
PROGNOSTIC OF CYTOGENETIC AND MOLECULAR ALTERATIONS IN MYELODYSPLASTIC SYNDROMES (MDS)



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PROGNOSTIC OF CYTOGENETIC AND MOLECULAR ALTERATIONS

IN MYELODYSPLASTIC **NEOPLASMS** (MDS)

NEW WHO 2022



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- **¿Debemos incorporar los estudios moleculares en pacientes con sospecha o diagnóstico de SMD?**
- **A) no deben realizarse**
- **B) son recomendables**
- **C) son obligatorios**

- **Technical and methodological aspects**
- **Prognostic value of cytogenetic findings: IPSS-R**
- **Cytogenetic/genetic changes and IPSS-M**
- **CONCLUSIONS**

- **Technical and methodological aspects**
- Prognostic value of cytogenetic findings: IPSS-R
- Cytogenetic/genetic changes and IPSS-M
- CONCLUSIONS

WHO (2017)

THE UPDATED WHO CLASSIFICATION OF HEMATOLOGICAL MALIGNANCIES

The 2016 revision to the World Health Organization classification of myeloid neoplasms and acute leukemia

Daniel A. Arber,¹ Attilio Orazi,² Robert Hasserjian,³ Jürgen Thiele,⁴ Michael J. Borowitz,⁵ Michelle M. Le Beau,⁶ Clara D. Bloomfield,⁷ Mario Cazzola,⁸ and James W. Vardiman⁹

Table 15. PB and BM findings and cytogenetics of MDS

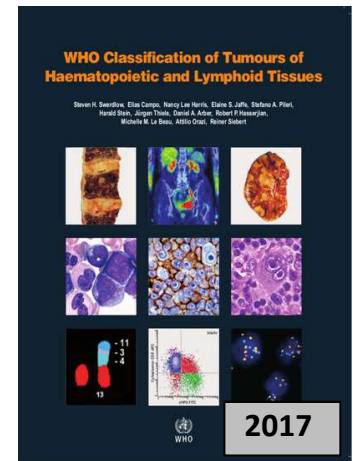
Name	Dysplastic lineages	Cytopenias*	Ring sideroblasts as % of marrow erythroid elements	BM and PB blasts	Cytogenetics by conventional karyotype analysis
MDS with single lineage dysplasia (MDS-SLD)	1	1 or 2	<15%/<5%†	BM <5%, PB <1%, no Auer rods	Any, unless fulfills all criteria for MDS with isolated del(5q)
MDS with multilineage dysplasia (MDS-MLD)	2 or 3	1-3	<15%/<5%†	BM <5%, PB <1%, no Auer rods	Any, unless fulfills all criteria for MDS with isolated del(5q)
MDS with ring sideroblasts (MDS-RS)					
MDS-RS with single lineage dysplasia (MDS-RS-SLD)	1	1 or 2	≥15%/≥5%†	BM <5%, PB <1%, no Auer rods	Any, unless fulfills all criteria for MDS with isolated del(5q)
MDS-RS with multilineage dysplasia (MDS-RS-MLD)	2 or 3	1-3	≥15%/≥5%†	BM <5%, PB <1%, no Auer rods	Any, unless fulfills all criteria for MDS with isolated del(5q)
MDS with isolated del(5q)	1-3	1-2	None or any	BM <5%, PB <1%, no Auer rods	del(5q) alone or with 1 additional abnormality except -7 or del(7q)
MDS with excess blasts (MDS-EB)					
MDS-EB-1	0-3	1-3	None or any	BM 5%-9% or PB 2%-4%, no Auer rods	Any
MDS-EB-2	0-3	1-3	None or any	BM 10%-19% or PB 5%-19% or Auer rods	Any
MDS, unclassifiable (MDS-U)					
with 1% blood blasts	1-3	1-3	None or any	BM <5%, PB = 1%, ‡ no Auer rods	Any
with single lineage dysplasia and pancytopenia	1	3	None or any	BM <5%, PB <1%, no Auer rods	Any
based on defining cytogenetic abnormality	0	1-3	<15%§	BM <5%, PB <1%, no Auer rods	MDS-defining abnormality
Refractory cytopenia of childhood	1-3	1-3	None	BM <5%, PB <2%	Any

*Cytopenias defined as: hemoglobin, <10 g/dL; platelet count, <100 × 10⁹/L; and absolute neutrophil count, <1.8 × 10⁹/L. Rarely, MDS may present with mild anemia or thrombocytopenia above these levels. PB monocytes must be <1 × 10⁹/L

†If *SE3B1* mutation is present

‡One percent PB blasts must be recorded on at least 2 separate occasions.

§Cases with ≥15% ring sideroblasts by definition have significant erythroid dysplasia, and are classified as MDS-RS-SLD.



NGS

CG

Arber *et al.* Blood (2016)

New WHO (2022)

Leukemia

www.nature.com/leu

REVIEW ARTICLE OPEN

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The 5th edition of the World Health Organization Classification of Haematolymphoid Tumours: Myeloid and Histiocytic/Dendritic Neoplasms

Joseph D. Khoury ^{1✉}, Eric Solary ^{2✉}, Oussama Abla³, Yasmine Akkari ⁴, Rita Alaggio⁵, Jane F. Apperley ⁶, Rafael Bejar ⁷, Emilio Berti⁸, Lambert Busque ⁹, John K. C. Chan¹⁰, Weina Chen ¹¹, Xueyan Chen¹², Wee-Joo Chng¹³, John K. Choi ¹⁴, Isabel Colmenero ¹⁵, Sarah E. Coupland¹⁶, Nicholas C. P. Cross ¹⁷, Daphne De Jong¹⁸, M. Tarek Elghetany¹⁹, Emiko Takahashi ²⁰, Jean-Francois Emile ²¹, Judith Ferry²², Linda Fogelstrand²³, Michaela Fontenay²⁴, Ulrich Germing²⁵, Sumeet Gujral²⁶, Torsten Haferlach ²⁷, Claire Harrison²⁸, Jennelle C. Hodge²⁹, Shimin Hu ¹, Joop H. Jansen³⁰, Rashmi Kanagal-Shamanna ¹, Hagop M. Kantarjian ³¹, Christian P. Kratz ³², Xiao-Qiu Li³³, Megan S. Lim³⁴, Keith Loeb³⁵, Sanam Loghavi ¹, Andrea Marcogliese¹⁹, Soheil Meshinchi³⁶, Phillip Michaels³⁷, Kikkeri N. Naresh ³⁵, Yasodha Natkunam ³⁸, Reza Nejati³⁹, German Ott⁴⁰, Eric Padron ⁴¹, Keyur P. Patel¹, Nikhil Patkar ⁴², Jennifer Picarsic⁴³, Uwe Platzbecker ⁴⁴, Irene Roberts⁴⁵, Anna Schuh ⁴⁶, William Sewell⁴⁷, Reiner Siebert⁴⁸, Prashant Tembhare ⁴², Jeffrey Tyner ⁴⁹, Srdan Verstovsek ³¹, Wei Wang ¹, Brent Wood⁵⁰, Wenbin Xiao ⁵¹, Cecilia Yeung ³⁵ and Andreas Hochhaus ^{52✉}

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Khoury et al. Leukemia (2022)

New WHO (2022)

MYELODYSPLASTIC NEOPLASMS (MDS)

NEW

Table 3. Classification and defining features of myelodysplastic neoplasms (MDS).

	Blasts	Cytogenetics	Mutations
MDS with defining genetic abnormalities			
MDS with low blasts and isolated 5q deletion (MDS-5q)	<5% BM and <2% PB	5q deletion alone, or with 1 other abnormality other than monosomy 7 or 7q deletion	
MDS with low blasts and <i>SF3B1</i> mutation ^a (MDS- <i>SF3B1</i>)		Absence of 5q deletion, monosomy 7, or complex karyotype	<i>SF3B1</i>
MDS with biallelic <i>TP53</i> inactivation (MDS-bi <i>TP53</i>)	<20% BM and PB	Usually complex	Two or more <i>TP53</i> mutations, or 1 mutation with evidence of <i>TP53</i> copy number loss or <i>cnLOH</i>
MDS, morphologically defined			
MDS with low blasts (MDS-LB)	<5% BM and <2% PB		
MDS, hypoplastic ^b (MDS-h)			
MDS with increased blasts (MDS-IB)			
MDS-IB1	5–9% BM or 2–4% PB		
MDS-IB2	10–19% BM or 5–19% PB or Auer rods		
MDS with fibrosis (MDS-f)	5–19% BM; 2–19% PB		

GEN

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^aDetection of $\geq 15\%$ ring sideroblasts may substitute for *SF3B1* mutation. Acceptable related terminology: MDS with low blasts and ring sideroblasts.

^bBy definition, $\leq 25\%$ bone marrow cellularity, age adjusted.

BM bone marrow, PB peripheral blood, *cnLOH* copy neutral loss of heterozygosity.

