Classificatie van AML

Acute myeloïde leukemie (AML) wordt geclassificeerd volgens de European LeukemiaNet (ELN) / International Consensus Classification (ICC) criteria.

Classificatie volgens ELN / ICC 2022

Tabellen

Bron: Diagnosis and management of AML in adults: 2022 recommendations from an international expert panel on behalf of the ELN – Blood 2022 – 140 (12): 1345-1377.

Table 1. AML and related neoplasms

AML and related neoplams	
AML with recurrent genetic abnormalities (requiring ≥10% blasts in BM or PB)* • APL with t(15;17)(q24.1;q21.2)/*PML*::*RARA*† • AML with t(8;21)(q22;q22.1)/*RUNX1*::*RUNX1T1* • AML with inv(16)(p13.1q22) or t(16;16)(p13.1;q22)/*CBFB*::*MYH11* • AML with t(9;11)(p21.3;q23.3)/*MLLT3*::*KMT2A*‡ • AML with t(6;9)(p22.3;q34.1)/*DEK*::*NUP214* • AML with inv(3)(q21.3q26.2) or t(3;3)(q21.3;q26.2)/*GATA2*, *MECOM(EVI1)*§ • AML with other rare recurring translocations‖ • AML with mutated *NPM1* • AML with in-frame bZIP mutated *CEBPA*¶ • AML with t(9;22)(q34.1;q11.2)/*BCR*::*ABL1**	**Myeloid sarcoma**
Categories designated AML (if ≥20% blasts in BM or PB) or MDS/AML (if 10-19% blasts in BM or PB) • AML with mutated *TP53*# • AML with myelodysplasia-related gene mutations Defined by mutations in *ASXL1*, *BCOR*, *EZH2*, *RUNX1*, *SF3B1*, *SRSF2*, *STAG2*, *U2AF1*, and/or *ZRSR2* • AML with myelodysplasia-related cytogenetic abnormalities** • AML not otherwise specified	**Myeloid proliferations related to Down syndrome** • Transient abnormal myelopoiesis associated with Down syndrome • Myeloid leukemia associated with Down syndrome **Blastic plasmacytoid dendritic cell neoplasm**
Diagnostic qualifiers†† Therapy-related‡‡ • Prior chemotherapy, radiotherapy, immune interventions Progressed from MDS • MDS should be confirmed by standard diagnostics and >3 mo prior to AML diagnosis Progressed from MDS/MPN (specify type) • MDS/MPN should be confirmed by standard diagnostics and >3 mo prior to AML diagnosis Germline predisposition (specify type)	

Classification adopted from reference 2. BM, bone marrow; MPAL, mixed phenotype acute leukemia.

*Bone marrow or peripheral blood blast count of ≥ 10% required, except for AML with t(9;22)(q34.1;q11.2)/*BCR*::*ABL1* which requires bone marrow or peripheral blood blast count of ≥ 20% due to its overlap with progression of chronic myeloid leukemia, *BCR*::*ABL1*-positive.

†Other recurring translocations involving *RARA* should be reported accordingly: eg, APL with t(1;17)(q42.3;q21.2)/*IRF2BP2*::*RARA*; APL with t(5;17)(q35.1;q21.2)/*NPM1*::*RARA*; APL with t(11;17)(q23.2;q21.2)/*ZBTB16*::*RARA*; APL with cryptic inv(17) or del(17)(q21.2q21.2)/*STAT5B*::*RARA*; *STAT3*::*RARA*; other genes rarely rearranged with *RARA: TBL1XR1* (3q26.3); *FIP1L1* (4q12); *BCOR* (Xp11.4).

‡Other recurring translocations involving *KMT2A* should be reported accordingly: eg, AML with t(4;11)(q21.3;q23.3)/*AFF1*::*KMT2A*; AML with t(6;11)(q27;q23.3)/*AFDN*::*KMT2A*; AML with t(10;11)(p12.3;q23.3)/*MLLT10*::*KMT2A*; AML with t(10;11)(q21.3;q23.3)/*TET1*::*KMT2A*; AML with t(11;19)(q23.3;p13.1)/*KMT2A*::*ELL*; AML with t(11;19)(q23.3;p13.3)/*KMT2A*::*MLLT1*.

§Other recurring translocations involving *MECOM* should be reported accordingly: eg, AML with t(2;3)(p11∼23;q26.2)/*MECOM*::?; AML with t(3;8)(q26.2;q24.2)/*MYC*, *MECOM*; AML with t(3;12)(q26.2;p13.2)/*ETV6*::*MECOM*; AML with t(3;21)(q26.2;q22.1)/*MECOM*::*RUNX1*.

‖Other rare recurring translocations: AML with t(1;3)(p36.3;q21.3)/*PRDM16*::*RPN1*; AML (megakaryoblastic) with t(1;22)(p13.3;q13.1)/*RBM15*::*MRTFA*; AML with t(3;5)(q25.3;q35.1)/*NPM1*::*MLF1*; AML with t(5;11)(q35.2;p15.4)/*NUP98*::*NSD1*; AML with t(7;12)(q36.3;p13.2)/*ETV6*::*MNX1*; AML with t(8;16)(p11.2;p13.3)/*KAT6A*::*CREBBP*; AML with t(10;11)(p12.3;q14.2)/*PICALM*::*MLLT10*; AML with t(11;12)(p15.4;p13.3)/*NUP98*::*KMD5A*; AML with *NUP98* and other partners; 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*.

