

MDS/MPN overlap syndromes

**Guide to the completion of the EBMT data collection form:
MDS/MPN_Core_Extended_v2.2**

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EBMT Registry

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Table of Contents

Introduction.....	4
MDS/MPN overlap syndromes.....	4
Disease.....	4
Date of diagnosis.....	4
MDS/MPN transformed into Acute Leukaemia and treatment was done for Acute Leukaemia?....	4
Classification (WHO 2022).....	5
CMML subtype.....	6
CMML subgroup.....	7
Therapy-related MDS/MPN.....	7
CPSS (for CMML only).....	7
CPSS-Mol (for CMML only).....	8
Extended dataset.....	9
Assessments at diagnosis.....	9
Haematological values.....	9
Peripheral blood.....	9
Haemoglobin (g/dL).....	9
Platelets (109/L).....	9
White blood cells (109/L).....	9
% blasts.....	9
% monocytes.....	9
% neutrophils.....	9
Bone marrow.....	9
% blasts.....	9
Precise blast count not available.....	10
Auer rods present.....	10
Bone marrow investigation.....	10
Fibrosis.....	10
Chromosome analysis.....	10
Chromosome analysis done before HCT/CT/IST treatment.....	10
Output of analysis.....	10
What were the results?.....	10
Date of chromosome analysis.....	11
Chromosome analysis details.....	11
Transcribe the complete karyotype.....	11
Molecular marker analysis.....	11
Molecular markers analysis done before HCT/CT/IST.....	11
Date of molecular marker analysis.....	11
Molecular marker analysis details.....	11
TP53 mutation.....	12
Extended dataset.....	12
PREVIOUS THERAPIES(between diagnosis and HCT/CT).....	12

Previous therapy lines before the HCT/CT:.....	12
Bibliography.....	13

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](#).

MDS/MPN overlap syndromes

MDS/MPN overlap syndromes are a group of chronic clonal myeloid malignancies in which there are features of both MDS and MPN at the time of presentation. This category is composed of the following major myeloid disorders: chronic myelomonocytic leukaemia (CMML), MDS/MPN with SF3B1 mutation and thrombocytosis and MDS/MPN with neutrophilia and MDS/MPN with ring sideroblasts and thrombocytosis (MDS/MPN-RS-T). Myeloid disease that shows features of both MDS and MPN but does not meet the criteria for any of the major MDS/MPN entities is designated as MDS/MPN-NOS (not otherwise specified).

All MDS/MPN subclassifications are negative for BCR::ABL1 fusions, or rearrangements involving PDGFRA, PDGFRB, FGFR1 and JAK2 and have <20% blasts in the peripheral blood (PB) and in the bone marrow (BM).

This form must be completed for all patients whose primary disease for which the HCT/CT treatment is being given is MDS/MPN. When the MDS/MPN has transformed to acute myelogenous leukaemia (AML) before HCT/CT, please complete both the MDS/MPN diagnosis form and the Acute Leukaemias 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/MPN transformed into Acute Leukaemia and treatment was done for Acute Leukaemia?

MDS/MPN 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/MPN, select **Yes** and complete the Acute Leukaemias diagnosis form in addition to the current form. Otherwise, check the **No** option.

Classification (WHO 2022)

According to the WHO 2022 (1) classification there are five subclassifications of the MDS/MPN overlap syndrome:

Chronic myelomonocytic leukaemia (CMML, CMML):

Prerequisite criteria

1. Persistent absolute ($\geq 0.5 \times 10^9/L$) and relative ($\geq 10\%$) peripheral blood monocytosis.
2. Blasts constitute $< 20\%$ of the cells in the peripheral blood and bone marrow.^a
3. Not meeting diagnostic criteria of chronic myeloid leukaemia or other myeloproliferative neoplasms.^b
4. Not meeting diagnostic criteria of myeloid/lymphoid neoplasms with tyrosine kinase fusions.^c

Supporting criteria

1. Dysplasia involving ≥ 1 myeloid lineages.^d
2. Acquired clonal cytogenetic or molecular abnormality.
3. Abnormal partitioning of peripheral blood monocyte subsets.^e

Requirements for diagnosis

- Pre-requisite criteria must be present in all cases.
- If monocytosis is $\geq 1 \times 10^9/L$: one or more supporting criteria must be met.
- If monocytosis is ≥ 0.5 and $< 1 \times 10^9/L$: supporting criteria 1 and 2 must be met.