New ICC (2022)



International Consensus Classification of Myeloid Neoplasms and Acute Leukemias: integrating morphologic, clinical, and genomic data

Daniel A. Arber,¹ Attilio Orazi,² Robert P. Hasserjian,³ Michael J. Borowitz,⁴ Katherine R. Calvo,⁵ Hans-Michael Kvasnicka,⁶ Sa A. Wang,⁷ Adam Bagg,⁸ Tiziano Barbui,⁹ Susan Branford,¹⁰ Carlos E. Bueso-Ramos,⁷ Jorge E. Cortes,¹¹ Paola Dal Cin,¹² Courtney D. DiNardo,⁷ Hervé Dombret,¹³ Eric J. Duncavage,¹⁴ Benjamin L. Ebert,¹⁵ Elihu H. Estey,¹⁶ Fabio Facchetti,¹⁷ Kathryn Foucar,¹⁸ Naseema Gangat,¹⁹ Umberto Gianelli,²⁰ Lucy A. Godley,¹ Nicola Gökbuget,²¹ Jason Gotlib,²² Eva Hellström-Lindberg,²³ Gabriela S. Hobbs,³ Ronald Hoffman,²⁴ Elias J. Jabbour,⁷ Jean-Jacques Kiladjian,¹³ Richard A. Larson,¹ Michelle M. Le Beau,¹ Mignon L.-C. Loh,²⁵ Bob Löwenberg,²⁶ Elizabeth Macintyre,²⁷ Luca Malcovati,²⁸ Charles G. Mullighan,²⁹ Charlotte Niemeyer,³⁰ Olatoyosi M. Odenike,¹ Seishi Ogawa,³¹ Alberto Orfao,³² Elli Papaemmanuil,³³ Francesco Passamonti,²⁸ Kimmo Porkka,³⁴ Ching-Hon Pui,²⁹ Jerald P. Radich,³⁵ Andreas Reiter,³⁶ Maria Rozman,³⁷ Martina Rudelius,³⁸ Michael R. Savona,³⁹ Charles A. Schiffer,⁴⁰ Annette Schmitt-Graeff,⁴¹ Akiko Shimamura,^{15,42} Jorge Sierra,⁴³ Wendy A. Stock,¹ Richard M. Stone,¹⁵ Martin S. Tallman,⁴⁴ Jürgen Thiele,⁴⁵ Hwei-Fang Tien,⁴⁶ Alexandar Tzankov,⁴⁷ Alessandro M. Vannucchi,⁴⁸ Paresh Vyas,⁴⁹ Andrew H. Wei,⁵⁰ Olga K. Weinberg,⁵¹ Agnieszka Wierzbowska,⁵² Mario Cazzola,²⁸ Hartmut Döhner,⁵³ and Ayalew Tefferi¹⁹

Arber *et al.* Blood (2022)

New ICC (2022)

Table 20. Myelodysplastic syndromes (MDS) and myelodysplastic syndrome/acute myeloid leukemia (MDS/AML)

	Dysplastic lineages	Cytopenias	Cytoses*	BM and PB Blasts	Cytogenetics ^{b***}	Mutations
MDS with mutated <i>SF3B1</i> (MDS- <i>SF3B1</i>)	Typically $\geq 1^c$	≥ 1	0	<5% BM <2% PB	Any, except isolated del(5q), -7/del(7q), abn3q26.2, or complex	<i>SF3B1</i> ($\geq 10\%$ VAF), without multi-hit <i>TP53</i> , or <i>RUNX1</i>
MDS with del(5q) [MDS-del(5q)]	Typically $\geq 1^c$	≥ 1	Thrombocytosis allowed	<5% BM <2% PB ^d	del(5q), with up to 1 additional, except -7/del(7q)	Any, except multi-hit <i>TP53</i>
MDS, NOS - without dysplasia	0	≥ 1	0	<5% BM <2% PB ^d	-7/del(7q) or complex	Any, except multi-hit <i>TP53</i> or <i>SF3B1</i> ($\geq 10\%$ VAF)
MDS, NOS - with single lineage dysplasia	1	≥ 1	0	<5% BM <2% PB ^d	Any, except not meeting criteria for MDS-del(5q)	Any, except multi-hit <i>TP53</i> ; not meeting criteria for MDS- <i>SF3B1</i>
MDS, NOS - with multilineage dysplasia	≥ 2	≥ 1	0	<5% BM <2% PB ^d	Any, except not meeting criteria for MDS-del(5q)	Any, except multi-hit <i>TP53</i> ; not meeting criteria for MDS- <i>SF3B1</i>

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Arber et al. Blood (2022)

New ICC (2022)

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MDS with excess blasts (MDS-EB)	Typically $\geq 1^c$	≥ 1	0	5-9% BM, 2-9% PB ^d	Any	Any, except multi-hit <i>TP53</i>
MDS/AML	Typically $\geq 1^c$	≥ 1	0	10-19% BM or PB ^e	Any, except AML-defining ^f	Any, except <i>NPM1</i> , <i>bZIP</i> , <i>CEBPA</i> or <i>TP53</i>



^aCytoses: Sustained white blood count $\geq 13 \times 10^9/L$, monocytosis ($\geq 0.5 \times 10^9/L$ and $\geq 10\%$ of leukocytes), or platelets $\geq 450 \times 10^9/L$; thrombocytosis is allowed in MDS-del(5q) or in any MDS case with inv(3) or t(3;3) cytogenetic abnormality.

^b*BCR::ABL1* rearrangement or any of the rearrangements associated with myeloid/lymphoid neoplasms with eosinophilia and tyrosine kinase gene fusions exclude a diagnosis of MDS, even in the context of cytopenia.

^cAlthough dysplasia is typically present in these entities, it is not required.

^dAlthough 2% PB blasts mandates classification of an MDS case as MDS-EB, the presence of 1% PB blasts confirmed on two separate occasions also qualifies for MDS-EB.

^eFor pediatric patients (<18 years), the blast thresholds for MDS-EB are 5-19% in BM and 2-19% in PB, and the entity MDS/AML does not apply.

^fAML-defining cytogenetics are listed in the AML section.

Arber *et al.* Blood (2022)

New ICC (2022)

Table 21. Myeloid neoplasms with mutated *TP53*

NEW

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Type	Cytopenia	Blasts	Genetics
MDS with mutated <i>TP53</i>	Any	0-9% bone marrow and blood blasts	Multi-hit <i>TP53</i> mutation ^a , or <i>TP53</i> mutation (VAF >10%) and complex karyotype often with loss of 17p ^b
MDS/AML with mutated <i>TP53</i>	Any	10-19% bone marrow or blood blasts	Any somatic <i>TP53</i> mutation (VAF >10%)
AML with mutated <i>TP53</i>	Not required	≥20% bone marrow or blood blasts or meets criteria for pure erythroid leukemia	Any somatic <i>TP53</i> mutation (VAF >10%)

^aDefined as two distinct *TP53* mutations (each VAF >10%) OR a single *TP53* mutation with either 1) 17p deletion on cytogenetics; 2) VAF of >50%; or 3) Copy-neutral loss of heterozygosity (LOH) at the 17p *TP53* locus.

^bIf *TP53* locus LOH information is not available

Arber *et al.* Blood (2022)

WHO vs ICC (2022)

Leukemia

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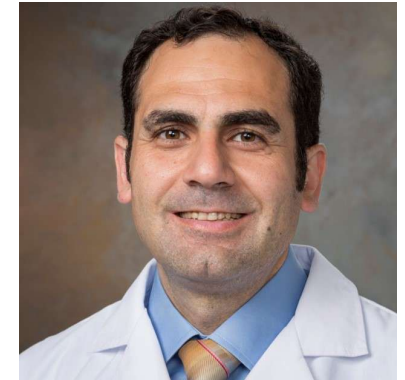
CORRESPONDENCE

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MYELODYSPLASTIC NEOPLASM

Finding consistency in classifications of myeloid neoplasms: a perspective on behalf of the International Workshop for Myelodysplastic Syndromes

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WHO vs ICC (2022)

CORRESPONDENCE

MYELODYSPLASTIC NEOPLASM

Finding consistency in classifications of myeloid neoplasms: a perspective on behalf of the International Workshop for Myelodysplastic Syndromes

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Table 1. Comparison of MDS subtype definitions in WHO 2016, WHO 2022, and ICC classification of MDS.

WHO 2016 [1]	WHO 2022 [3]	ICC [5]
MDS with single lineage dysplasia (MDS-SLD)	Not included MDS with low blasts (MDS-LB) < 5% BM and <2% PB	MDS, not otherwise specified with single lineage dysplasia (MDS, NOS-SLD)
MDS with multi-lineage dysplasia (MDS-MLD)	MDS with low blasts (MDS-LB) < 5% BM and <2% PB	MDS, not otherwise specified with multi-lineage dysplasia (MDS, NOS-MLD)
MDS with ring sideroblasts • With single lineage dysplasia (MDS-RS-SLD) • With multi-lineage dysplasia (MDS-RS-MLD)	MDS with low blasts and mutated <i>SF3B1</i> or MDS with ring sideroblasts (if ≥ 15% RS and <i>SF3B1</i> wild-type)	MDS with mutated <i>SF3B1</i>
MDS with isolated del(5q)	MDS with low blasts and isolated 5q deletion (MDS-5q)	MDS with del(5q)
MDS unclassifiable	Not included	Not included
Not included	Not included	MDS, not otherwise specified without dysplasia (e.g., monosomy 7/del(7q)) ^a
MDS excess blasts-1 (MDS-EB1; 5–9% bone marrow blasts)	MDS with increased blasts-1 (MDS-IB1; 5–9% bone marrow and/or 2–4% peripheral blood blasts)	MDS excess blasts (5–9% bone marrow and/or 2–9% peripheral blood blasts)
MDS excess blasts-2 (MDS-EB2; 10–19% bone marrow or peripheral blood blasts or Auer rods)	MDS with increased blasts-2 (MDS-IB2; 10–19% bone marrow or 5–19% peripheral blood blasts or Auer rods)	MDS/AML (10–19% bone marrow or peripheral blood blasts)
AML-defining genetics ^b	AML-defining genetics independent of bone marrow and peripheral blood blast count	AML-defining genetics with ≥10% bone marrow and peripheral blood blasts
AML (≥20% bone marrow and peripheral blood blasts)	AML (≥20% bone marrow and peripheral blood blasts)	AML (≥20% bone marrow and peripheral blood blasts)
Not included	MDS with biallelic <i>TP53</i> inactivation (Two or more <i>TP53</i> mutations, or 1 mutation with evidence of <i>TP53</i> copy number loss or cnLOH)	MDS with mutated <i>TP53</i> (Multi-hit <i>TP53</i> mutation, or <i>TP53</i> mutation (VAF > 10%) and loss of 17p) and MDS/AML with mutated <i>TP53</i> (Any somatic <i>TP53</i> mutation (VAF > 10%))
Not included	MDS, hypoplastic (MDS-h)	Not included
Not included	MDS with fibrosis (MDS-f)	Not included
Not included	Clonal hematopoiesis (CHIP, CCUS) ^c	Pre-malignant clonal cytopenias and CCUS ^c

^aThis would have been classified as MDS-unclassifiable (MDS-U) in the WHO 2016 classification.

