MDS-SLD, MDS with single lineage dysplasia; mOS, median overall survival; WHO, World Health Organization.

Ball S, et al. *Blood*. 2022;140(Suppl. 1):1118–20.

Impact of WHO and ICC 2022 on AML diagnosis

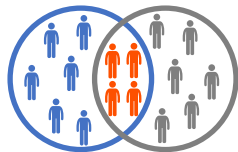
1,451 non-therapy-related cases with MDS or AML according to 2017 revised 4th edition WHO guidelines

WHO 2022 guidelines

- 746 patients diagnosed with AML
- **<1%** of cases were **upgraded from MDS to AML** compared with the revised 4th edition WHO guidelines

ICC 2022 guidelines

- 742 patients diagnosed with AML
- 137 patients diagnosed with MDS/AML
- **10%** of cases were **upgraded from MDS to AML** compared to the revised 4th edition WHO guidelines, **mainly due to the introduction of the MDS/AML class**



4/16 patients with **MDS-EB2** according to the revised 4th edition WHO guidelines were **upgraded to AML** using both the WHO 2022 and ICC 2022 guidelines

Updated prognostic risk stratification and its impact on patient management

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Vrije Universiteit University Medical Center,
Amsterdam, Netherlands



Comparison between IPSS-R and IPSS-M

IPSS-R

Risk based on haematologic and cytogenetic features

- 5 cytogenetic risk categories
- Haemoglobin level
- Marrow blast percentage
- Platelet count

Factors from IPSS-R conserved in IPSS-M

IPSS-M

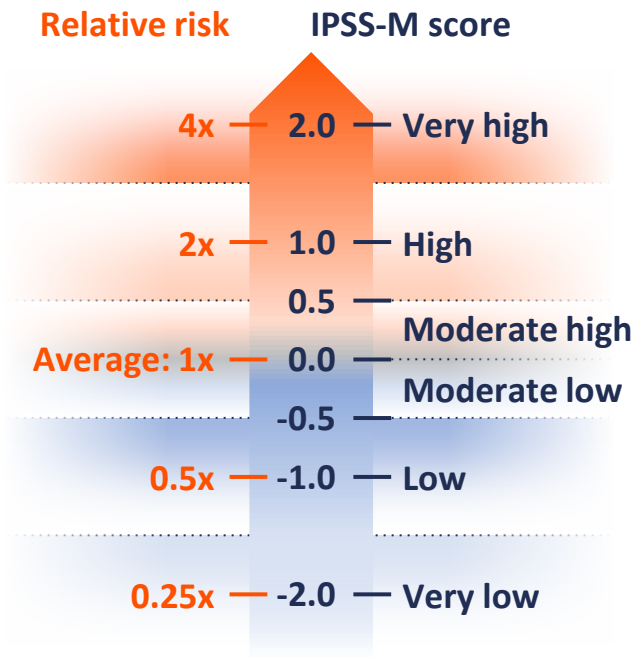
Risk based on haematologic parameters, cytogenetic abnormalities and somatic mutations

Additional factors in IPSS-M

- 16 main effect genes
- 15 residual genes
- Mutations associated with worse outcome:
 - *TP53*^{multihit}
 - *FLT3*
 - *MLL*^{PTD}

IPSS-M risk categories

The IPSS-M score corresponds to the relative risk compared with an 'average' patient



A patient's IPSS-M score can be calculated using the [IPSS-M web calculator*](#)

*www.mds-risk-model.com

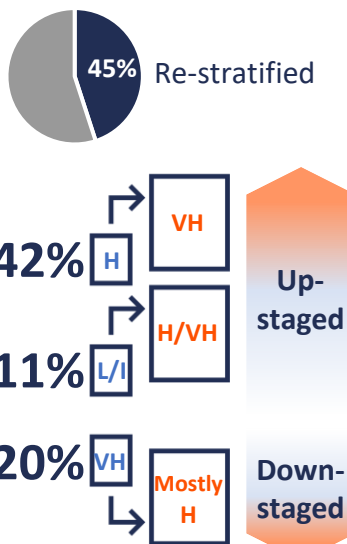
IPSS-M, Molecular International Prognostic Scoring System.

Bernard E, et al. *NEJM Evidence*. 2022;1:EVIDoa2200008.

