EBMT Registry

Myelodysplastic syndromes (MDS)

Guide to the completion of the EBMT data collection form: MDS_v2.0

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EBMT Registry

EBMT Clinical Research & Registry Department

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Introduction

Please make sure you have already checked the **Introduction to the EBMT Registry Completion Guidelines** document latest version available under *Manuals and Reference Documents* section on EBMT website.

Myelodysplastic neoplasms (MDS)

MDS is a heterogeneous group of clonal haematopoietic stem cell disorders characterised by ineffective, dysplastic haematopoiesis, peripheral cytopenia and a variable rate of progression to acute myelogenous leukaemia (AML).

This form must be completed for all patients whose primary disease for which the HCT/CT treatment is given is MDS. If the MDS has transformed to AML before the HCT/CT treatment, please complete both the MDS diagnosis form and the Acute Leukaemias diagnosis form.

If MDS originated from Fanconi Anaemia (FA) or Aplastic Anaemia (AA) and the patient received treatment for these diagnoses, please complete the Bone Marrow Failure Syndromes (BMF) incl. Aplastic Anaemia (AA) diagnosis form in addition to the MDS diagnosis form. If no treatment was given for FA or AA, please complete the Non-indication diagnosis form in addition to the MDS diagnosis form.

No data items should be left blank unless specifically stated in the definition.

Disease

Date of diagnosis

Report the date of the first pathological diagnosis of the disease. This is the date when the sample was collected for examination or (in its absence) the date indicated by a physician within the patient's medical record.

MDS transformed into Acute Leukaemia and treatment was done for Acute Leukaemia?

MDS can progress through different phases (subclassifications) from the time of diagnosis to transplantation. One of these phases can be AML.

If the patient is being transplanted for AML that has transformed from MDS, select **Yes** and complete the Acute Leukaemias diagnosis form in addition to the current form. Otherwise, check the **No** option.

MDS classification at diagnosis (WHO 2022)

Please see the tables 1,2 and 3 below for definitions of the MDS subclassifications according to WHO 2022 (1).

Classification	Blasts	Cytogenetics	Mutations
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 SF3B1 mutation[a] (MDS-SF3B1)	<5% BM and <2% PB	Absence of 5q deletion, monosomy 7, or complex karyotype	SF3B1
MDS with biallelic TP53 inactivation (MDS-biTP53)	<20% BM and PB	Usually complex	Two or more TP53 mutations, or 1 mutation with evidence of TP53 copy number loss or cnLOH

Table 1. MDS with defining genetic abnormalities (WHO 2022).

[a] Detection of ≥15% ring sideroblasts may substitute for SF3B1 mutation

Classification	Blasts
MDS with low blasts (MDS-LB)	<5% BM and <2% PB
MDS, hypoplastic[a] (MDS-h)	
MDS with increased blasts (MDS-IB1)	5–9% BM or 2–4% PB
MDS with increased blasts (MDS-IB2)	10– 9% BM or 5–19% PB or Auer rods
MDS with fibrosis (MDS-f)	5–19% BM; 2–19% PB

Table 2. MDS, morphologically defined (WHO 2022).

[a] By definition, ≤25% bone marrow cellularity, age adjusted

Classification	Blasts
Childhood MDS[a] with low blasts	<5% BM; <2% PB
Childhood MDS[a] with increased blasts	5–19% BM; 2–19% PB

Table 3. Childhood MDS (WHO 2022).

[a] A clonal haematopoietic stem cell neoplasm arising in children and adolescents (<18 years of age)

Therapy-related MDS

Indicate if MDS developed due to medical treatment (therapeutic agents or radiation).

IPSS-R

The Revised International Prognostic Scoring System (IPSS-R) (2) consists of the following:

- Haemoglobin value
- Absolute Neutrophil Count (ANC)
- Platelet count
- Bone marrow blasts (%)
- Cytogenetic risk group

Please see tables 4, 5 and 6 how to calculate this score. There are online calculators available, one example is: https://www.mds-foundation.org/ipss-r-calculator/

Cytogenetic risk groups	Cytogenetic abnormalities
Very good	-Y, del(11q)
Good	Normal, del(5q), del(12p), del(20q), double including del(5q)
Intermediate	del(7q), +8, +19, i(17q), any other single or double independent clones
Poor	-7, inv(3)/t(3q)/del(3q), double including -7/del(7q), Complex: 3 abnormalities
Very poor	Complex: >3 abnormalities

Table 4. Cytogenetic risk groups.

Prognostic variable	0	0.5	1	1.5	2	3	4
Cytogenetics	Very Good		Good		Intermediate	Poor	Very Poor
BM Blast (%)	<=2		>2-<5%		5-10%	>10%	
Haemoglobin (g/dL)	=>10		8-<10	<8			
Platelets (10^9/L)	=>100	50-<100	<50				
ANC (10^9/L)	=>0.8	<0.8					

Table 5. IPSS-R points.

Risk category	Risk score
Very Low	<=1.5
Low	>1.5 – 3
Intermediate	>3 – 4.5
High	>4.5 – 6
Very High	>6

Table 6. IPSS-R risk categories.