^bAML-defining genetic abnormalities: Acute promyelocytic leukemia (APL) with t(15;17)(q24.1;q21.2)/*PML::RARA*; APL with other *RARA* rearrangements; AML with t(8;21)(q22;q22.1)/*RUNX1::RUNX1T1*; AML with inv(16)(p13.1;q22) or t(16;16)(p13.1;q22)/*CBFB::MYH11*; AML with t(9;11)(p21.3;q23.3)/*MLLT3::KMT2A*; AML with other *KMT2A* rearrangements; AML with t(6;9)(p22.3;q34.1)/*DEK::NUP214*; AML with inv(3)(q21.3;q26.2) or t(3;3)(q21.3;q26.2)/*GATA2::MECOM(EVI1)*; AML with other *MECOM* rearrangements; AML with other rare recurring translocations; AML with mutated *NPM1*; AML with in-frame bZIP *CEBPA* mutations (ICC only); AML with *RBM15::MRTFA* fusion (WHO only); AML with *NUP98*-rearrangement (WHO only).

^ccytopenias are defined as follows: hemoglobin <13 g/dL in males and <12 g/dL in females for anemia, absolute neutrophil count <1.8 × 10⁹/L for leukopenia, and platelets <150 × 10⁹/L for thrombocytopenia.

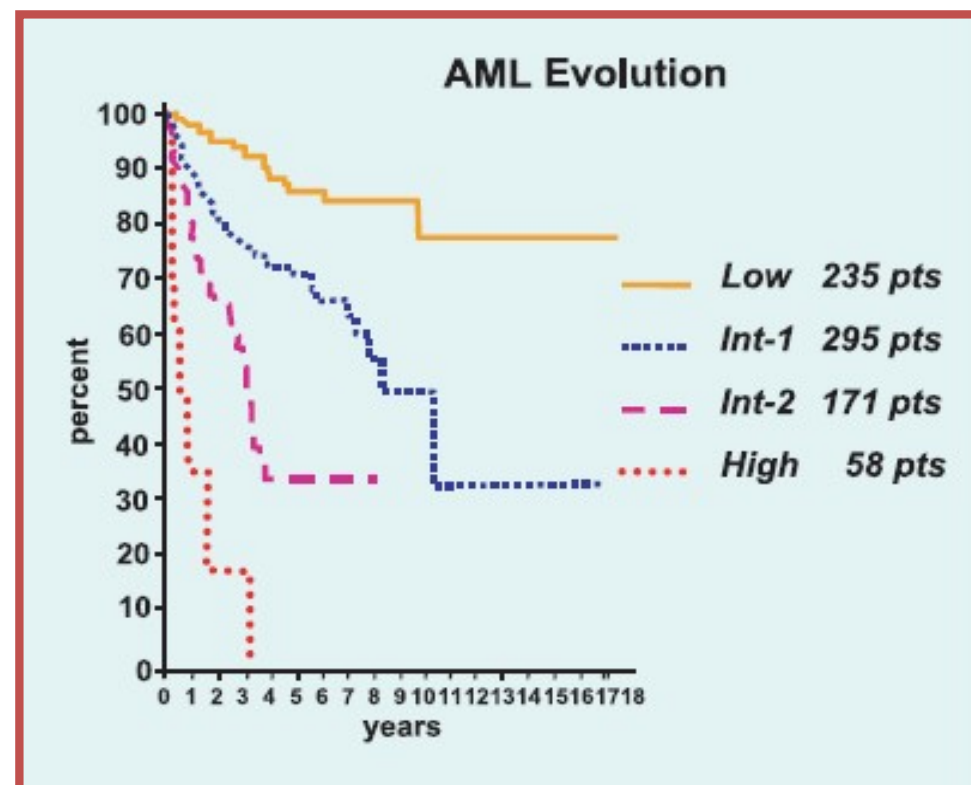
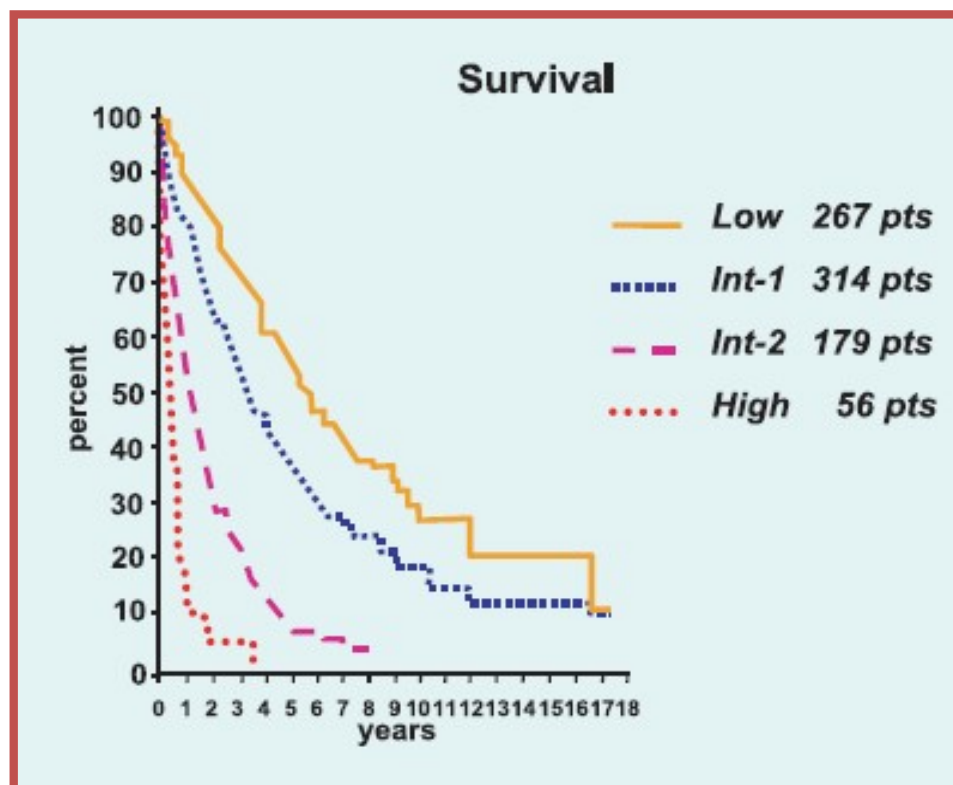
- Technical and methodological aspects
- **Prognostic value of cytogenetic findings: IPSS-R**
- Cytogenetic/genetic changes and IPSS-M
- CONCLUSIONS


International Scoring System for Evaluating Prognosis in Myelodysplastic Syndromes

By Peter Greenberg, Christopher Cox, Michelle M. LeBeau, Pierre Fenaux, Pierre Morel, Guillermo Sanz, Miguel Sanz, Teresa Vallespi, Terry Hamblin, David Oscier, Kazuma Ohyashiki, Keisuke Toyama, Carlo Aul, Ghulam Mufti, and John Bennett

N= 816


Blood, Vol 89, No 6 (March 15), 1997: pp 2079-2088



<p>ALTERATIONS WITH GOOD PROGNOSIS</p>	<p>del(5q) del(20q) loss of Y chromosome normal karyotype</p>
<p>ALTERATIONS WITH INTERMEDIATE PROGNOSIS</p>	<p>other alterations</p> 
<p>ALTERATIONS WITH POOR PROGNOSIS</p>	<p>alterations of chr. 7 complex karyotype (≥ 3 alterations)</p>

Only 4 different cytogenetic
alterations considered!!!!

Greenberg *et al.* (1997)

<p>ALTERATIONS WITH GOOD PROGNOSIS</p>	<p>del(5q) del(20q) loss of Y chromosome normal karyotype</p>
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<p>ALTERATIONS WITH POOR PROGNOSIS</p>	<p>alterations of chr. 7 complex karyotype (≥ 3 alterations)</p>

Only 4 different cytogenetic
alterations considered!!!!

Greenberg *et al.* (1997)

- **Patients obtained from registries:**
 - *IPSS (IMRAW)*
 - **German-Austrian Group**
 - **GCECGH (Spain)**
 - **International Working Group on MDS Cytogenetics from the MDS Foundation**

N= 2902

JOURNAL OF CLINICAL ONCOLOGY

ORIGINAL REPORT

N= 2902



New Comprehensive Cytogenetic Scoring System for Primary Myelodysplastic Syndromes (MDS) and Oligoblastic Acute Myeloid Leukemia After MDS Derived From an International Database Merge

Julie Schanz, Heinz Tüchler, Francesc Solé, Mar Mallo, Elisa Luño, José Cervera, Isabel Granada, Barbara Hildebrandt, Marilyn L. Slovak, Kazuma Ohyashiki, Christian Steidl, Christa Fonatsch, Michael Pfeilstöcker, Thomas Nösslinger, Peter Valent, Aristoteles Giagounidis, Carlo Aul, Michael Lübbert, Reinhard Stauder, Otto Krieger, Guillermo Garcia-Manero, Stefan Faderl, Sherry Pierce, Michelle M. Le Beau, John M. Bennett, Peter Greenberg, Ulrich Germing, and Detlef Haase

Schanz *et al.*, JCO (2012)

**VERY
GOOD**

Single:
del(11q)
-Y

OS 60.8m
HR 0.47
(0.3-0.7)

GOOD

Normal
Single:
der(1;7)
del(5q)
del(12p)
del(20q)

Double with 5q-

OS 48.5m
HR 1
(0.8-1.3)

INT.

Single:
7q-
+8
i(17q)
+19
+21
Other singles
unrelated

Other doubles

OS 25.0 m
HR 1.59
(1.4-1.9)

POOR

Single:
der(3)(q21q26)
-7

Complex 3 alt.