Validation of the IPSS-M: Data from ASH 2022

Aguirre LEE, et al.¹

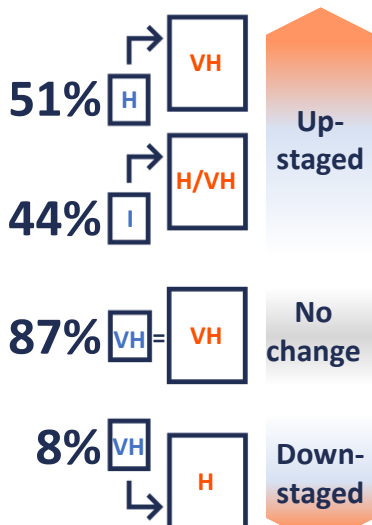
N=2,333



Percentage of each IPSS-R risk group

Santini V, et al.²

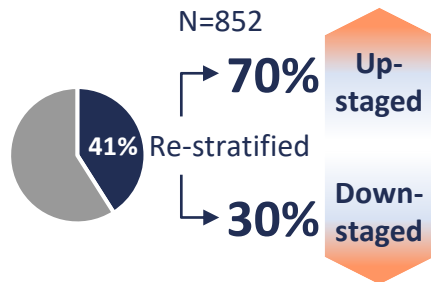
N=512



Percentage of each IPSS-R risk group

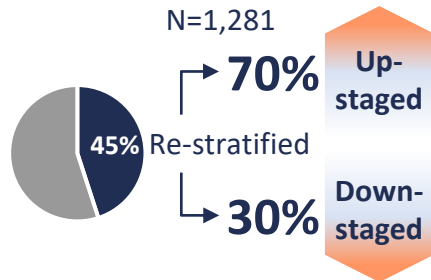
Wu J, et al.³

N=852



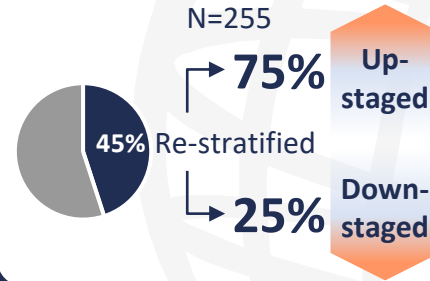
Kewan T, et al.⁴

N=1,281



Ma J, et al.⁵

N=255

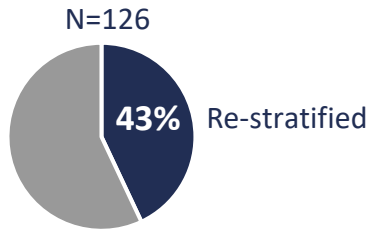


ASH, American Society of Hematology; H, high risk; I, intermediate risk; IPSS, International Prognostic Scoring System; L, low risk; M, Molecular; R, Revised. sig, significant; VH, very high risk. 1. Aguirre LEE, et al. Presented at: 64th ASH Annual Meeting, New Orleans, LA, USA. 10–13 December 2022. Abstr 465; 2. Santini V, et al. Presented at: 64th ASH Annual Meeting, New Orleans, LA, USA. 10–13 December 2022. Abstr 559; 3. Wu J, et al. Presented at: 64th ASH Annual Meeting, New Orleans, LA, USA. 10–13 December 2022. Abstr 1780; 4. Kewan T, et al. Presented at: 64th ASH Annual Meeting, New Orleans, LA, USA. 10–13 December 2022. Abstr 3087; 5. Ma J, et al. Presented at: 64th ASH Annual Meeting, New Orleans, LA, USA. 10–13 December 2022. Abstr 4400.

Real-world use of IPSS-R vs IPSS-M: Data from ASH 2022

Jáuregui SN, et al.

Patients with MDS
from a single centre



17.4% of re-stratifications of patients had a potential impact on therapeutic choices

- Of these, 11.9% of patients were up-staged, 5.6% were down-staged



9.5% would have actually been treated differently if IPSS-M was initially applied

- Some of the higher-risk patients were not candidates for intensive care due to age and comorbidities

ELN 2022: Genetic risk classification changes

- ***FLT3*-ITD allelic ratio is no longer considered in the risk classification**
 - AML with *FLT3*-ITD (without adverse-risk genetic lesions) is categorized in the intermediate-risk group, irrespective of allelic ratio or concurrent presence of an *NPM1* mutation
- **AML with myelodysplasia-related gene mutations are now in the adverse-risk group**
 - Mutations include pathologic variants in at least one of the following:
 - *ASXL1*, *BCOR*, *EZH2*, *RUNX1*, *SF3B1*, *SRSF2*, *STAG2*, *U2AF1*, or *ZRSR2*
- **In-frame mutations in the leucine zipper region of *CEBPA* are now classified in the favourable-risk group**
 - Classification is irrespective of biallelic or monoallelic mutations
- **The presence of adverse-risk cytogenetic abnormalities in *NPM1*-mutated AML are now classified as adverse risk**
- **Additional disease-defining, recurring cytogenetic abnormalities are now in the adverse-risk group**
 - Include mutations in t(3q26.2;v) involving the *MECOM* gene, or t(8;16)(p11.2;p13.3) associated with *KAT6A::CREBBP* gene fusion
- **Hyperdiploid karyotypes with multiple trisomies are no longer on the list of complex karyotypes or in the adverse risk group**