IPSS-M

The Molecular International Prognostic Scoring System (IPSS-M) (3) combines genomic risk factors with haematological and cytogenetic risk factors and consists of the following:

- Haemoglobin value
- Platelet count
- Bone marrow blasts
- IPSS-R cytogenetic risk groups (see IPSS-R section above, table 4)
- Molecular information on 31 genes (see table 7)

There are online calculators available, one example is: https://mds-risk-model.com/

Prognostic genes	Additional genes
ASXL1	BCOR
CBL	BCORL1
DNMT3A	CEBPA
ETV6	ETNK1
EZH2	GATA2
FLT3	GNB1
IDH2	IDH1
KRAS	NF1
MLL PTD	PHF6
NPM1	PPM1D
NRAS	PRPF8
RUNX1	PTPN11
SF3B15q/SF3B1α	SETBP1
SRSF2	STAG2
TP53 multihit	WT1
U2AF1	

Table 7. Molecular information for IPSS-M.

Risk category	Risk score
Very Low	<=-1.5
Low	>-1.5 – -0.5
Moderate Low	>-0.5 – 0
Moderate High	>0 – 0.5
High	>0.5 – 1.5
Very High	>1.5

Table 8. IPSS-M risk categories.

Chromosome analysis

Chromosome analysis done before HCT/CT/IST treatment

In this section describe the results of all chromosome analyses (all methods including FISH) performed at/after diagnosis but before the HCT/CT/IST treatment. If there were multiple chromosome analysis tests done on different dates, the results can be registered separately along with the test date.

Indicate if chromosome analysis was done or not before the HCT/CT/IST treatment. Check **Unknown** if it is not known whether it was performed.

Output of analysis

Indicate if the output of the chromosome analysis will be reported as **separate abnormalities** or as a **full karyotype**.

What were the results?

Normal - the chromosome analysis has been performed and the results have been found normal

Abnormal - the chromosome analysis has been performed and abnormalities have been found. In addition, indicate the total number of different abnormalities present (**number of abnormalities present**).

Failed - the chromosome analysis was done but failed

Date of chromosome analysis

Indicate the date of the chromosome analysis. Check **Unknown** if it is not known when it was performed.

Chromosome analysis details

Indicate for each abnormality in the table whether it was **Absent, Present** or **Not evaluated**.

If a chromosome abnormality was checked, but not listed as an option in the table, select **Other** and specify the abnormality, marking whether it was **Absent** or **Present**.

Transcribe the complete karyotype

If it is not possible to report the chromosome analysis results as per the abnormalities table please enter the complete karyotype. Describe all abnormalities according to the ISCN karyotype nomenclature. This notation includes the total number of chromosomes, the sex chromosomes, and any extra, missing or mutated autosomal chromosomes. For example, **47, XY, +18** indicates that the patient has 47 chromosomes, is a male, and has an extra autosomal chromosome 18.

Molecular marker analysis

Molecular markers analysis done before HCT/CT/IST treatment

In this section, describe the results of all molecular marker analyses (performed at/after diagnosis but before the HCT/CT/IST treatment). If there were multiple molecular marker analyses tests done on different dates, the results can be registered separately along with the test date.

Indicate if molecular marker analysis was done or not before the HCT/CT/IST treatment. Check **Unknown** if it is not known whether it was performed.

Date of molecular marker analysis

Indicate the date of the molecular marker analysis. If there were multiple molecular tests done on different dates, the results can be registered separately along with the test date.

Molecular marker analysis details

If molecular marker analysis was performed, indicate for each marker in the table whether it was **Absent, Present** or **Not evaluated**.

If a molecular marker was evaluated, but not listed as an option in the table, select **Other** and specify the marker, indicating whether it was **Absent** or **Present**.

TP53 mutation type

If TP53 mutation is present, indicate the mutation type if known. A TP53 mutation is considered a multi hit if it fulfils one of the following criteria

- 2 or more distinct mutations of TP53 with a VAF of ≥ 10%
- 1 mutation and 1 deletion involving the TP53 locus
- 1 mutation with VAF ≥ 50%
- 1 mutation with complex karyotype

A TP53 mutation is considered single hit if either one of the following criteria is fulfilled:

- a single TP53 mutation with VAF < 50%
- loss of 17p13 involving TP53 locus without TP53 mutations

If the lab report does not specify the type, select **Unknown**.

Bibliography

1. Khoury JD, Solary E, Abla O, Akkari Y, Alaggio R, Apperley JF, et al. The 5th edition of the World Health Organization classification of haematolymphoid tumours: myeloid and histiocytic/dendritic neoplasms. Leukemia. 2022;36:1703–19. doi: 10.1038/s41375-022-01613-1.

2. Greenberg PL, Tuechler H, Schanz J, et al. Revised International Prognostic Scoring System for Myelodysplastic Syndromes. Blood. 2012;120(12):2454-2465. doi:10.1182/blood-2012-03-420489.

3. Bernard E, Tuechler H, Greenberg Peter L, Hasserjian Robert P, Arango Ossa Juan E, Nannya Y, et al. Molecular international prognostic scoring system for myelodysplastic syndromes. NEJM Evid (2022) 1:EVIDoa2200008. doi: 10.1056/EVIDoa2200008