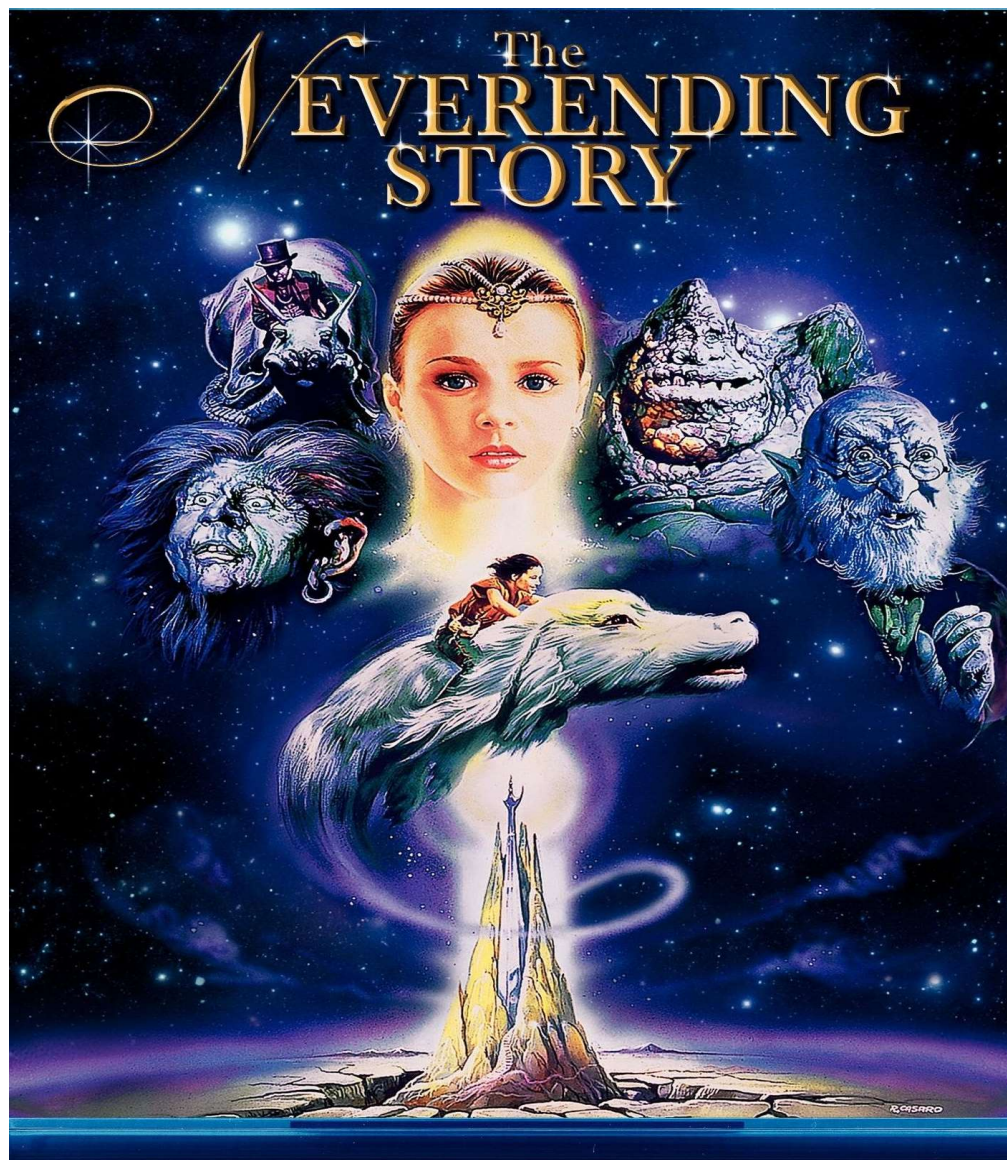
Double with
-7/7q-

OS 15.0 m
HR 2.83
(2.2-3.7)

**VERY
POOR**

Complex >3 alt.

OS 5.7 m
HR 4.37
(3.5-5.5)



*From 2008 to 2012

Revised International Prognostic Scoring System for Myelodysplastic Syndromes

Peter L. Greenberg,¹ Heinz Tuechler,² Julie Schanz,³ Guillermo Sanz,⁴ Guillermo Garcia-Manero,⁵ Francesc Solé,⁶ John M. Bennett,⁷ David Bowen,⁸ Pierre Fenaux,⁹ Francois Dreyfus,¹⁰ Hagop Kantarjian,⁵ Andrea Kuendgen,¹¹ Alessandro Levis,¹² Luca Malcovati,¹³ Mario Cazzola,¹³ Jaroslav Cermak,¹⁴ Christa Fonatsch,¹⁵ Michelle M. Le Beau,¹⁶ Marilyn L. Slovak,¹⁷ Otto Krieger,¹⁸ Michael Luebbert,¹⁹ Jaroslaw Maciejewski,²⁰ Silvia M. M. Magalhaes,²¹ Yasushi Miyazaki,²² Michael Pfeilstöcker,² Mikkael Sekeres,²⁰ Wolfgang R. Sperr,¹⁵ Reinhard Stauder,²³ Sudhir Tauro,²⁴ Peter Valent,¹⁵ Teresa Vallespi,²⁵ Arjan A. van de Loosdrecht,²⁶ Ulrich Germing,¹¹ and Detlef Haase³

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Parameters	0	0.5	1	1.5	2	3	4
Cytogenetics	Very good		Good		Int.	Poor	Very poor
Blasts MO %	≤2		>2-5%		5-10%	>10%	
Hb	≥10		8-<10	<8			
Platelets	≥100	50-<100	<50				
Neut.	≥0.8	<0.8					

- Technical and methodological aspects
- Prognostic value of cytogenetic findings: IPSS-R
- **Cytogenetic/genetic changes and IPSS-M**
- CONCLUSIONS

– Karyotype Features and *TP53*

nature
medicine

LETTERS

<https://doi.org/10.1038/s41591-020-1008-z>

Check for updates

IWG-PM
INTERNATIONAL WORKING GROUP
FOR THE PROGNOSIS OF MDS



Implications of *TP53* allelic state for genome stability, clinical presentation and outcomes in myelodysplastic syndromes

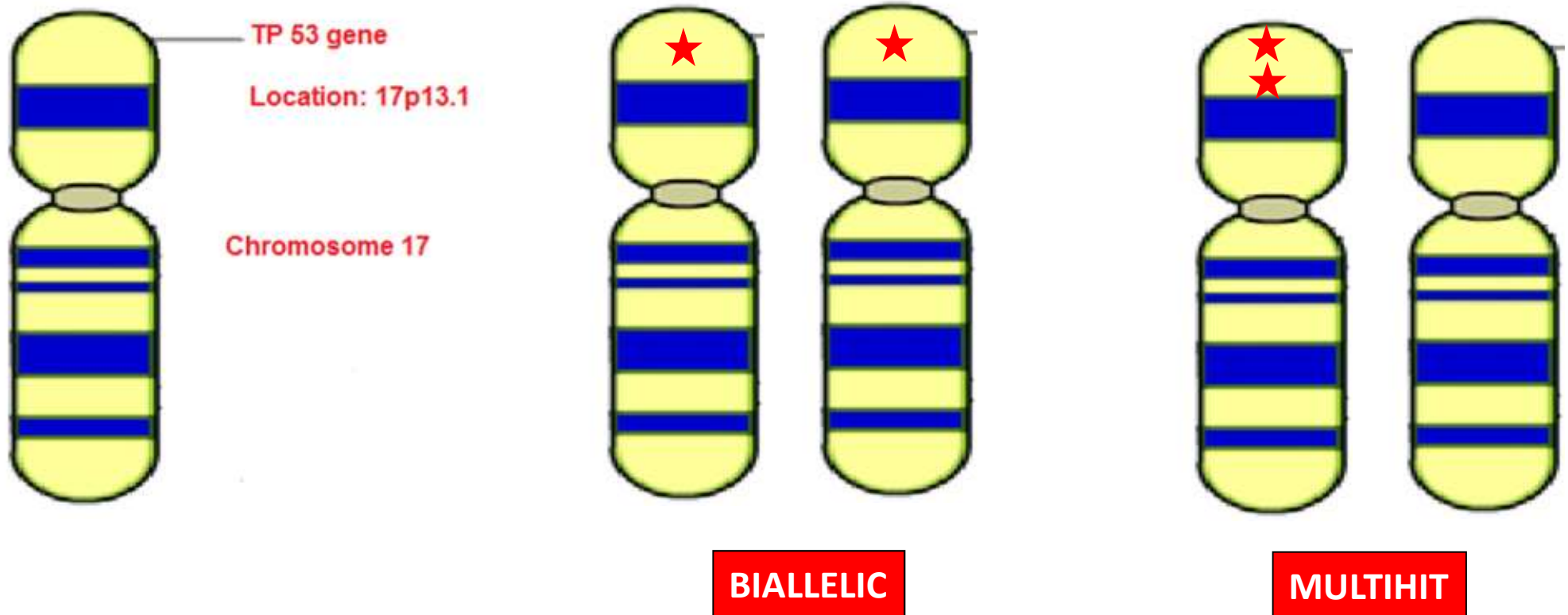
Elsa Bernard^{1,2}, Yasuhito Nannya³, Robert P. Hasserjian⁴, Sean M. Devlin⁵, Heinz Tuechler⁶, Juan S. Medina-Martinez^{1,2}, Tetsuichi Yoshizato³, Yusuke Shiozawa³, Ryunosuke Saiki³, Luca Malcovati^{7,8}, Max F. Levine^{1,2}, Juan E. Arango^{1,2}, Yangyu Zhou^{1,2}, Francesc Solé⁹, Catherine A. Cargo¹⁰, Detlef Haase¹¹, Maria Creignou¹², Ulrich Germing¹³, Yanming Zhang¹⁴, Gunes Gundem¹, Araxe Sarian², Arjan A. van de Loosdrecht¹⁵, Martin Jädersten¹², Magnus Tobiasson¹², Olivier Kosmider¹⁶, Matilde Y. Follo¹⁷, Felicitas Thol¹⁸, Ronald F. Pinheiro¹⁹, Valeria Santini²⁰, Ioannis Kotsianidis²¹, Jacqueline Boulton²², Fabio P. S. Santos²³, Julie Schanz¹¹, Senji Kasahara²⁴, Takayuki Ishikawa²⁵, Hisashi Tsurumi²⁶, Akifumi Takaori-Kondo²⁷, Toru Kiguchi²⁸, Chantana Polprasert²⁹, John M. Bennett³⁰, Virginia M. Klimek³¹, Michael R. Savona³², Monika Belickova³³, Christina Ganster¹¹, Laura Palomo⁹, Guillermo Sanz^{34,35}, Lionel Ades³⁶, Matteo Giovanni Della Porta³⁷, Alexandra G. Smith³⁸, Yesenia Werner¹, Minal Patel², Agnès Viale³⁹, Katelynd Vanness³⁹, Donna S. Neuberg⁴⁰, Kristen E. Stevenson⁴⁰, Kamal Menghrajani³¹, Kelly L. Bolton³¹, Pierre Fenaux³⁶, Andrea Pellagatti²², Uwe Platzbecker⁴¹, Michael Heuser¹⁸, Peter Valent⁴², Shigeru Chiba⁴³, Yasushi Miyazaki⁴⁴, Carlo Finelli⁴⁵, Maria Teresa Voso⁴⁶, Lee-Yung Shih⁴⁷, Michaela Fontenay¹⁶, Joop H. Jansen⁴⁸, José Cervera⁴⁹, Yoshiko Atsuta⁵⁰, Norbert Gattermann¹³, Benjamin L. Ebert⁵¹, Rafael Bejar⁵², Peter L. Greenberg⁵³, Mario Cazzola^{7,8}, Eva Hellström-Lindberg¹², Seishi Ogawa^{3,54} and Elli Papaemmanuil^{1,2,54} ✉