^aBlasts and blast equivalents include myeloblasts, monoblasts and promonocytes.

^bMyeloproliferative neoplasms (MPN) can be associated with monocytosis at presentation or during the course of the disease; such cases can mimic CMML. In these instances, a documented history of MPN excludes CMML. The presence of MPN features in the bone marrow and/or high burden of MPN-associated mutations (JAK2, CALR or MPL) tends to support MPN with monocytosis rather than CMML.

^cCriteria for myeloid/lymphoid neoplasms with tyrosine kinase fusions should be specifically excluded in cases with eosinophilia.

^dMorphologic dysplasia should be present in $\geq 10\%$ of cells of a haematopoietic lineage in the bone marrow.

^eBased on detection of increased classical monocytes (>94%) in the absence of known active autoimmune diseases and/or systemic inflammatory syndromes.

MDS/MPN with SF3B1 mutation and thrombocytosis:

- Platelet count $\geq 450 \times 10^9/L$.
- 15% ring sideroblasts in the BM or >5% with SF3B1 mutation.
- Presence of megakaryocytic atypia resembling ET or MF.

MDS/MPN with neutrophilia (Atypical CML (t(9;22) negative and BCR::ABL1 negative):

- WBC count $> 13 \times 10^9/L$ with increased and dysplastic neutrophils (immature myeloid cells $\geq 10\%$).
- No or minimal absolute basophils and monocytosis.
- Hypercellular BM with granulocytic proliferation and dysplasia.

MDS/MPN with ring sideroblasts and thrombocytosis (MDS/MPN-RS-T):

- Platelet count $\geq 450 \times 10^9/L$.
- 15% ring sideroblasts in the BM or >5% with wild-type SF3B1.
- Presence of megakaryocytic atypia resembling ET or MF.

MDS/MPN-NOS (not otherwise specified):

Myeloid neoplasm with mixed MDS and MPN features, not meeting WHO criteria for other MDS/MPN overlap neoplasms, MDS or MPN.

CMML subtype

The prototype and most common MDS/MPN is chronic myelomonocytic leukaemia (CMML), which is characterised by sustained peripheral blood monocytosis and various combinations of somatic mutations involving epigenetic regulation, spliceosome, and signal transduction genes.

Two main phenotypic types of CMML can be distinguished:

CMML subtype	Subtyping criteria
Myelodysplastic (MD-CMML)	WBC $< 13 \times 10^9/L$
Myeloproliferative (MP-CMML)	WBC $> 13 \times 10^9/L$

Table 1. CMML subtypes.

Patients with myeloproliferative type tend to have bulkier splenomegaly and more often have extramedullary infiltrations. MP-CMML is commonly associated with activating RAS pathway mutations and adverse clinical outcomes. Even though no difference exists with regard to the AML transformation rate, patient life expectancy is generally shorter in MP-CMML than in MD-CMML.

CMML subgroup

According to the WHO 2022 (1), CMML can be further subclassified according to the percentage of blasts in peripheral blood and in bone marrow into CMML-1 and CMML-2:

CMML subgroup	Subgrouping criteria
CMML-1	<5% blasts in the blood and <10% blasts in the bone marrow
CMML-2	5-19% blasts in the blood and 10-19% blasts in the bone marrow

Table 2. WHO 2022 CMML subgroups.

Therapy-related MDS/MPN

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

CPSS (for CMML only)

The CMML-specific prognostic scoring system (CPSS) combines clinical and cytogenetic data. Patients can be categorised into 4 risk groups according to following points:

- CMML-2 according to WHO 2022 (1 point)
 - WBC $\geq 13 \times 10^9/L$ (1 point)
 - RBC transfusion dependency (1 point)
 - Cytogenetic risk group:
 - Low (normal and -Y) (0 points)
 - Intermediate (other abnormalities) (1 point)
 - High (trisomy 8, complex and abnormalities of chromosome 7) (2 points)

Risk category	Risk score
Low	0
Intermediate-1	1
Intermediate-2	2-3

High	4-5
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Table 3. CPSS risk groups.