¶AML with in-frame mutation in the bZIP domain of the *CEBPA* gene, either monoallelic or biallelic.

#The presence of a pathogenic somatic *TP53* mutation (at a variant allele fraction of at least 10%, with or without loss of the wild-type *TP53* allele) defines the entity AML with mutated *TP53*.

**Cytogenetic abnormalities sufficient for the diagnosis of AML with MDS-related cytogenetic abnormalities and the absence of other AML-defining disease categories. Complex karyotype: ≥3 unrelated chromosome abnormalities in the absence of other class-defining recurring genetic abnormalities; excludes hyperdiploid karyotypes with three or more trisomies (or polysomies) without structural abnormalities. Unbalanced clonal abnormalities: del(5q)/t(5q)/add(5q); −7/del(7q); +8; del(12p)/t(12p)/(add)(12p); i(17q), −17/add(17p) or del(17p); del(20q); and/or idic(X)(q13).

††Examples: AML with myelodysplasia-related cytogenetic abnormality, therapy-related; AML with myelodysplasia-related gene mutation, prior myelodysplastic syndrome; AML with myelodysplasia-related gene mutation, germline *RUNX1* mutation.

‡‡Prior therapy for nonmyeloid neoplasms.

Bron: International consensus classification of myeloid neoplasms and acute leukemias: integrating morphologic, clinical and genomic data – Arber et al. – Blood 2022 – 140 (11): 1200-1228.

Table 25. Classification of AML with percentage of blasts required for diagnosis

Acute promyelocytic leukemia (APL) with t(15;17)(q24.1;q21.2)/*PML*::*RARA* ≥ 10%
APL with other *RARA* rearrangements* ≥ 10%
AML with t(8;21)(q22;q22.1)/*RUNX1*::*RUNX1T1* ≥ 10%
AML with inv(16)(p13.1q22) or t(16;16)(p13.1;q22)/*CBFB*::*MYH11* ≥ 10%
AML with t(9;11)(p21.3;q23.3)/*MLLT3*::*KMT2A* ≥ 10%
AML with other *KMT2A* rearrangements† ≥ 10%
AML with t(6;9)(p22.3;q34.1)/*DEK*::*NUP214* ≥ 10%
AML with inv(3)(q21.3q26.2) or t(3;3)(q21.3;q26.2)/*GATA2*; *MECOM*(*EVI1*) ≥ 10%
AML with other *MECOM* rearrangements‡ ≥ 10%
AML with other rare recurring translocations (see supplemental Table 5) ≥ 10%
AML with t(9;22)(q34.1;q11.2)/*BCR*::*ABL1*§ ≥ 20%
AML with mutated *NPM1* ≥ 10%
AML with in-frame bZIP *CEBPA* mutations ≥ 10%
AML and MDS/AML with mutated *TP53*† 10-19% (MDS/AML) and ≥ 20% (AML)
AML and MDS/AML with myelodysplasia-related gene mutations 10-19% (MDS/AML) and ≥ 20% (AML) Defined by mutations in *ASXL1*, *BCOR*, *EZH2*, *RUNX1*, *SF3B1*, *SRSF2*, *STAG2*, *U2AF1*, or *ZRSR2*
AML with myelodysplasia-related cytogenetic abnormalities 10-19% (MDS/AML) and ≥ 20% (AML) Defined by detecting a complex karyotype (≥ 3 unrelated clonal chromosomal abnormalities in the absence of other class-defining recurring genetic abnormalities), del(5q)/t(5q)/add(5q), −7/del(7q), +8, del(12p)/t(12p)/add(12p), i(17q), −17/add(17p) or del(17p), del(20q), and/or idic(X)(q13) clonal abnormalities
AML not otherwise specified (NOS) 10-19% (MDS/AML) and ≥ 20% (AML)
Myeloid sarcoma

*Includes AMLs with t(1;17)(q42.3;q21.2)/*IRF2BP2*::*RARA*; t(5;17)(q35.1;q21.2)/*NPM1*::*RARA*; t(11;17)(q23.2;q21.2)/*ZBTB16*::*RARA*; cryptic inv(17q) or del(17) (q21.2q21.2)/*STAT5B*::*RARA*, *STAT3*::*RARA*; Other genes rarely rearranged with *RARA*:*TBL1XR1* (3q26.3), *FIP1L1* (4q12), *BCOR* (Xp11.4).

†Includes AMLs with t(4;11)(q21.3;q23.3)/*AFF1*::*KMT2A*#; t(6;11)(q27;q23.3)/*AFDN*::*KMT2A*; t(10;11)(p12.3;q23.3)/*MLLT10*::*KMT2A*; t(10;11)(q21.3;q23.3)/*TET1*::*KMT2A*; t(11;19)(q23.3;p13.1)/*KMT2A*::*ELL*; t(11;19)(q23.3;p13.3)/*KMT2A*::*MLLT1* (occurs predominantly in infants and children).

‡Includes AMLs with t(2;3)(p11∼23;q26.2)/*MECOM*::?; t(3;8)(q26.2;q24.2)/*MYC*, *MECOM*; t(3;12)(q26.2;p13.2)/*ETV6*::*MECOM*; t(3;21)(q26.2;q22.1)/*MECOM*::*RUNX1*.

§The category of MDS/AML will not be used for AML with *BCR*::*ABL1* due to its overlap with progression of CML, *BCR*::*ABL1*-positive.

Flowschema

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