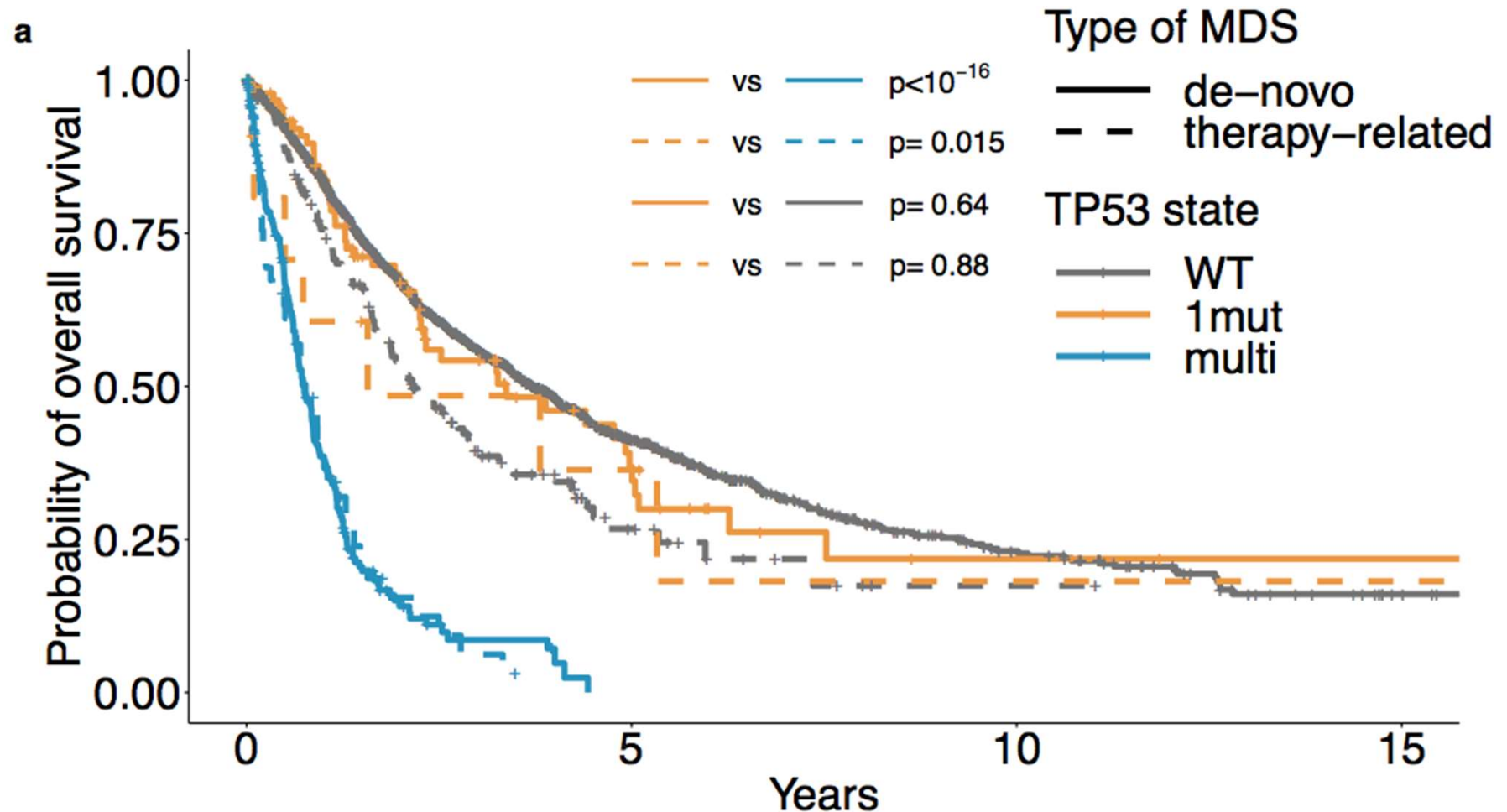
N= 3324

Bernard *et al.* Nat Med (2020)

– Karyotype Features and *TP53*



– Karyotype Features and *TP53*



MULTI HIT: ≥ 2 mutations, 1 mutation + 1 deleted or 1 mutated and LOH

Defined as two distinct *TP53* mutations (each VAF >10%) OR a single *TP53* mutation with either 1) 17p deletion on cytogenetics; 2) VAF of >50%; or 3) Copy-neutral loss of heterozygosity (LOH) at the 17p *TP53* locus.

New Proposal. IPSS-M

*From 2018 to 2022



ORIGINAL ARTICLE

Molecular International Prognostic Scoring System for Myelodysplastic Syndromes

Elsa Bernard, Ph.D.,¹ Heinz Tuechler, Peter L. Greenberg, M.D.,² Robert P. Hasserjian, M.D.,³ Juan E. Arango Ossa, M.S.,¹ Yasuhito Nannya, M.D., Ph.D.,^{4,5} Sean M. Devlin, Ph.D.,¹ Maria Creignou, M.D.,⁶ Philippe Pinel, M.S.,¹ Lily Monnier, M.S.,¹ Gunes Gundem, Ph.D.,¹ Juan S. Medina-Martinez, M.S.,¹ Dylan Domenico, B.S.,¹ Martin Jädersten, M.D., Ph.D.,⁶ Ulrich Germing, M.D.,⁷ Guillermo Sanz, M.D., Ph.D.,^{8,9,10} Arjan A. van de Loosdrecht, M.D., Ph.D.,¹¹ Olivier Kosmider, M.D., Ph.D.,¹² Matilde Y. Follo, Ph.D.,¹³ Felicitas Thol, M.D.,¹⁴ Lurdes Zamora, Ph.D.,¹⁵ Ronald F. Pinheiro, Ph.D.,¹⁶ Andrea Pellagatti, Ph.D.,¹⁷ Harold K. Elias, M.D.,¹⁸ Detlef Haase, M.D., Ph.D.,¹⁹ Christina Ganster, Ph.D.,¹⁹ Lionel Ades, M.D., Ph.D.,²⁰ Magnus Tobiasson, M.D., Ph.D.,⁷ Laura Palomo, Ph.D.,²¹ Matteo Giovanni Della Porta, M.D.,²² Akifumi Takaori-Kondo, M.D., Ph.D.,²³ Takayuki Ishikawa, M.D., Ph.D.,²⁴ Shigeru Chiba, M.D., Ph.D.,²⁵ Senji Kasahara, M.D., Ph.D.,²⁶ Yasushi Miyazaki, M.D., Ph.D.,²⁷ Agnes Viale, Ph.D.,²⁸ Kety Huberman, B.S.,²⁸ Pierre Fenaux, M.D., Ph.D.,²⁰ Monika Belickova, Ph.D.,²⁹ Michael R. Savona, M.D.,³⁰ Virginia M. Klimek, M.D.,¹⁸ Fabio P. S. Santos, M.D., Ph.D.,³¹ Jacqueline Boulwood, Ph.D.,¹⁷ Ioannis Kotsianidis, M.D., Ph.D.,³² Valeria Santini, M.D.,³³ Francesc Solé, Ph.D.,¹⁵ Uwe Platzbecker, M.D.,³⁴ Michael Heuser, M.D.,¹⁴ Peter Valent, M.D.,^{35,36} Kazuma Ohyashiki, M.D., Ph.D.,³⁷ Carlo Finelli, M.D.,³⁸ Maria Teresa Voso, M.D.,³⁹ Lee-Yung Shih, M.S.,⁴⁰ Michaela Fontenay, M.D., Ph.D.,¹² Joop H. Jansen, Ph.D.,⁴¹ José Cervera, M.D., Ph.D.,⁴² Norbert Gattermann, M.D.,⁷ Benjamin L. Ebert, M.D., Ph.D.,⁴³ Rafael Bejar, M.D., Ph.D.,⁴⁴ Luca Malcovati, M.D.,⁴⁵ Mario Cazzola, M.D.,⁴⁵ Seishi Ogawa, M.D., Ph.D.,^{4,46,47} Eva Hellström-Lindberg, M.D., Ph.D.,⁶ and Elli Papaemmanuil, Ph.D.¹