CPSS-Mol (for CMML only)

The CMML-specific prognostic scoring system Molecular (CPSS-Mol) combines clinical, cytogenetic and molecular data. Patients can be categorised into 4 risk groups according to following points:

- WBC $\geq 13 \times 10^9/L$ (1 point)
- Bone marrow blasts (%) $\geq 5\%$ (1 point)
- RBC transfusion dependency (1 point)
- Cytogenetic risk group:
 - Low (normal and -Y) (0 points)
 - Intermediate (other abnormalities) (1 point)
 - High (trisomy 8, complex and abnormalities of chromosome 7) (2 points)
- ASXL1 mutation (1 point)
- NRAS mutation (1 point)
- RUNX1 mutation (2 points)
- SETBP1 mutation (1 point)

Please see the table below for the risk groups. The score can be calculated with an online tool, such as: https://gxmd.com/calculate/calculator_609/cmml-cpss-mol

Risk category	Risk score
Low	0
Intermediate-1	1
Intermediate-2	2-3
High	≥ 4

Table 4. CPSS-Mol risk groups.

*Extended dataset**Assessments at diagnosis***Haematological values**

Report the values from the blood tests performed at diagnosis.

Peripheral blood*Haemoglobin (g/dL)*

Report the haemoglobin in grams per deciliter (g/dL). If the haemoglobin was not tested, select **not evaluated**. If the value is not known, select **unknown**.

Platelets ($10^9/L$)

Report the platelets in 10^9 cells per litre ($10^9/L$). If the platelets were not tested, select **not evaluated**. If the value is not known, select **unknown**.

White blood cells ($10^9/L$)

Report the white blood cells in 10^9 cells per litre ($10^9/L$). If the white blood cells were not tested, select **not evaluated**. If the value is not known, select **unknown**.

% blasts

Report the blasts as a percentage. If the blasts were not tested, select **not evaluated**. If the value is not known, select **unknown**.

% monocytes

Report the monocytes as a percentage. If the monocytes were not tested, select **not evaluated**. If the value is not known, select **unknown**.

% neutrophils

Report the neutrophils as a percentage. If the neutrophils were not tested, select **not evaluated**. If the value is not known, select **unknown**.

Bone marrow

Report the findings of the bone marrow investigation at diagnosis.

% blasts

Report the blasts as a percentage. If the blasts were not tested, select **not evaluated**. If the value is not known, select **unknown**.

Precise blast count not available

If the precise blast count is not available, indicate whether it was **below or equal to 5%, above 5%, Not evaluated**, or **Unknown**.

Auer rods present

Indicate if auer rods were present at the time of diagnosis. If auer rods presence was not tested, select **not evaluated**. If it is not known if auer rods were present, select **unknown**.

Bone marrow investigation

Report the findings of the bone marrow investigation at diagnosis.

Fibrosis

Indicate if the bone marrow biopsy revealed any signs of fibrosis at time of diagnosis. If this was not checked, select **not evaluated**. If it is not known if there was bone marrow fibrosis, select **unknown**.

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. If the date is unavailable, select **Unknown**.

Chromosome analysis details

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

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 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

In this section, describe the results of all molecular marker analyses (performed at/after diagnosis but before HCT/CT/IST). 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 HCT/CT/IST. 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**, **Not evaluated** or **Unknown**.

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

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 $\geq 10\%$
- 1 mutation and 1 deletion involving the TP53 locus
- 1 mutation with VAF $\geq 50\%$
- 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**.

Extended dataset

PREVIOUS THERAPIES(between diagnosis and HCT/CT)

Previous therapy lines before the HCT/CT:

Indicate if the patient underwent any previous therapy lines related to MDS/MPN overlap syndromes before the HCT/CT/GT treatment. A treatment is considered a new line of therapy when switching to a different drug (or different combination of drugs) due to toxicity or for progression or relapse of the disease. If answered **Yes**, complete the “Treatment non-HCT/CT/GT/IST” form.

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.