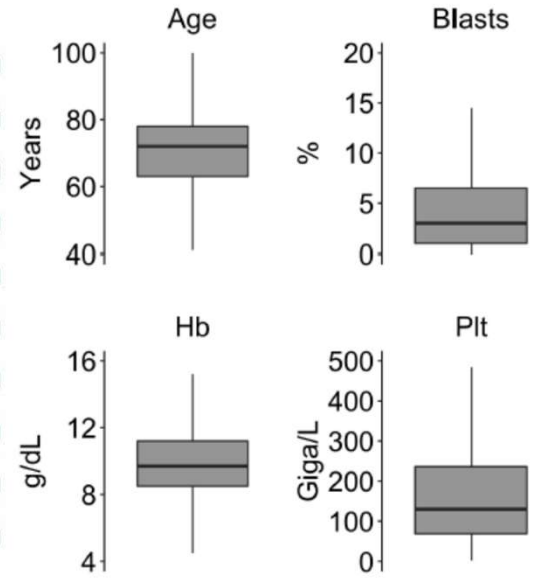
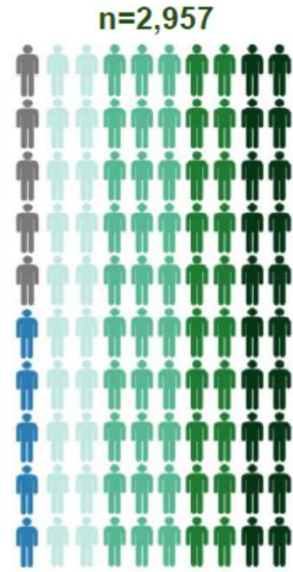
Bernard *et al.* NEJM-Evidence (2022)

New IPSS: IPSS-M

IPSS n = 816

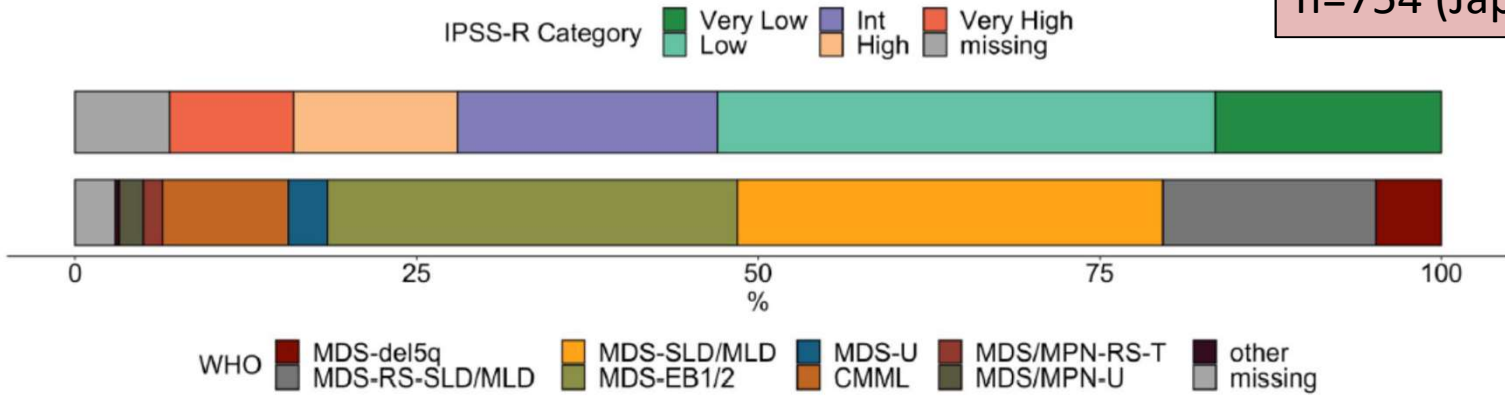
IPSS-R n = 7012

A.



Validation cohort:
n=754 (Japan, SO)

B.



New IPSS: IPSS-M

A

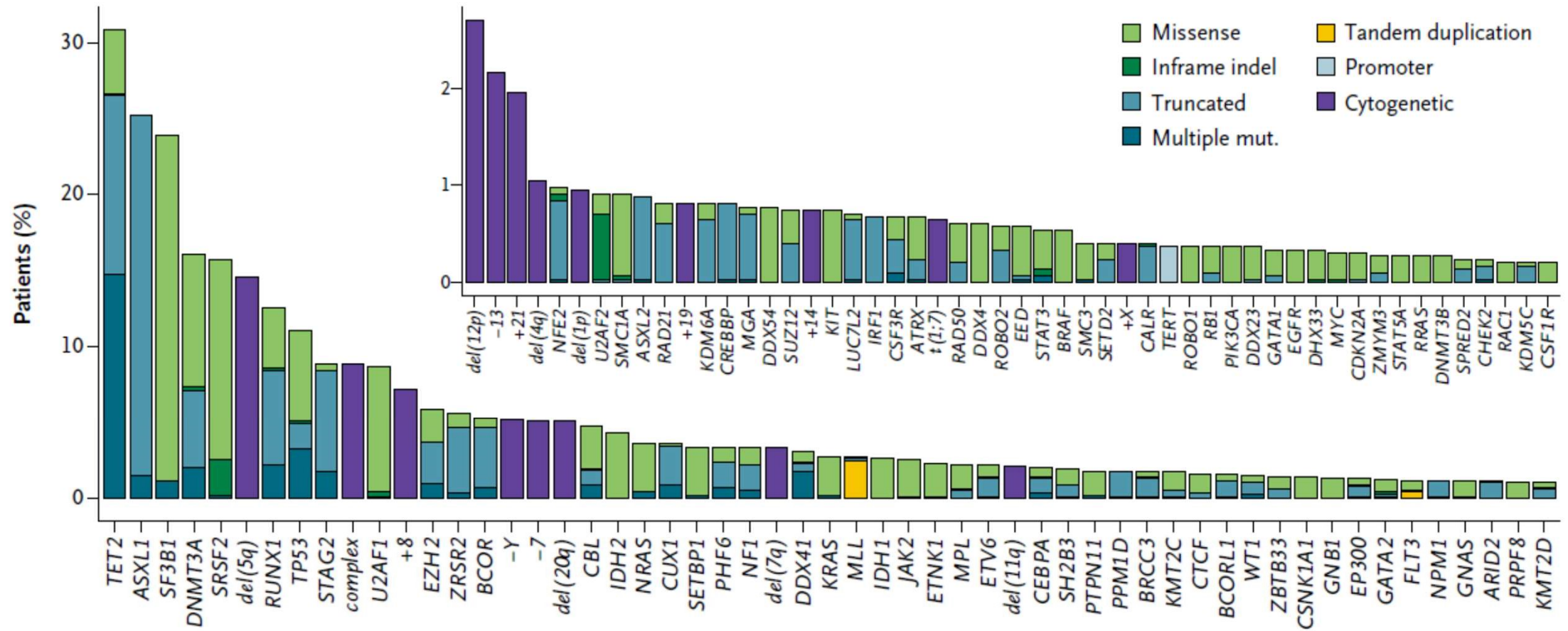


Figure 1 | IWG-PM cohort characteristics.

New IPSS: IPSS-M

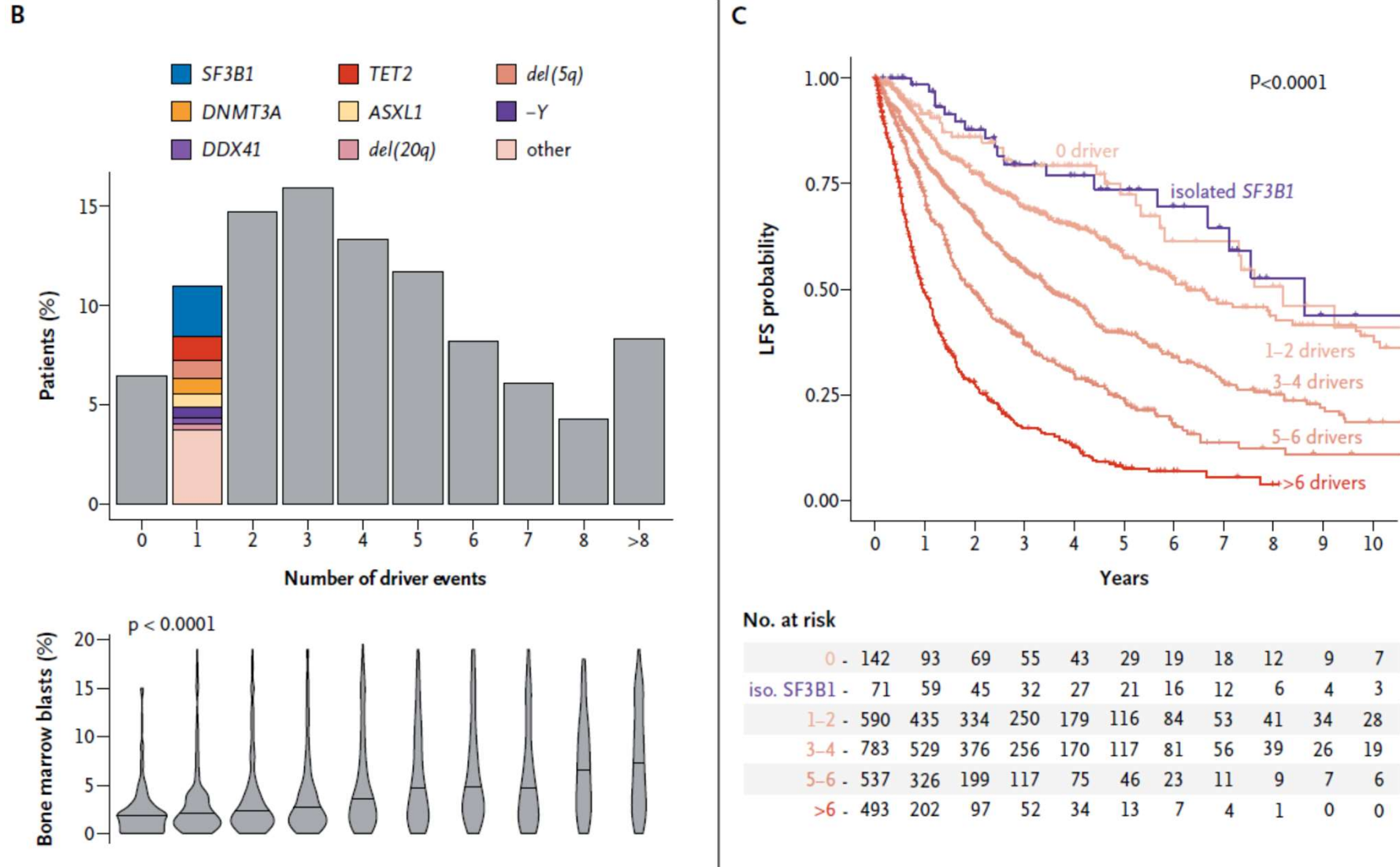


Figure 1 | IWG-PM cohort characteristics.

Figure 2 | IPSS-M score construction.

Table 1. IPSS-M Risk Score Construction from an Adjusted Cox Multivariable Regression for Leukemia-Free Survival.*		
Category and Variable	Adjusted Hazard Ratio (95% CI)†	Model Weight‡
Clinical		
Bone marrow blasts — %	1.07 (1.05–1.09)	0.0704
min(Platelets,250) — $\times 10^9/l$	0.998 (0.997–0.999)	–0.00222
Hemoglobin — g/dl	0.84 (0.81–0.88)	–0.171
Cytogenetic		
IPSS-R cytogenetic category§	1.33 (1.21–1.47)	0.287
Gene main effects (17 variables, 16 genes)¶		
<i>TP53</i> ^{multihit}	3.27 (2.38–4.48)	1.18
<i>MLL</i> ^{PTD}	2.22 (1.49–3.32)	0.798
<i>FLT3</i> ^{ITD+TKD}	2.22 (1.11–4.45)	0.798
<i>SF3B1</i> ^{5q}	1.66 (1.03–2.66)	0.504
<i>NPM1</i>	1.54 (0.78–3.02)	0.430
<i>RUNX1</i>	1.53 (1.23–1.89)	0.423
<i>NRAS</i>	1.52 (1.05–2.20)	0.417
<i>ETV6</i>	1.48 (0.98–2.23)	0.391
<i>IDH2</i>	1.46 (1.05–2.02)	0.379
<i>CBL</i>	1.34 (0.99–1.82)	0.295
<i>EZH2</i>	1.31 (0.98–1.75)	0.270
<i>U2AF1</i>	1.28 (1.01–1.61)	0.247
<i>SRSF2</i>	1.27 (1.03–1.56)	0.239
<i>DNMT3A</i>	1.25 (1.02–1.53)	0.221
<i>ASXL1</i>	1.24 (1.02–1.51)	0.213
<i>KRAS</i>	1.22 (0.84–1.77)	0.202
<i>SF3B1</i> ⁷	0.92 (0.74–1.16)	–0.0794
Gene residuals (1 variable, 15 genes; possible values of 0, 1, or 2) 		
min(Nres,2)	1.26 (1.12–1.42)	0.231

*Hazard ratio for the risk of leukemic transformation or death, adjusted for age, sex, and therapy-related versus primary MDS. CI: confidence interval. The Cox regression was performed on 2,428 patients with available covariables and leukemia-free survival data.

†The model weights, derived from the logarithm of the raw hazard ratios up to three significant digits, used to calculate the IPSS-M risk score. The following formula applies: IPSS-M score = $1.15467 + (\sum_{\text{variables}} w_j x_j) / \log(2)$, where w_j denotes the weight of variable j , and x_j the value of the variable j observed in a given patient.

‡0=Very Good; 1=Good; 2=Intermediate; 3=Poor; 4=Very Poor.

§Nres is defined as the number of mutated genes within the following list: *BCOR, BCORL1, CEBPA, ETNK1, GATA2, GNB1, IDH1, NF1, PHF6, PPM1D, PRPF8, PTPN11, SETBP1, STAG2, WT1*. The variable min(Nres,2) can therefore take the value 0, 1 or 2.

¶PTD: partial tandem duplication; ITD: internal tandem duplication; TKD: tyrosine kinase domain.

¶*SF3B1*^{5q}: *SF3B1* mutation in the presence of isolated del(5q), i.e. del(5q) only or with one additional aberration excluding -7/del(7q).

¶*SF3B1*⁷: *SF3B1* mutation without co-mutations in *BCOR, BCORL1, RUNX1, NRAS, STAG2, SRSF2*, and del(5q).

IPSS-R

IPSS-R Blasts, HB, plat

IPSS-R Cytogenetics

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IPSS-R

IPSS-R Blasts, HB, plat

IPSS-R Cytogenetics

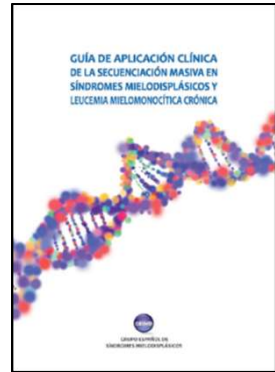
Genes with independent prognostic

Number of mutated genes

bjh guideline

Spanish Guidelines for the use of targeted deep sequencing in myelodysplastic syndromes and chronic myelomonocytic leukaemia

Lauro Palomo,¹ Marian Ibáñez,^{2,3,4} María Abellán,² Iñe Vázquez,^{5,6} Sara Álvarez,^{6,7} María Cabanero,⁸ Bárbara Tardón-Vega,^{9,10} Inmaculada Rapado,^{11,12,13} Francisco Fuster-Torres,¹⁴ José Carverá,^{2,3,15} Rocío Benito,² María J. Larrazo,^{6,7} Juan C. Cigudosa,⁶ Lurdes Zamora,⁶ David Valcárcel,^{16,17} María T. Cedeno,^{18,19,20} Pamela Acha,¹ Jesús M. Hernández-Sánchez,^{21,22} Marta Fernández-Mercado,^{6,23,24} Guillermo Sanz,²⁵ Jesús M. Hernández-Rivas,^{2,16,19} María J. Calasanz,^{6,7} Francisco Solís,²⁶ and Esperanza Such,^{2,26} On behalf of the Spanish Group of MDS (GESMD)



Application to calculate the IPSS-M

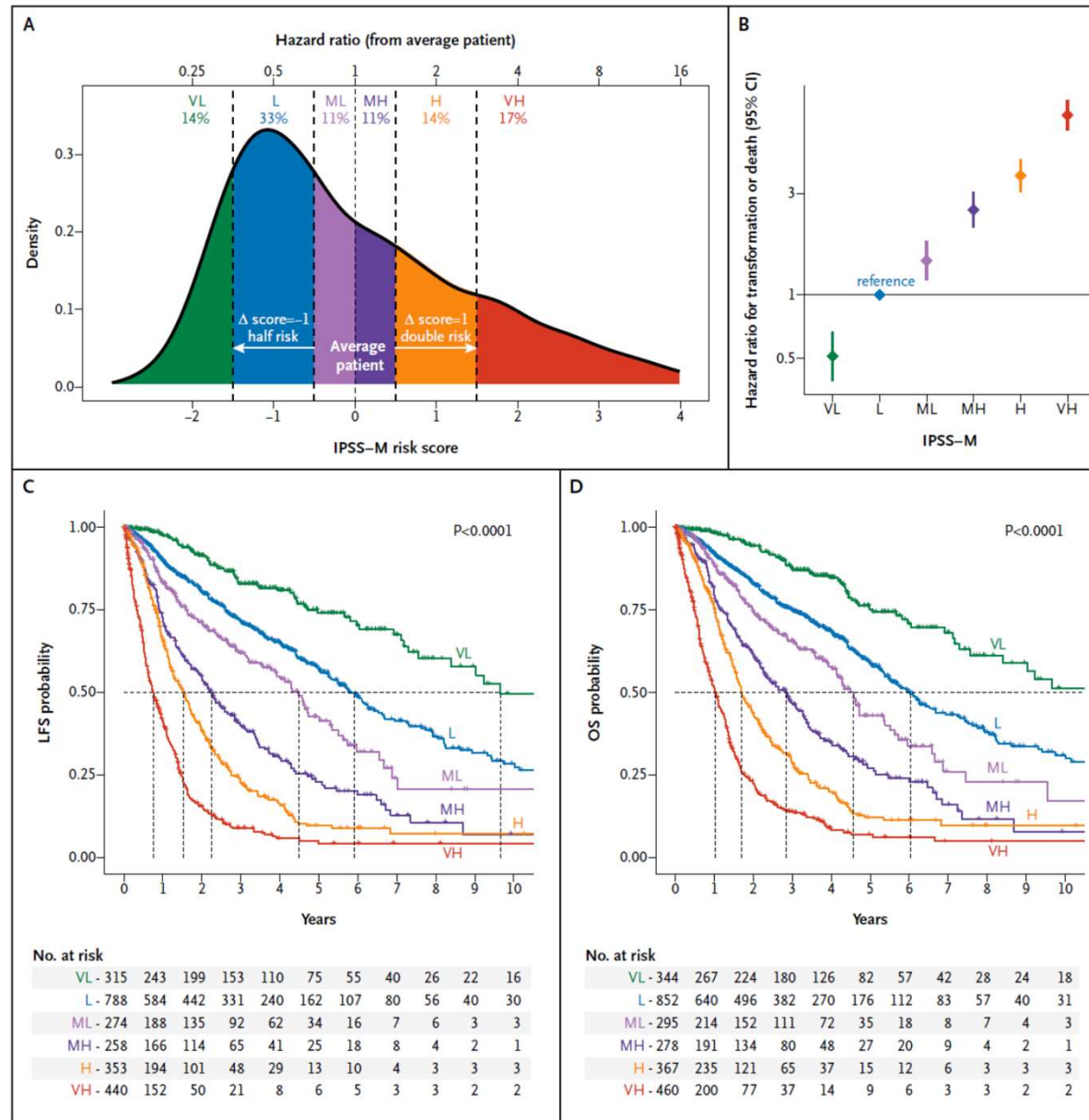
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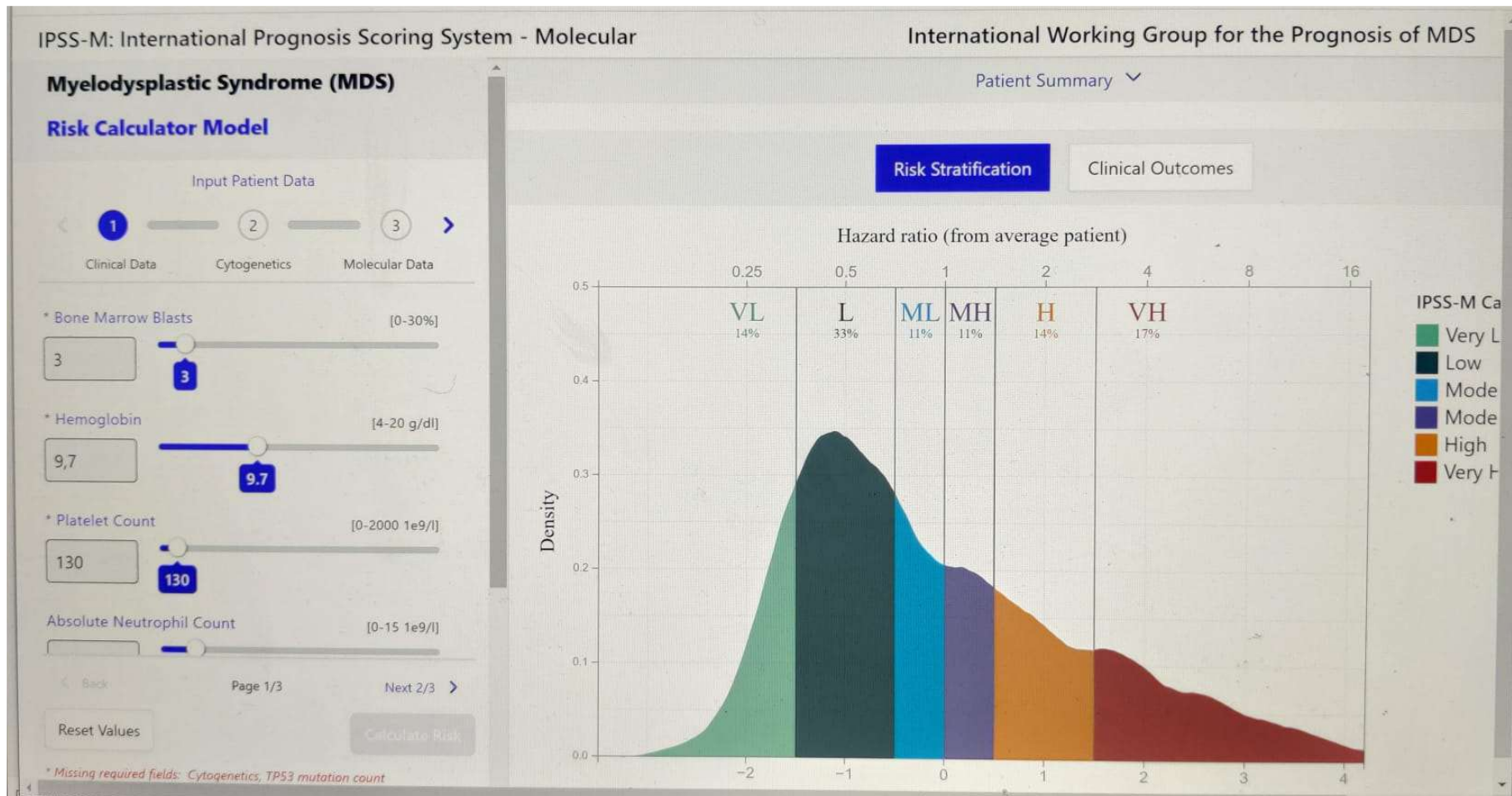
New IPSS: IPSS-M

6 CATEGORIES: VL, L, ML, MH, H, and VH



New IPSS: IPSS-M. Calculator

6 CATEGORIES: VL, L, ML, MH, H, and VH



<https://mds-risk-model.com/>

New IPSS: IPSS-M. Calculator

Translated to Spanish, French, German, Japanese...

The image displays three sequential screenshots of the IPSS-M Risk Calculator Model interface, illustrating the input phase and the resulting density plot.

Screenshot 1 (Left): Shows the 'Input Patient Data' section with three steps: Clinical Data, Cytogenetics, and Molecular Data. The 'Clinical Data' step is active, showing sliders for Bone Marrow Blasts (3), Hemoglobin (4.0), Platelet Count (130), and Absolute Neutrophil Count (1.9). A 'Skip Variable' checkbox is present. The density plot on the right shows a peak at 0.0.

Screenshot 2 (Middle): Shows the 'Cytogenetics' step. It includes a table for 'Presence of' cytogenetic abnormalities:

del(5q)	No	Yes
-7/del(7q)	No	Yes
-17/del(17p)	No	Yes
Complex Karyotype	No	Yes

It also shows a 'Cytogenetics Category' with radio buttons for Very Good, Good, Intermediate, Poor, and Very Poor. The 'Prognostic Subgroups' table shows 'Very good' and 'Cytogenetic Abnormalities' as '-Y, del(11q)'. The density plot on the right shows a peak at 0.0.

Screenshot 3 (Right): Shows the 'Molecular Data' step. It includes radio buttons for 'Number of TP53 mutations' (0, 1, 2 or more), 'Loss of heterozygosity at TP53 locus' (No, Yes, N/A), and 'MLL and FLT3 Mutations' (MLL PTD, FLT3 ITD or TKD). The density plot on the right shows a peak at 0.0.

Each screenshot includes a 'Reset Values' button and a 'Calculate Risk' button. A red asterisk indicates missing required fields: Cytogenetics, TP53 mutation count.

<https://mds-risk-model.com/>

New IPSS: IPSS-M

Tweet, 30 th October, 2022

Elli Papaemmanuil, PhD

@PapaemmanuilLab

4months since publication (<https://bit.ly/3aNEU64>), >5K unique users from 65 countries have used the IPSS-M model (<https://mds-risk-model.com>) to compute risk for 42,500 patient profiles.



**High IF journal editor said "not ready for prime time".
This is my type of impact factor.**

New IPSS: IPSS-M

Tweet, 5th November, 2022

6:52

Hilo

 **Elli Papaemmanuil, PhD**
@PapaemmanuilLab

39 abstracts on IPSS-M at #ASH22. Diagnostic & clinical utility validated in >10,000 patients, including secondary & therapy related MDS.

Validation at scale & within 6wks to ASH deadline enabled by R package developed by @Elsa2Bernard
github.com/papaemmelab/ip...
#opensource

[Traducir Tweet](#)

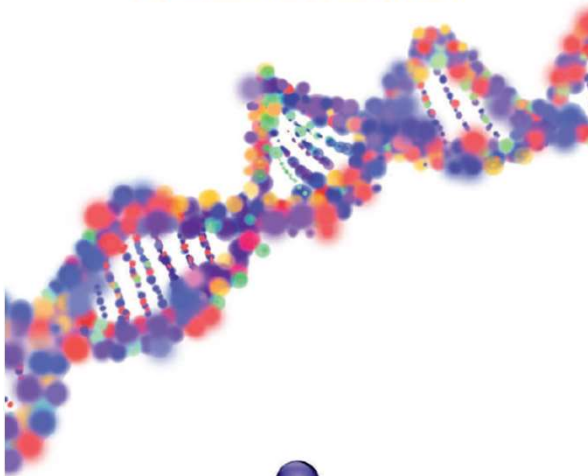
Twittea tu respuesta





GRUPO ESPAÑOL DE SÍNDROMES MIELODISPLÁSICOS

GUÍA DE APLICACIÓN CLÍNICA
DE LA SECUENCIACIÓN MASIVA EN
SÍNDROMES MIELODISPLÁSICOS Y
LEUCEMIA MIELOMONOCÍTICA CRÓNICA




GRUPO ESPAÑOL DE
SÍNDROMES MIELODISPLÁSICOS
2017

GUÍAS
ESPAÑOLAS DE
SMD Y LMMC
Edición 2020



GUÍA DE CONSENSO DE LA HEMATOPOYESIS CLONAL DE POTENCIAL INDETERMINADO GESMD - I Edición - Enero de 2022

GUÍA DE CONSENSO DE LA
HEMATOPOYESIS CLONAL
DE POTENCIAL INDETERMINADO
GESMD
I Edición - Enero de 2022



- **¿Debemos incorporar los estudios moleculares en pacientes con sospecha o diagnóstico de SMD?**
- **A) no deben realizarse**
- **B) son recomendables**
- **C) son obligatorios**

- Technical and methodological aspects
- Prognostic value of cytogenetic findings: IPSS-R
- Cytogenetic/genetic changes and IPSS-M
- **CONCLUSIONS**

To conclude: What should we do?

Apply in all cases

IPSS-R (MDS)
CPSS (CMML)

Apply in selected cases

Karyotype

FISH

Start to introduce

IPSS-M (MDS)

Apply in cases
with normal CG or
without mitosis

Arrays

+

OGM

Sequencing
(panel of genes)

