Leukaemia Section
Short Communication

-20 or monosomy 20
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Published in Atlas Database: April 2018
Online updated version: http://AtlasGeneticsOncology.org/Anomalies/mono20ID1079.html
Printable original version: http://documents.trevues.inist.fr/bitstream/handle/2042/70530/04-2018-mono20ID1079.pdf
DOI: 10.4267/2042/70530
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Abstract
Chromosome 20 anomalies are well-known in hematological malignancies, being del(20q) and dicentric chromosome 20 the most frequent. In contrast, monosomy 20 that occurs in a variety of hematological neoplasms is less well characterized.

Keywords
Numerical chromosome anomalies, chromosome 20, del(20q), gene repression.

Clinics and pathology

Disease
Chronic and acute myeloid malignancies, myelodysplastic syndromes (MDS), acute lymphoblastic leukemia (ALL) and plasma cell neoplasms.

Etiology
Detected in both myeloid and lymphoid malignancies.

Epidemiology
Chronic myeloproliferative disorder in 20 (9M/11F aged 29 to 80 years, median 65 years): 6 myelofibrosis (MF), 6 polycythemia vera (PV), 3 essential thrombocythemia (ET), 1 chronic myeloproliferative disorder (MPD), 1 MDS/MPD and there were 3 patients with chronic myelomonocytic leukemia.

Chronic myeloid leukemia (CML) was diagnosed in 56 patients at different time points and disease stages (29M/27F aged 8 to 85 years, median 49 years).

Myelodysplastic syndromes: 149 patients aged 1 to 84 years have been reported (99M/49F, 1 unknown); most patients were diagnosed with refractory anemia with excess of blasts (RAEB) (68 patients), followed by myelodysplastic syndrome, NOS (35 patients), refractory anemia (RA) (25 patients), refractory cytopenia with multilineage dysplasia (12 patients) and refractory anemia with ringed sideroblasts (9 patients). Among them, 25 patients developed MDS after chemotherapy and/or radiation therapy for previous tumors.

Acute myeloid leukaemia (AML): More than 400 patients with various AML types have been reported: 165 acute myeloid leukemia, NOS, 17 acute myeloblastic leukemia with minimal differentiation (AML-M0), 29 acute myeloblastic leukemia without maturation (AML-M1), 71 acute myeloblastic leukemia with maturation (AML-M2), 5acute promyelocytic leukemia (AML- M3), 35 acute myelomonocytic leukemia (AML-M4), 16 acute monoblastic leukemia (AML-M5), 69 acute erythroleukemia (AML-M6) and 19 acute megakaryoblastic leukemia (AML-M7). The estimated frequency of monosomy 20 in patients with myeloid malignancies and abnormal karyotypes is about 11% (Raza et al., 2011).

Lymphoid malignancies

Acute lymphoblastic leukaemia More than 450 reported patients; however up to half of these patients had hyperdiploid/polyplody or hypodiploid karyotypes with unknown significance of -20. The estimated frequency of isolated monosomy 20 in cytogenetically abnormal childhood ALL is about 3% (Betts et al., 1990).

Bilineage or biphenotypic leukemia (BAL) was diagnosed in 9 patients (4M/5F aged 9 to 60 years, median 27 years).

Other malignancies Chronic lymphocytic leukemia (CLL) in 44, T-prolymphocytic leukemia
in 12 and about 200 patients with plasma cell neoplasm. However, because monosomy 20 was detected in various disease stages in these patients, it is unclear if its occurrence is related to clonal evolution or to previous therapies and is a sign of therapy-related hidden myelodysplastic syndrome.

**Prognosis**

The presence of isolated monosomy 20 may be associated with premalignant haematological conditions and an indolent clinical course in chronic myeloproliferative disorders with similar prognosis as in patients with del(20q).

In AML, monosomy 20 occurs in both noncomplex and highly complex karyotypes, therefore the presence of primary anomalies and the number of additional anomalies may be a strong prognostic factor. In these patients, monosomy 20 frequently occurs as part of highly complex karyotypes with combination of chromosome 5 and 7 abnormalities, conferring unfavorable prognosis and poor response to chemotherapy. Isolated monosomy 20 in childhood ALL may indicate favorable prognosis (Betts et al., 1990; Silengo et al., 1992) while in complex karyotypes the prognosis may depend on the presence of additional anomalies.

Figure 1. Karyotype and partial karyotypes showing monosomy of chromosome 20.

**Figure 2.** True monosomy can be confirmed with the use of fluorescence in situ hybridization techniques applying locus specific LSI D20S108 (A) or chromosome 20 painting probes (Abbott Molecular/Vysis, US) showing (B).
Cytogenetics

Identification of 20 monosomy in complex karyotypes or its combination with marker chromosomes may be an indicator of unbalanced rearrangements, such as the dic(17;20) in myeloid malignancy or dic(9;20) in acute lymphoid leukaemia. Therefore, to confirm true monosomy 20, accurate karyotyping and the use of fluorescence in situ hybridization techniques with locus specific or chromosome painting probes is recommended. Because apparent monosomy 20 in complex karyotypes can be frequently misclassification of unbalanced chromosome 20 rearrangements, it is probably that true monosomy 20 is less frequent than it is reported.

Additional anomalies

Chronic myeloproliferative disorders: most patients had simple karyotypes and only 5 of them had highly complex aberrations; sole anomaly in 2, found in association with del(20q) in 3, +8 in 4, del(5q)/-5 in 5, del(13q) in 2 and monosomy 7 in 2.

CML: In 11 patients receiving tyrosine kinase inhibitor therapy or bone marrow transplant, monosomy 20 was detected in Philadelphia-negative cells. Among them, it was a sole anomaly in 5 and in 4 it was found in association with monosomy 22. Found as a sole additional anomaly tot(9;22) in 1 and with +der(22)t(9;22) in 21 patients.

MDS: Sole anomaly in 1, found in a sideline 45,XY,-3/45,XY,-4/45,XY,-7/45,XY,-20 in 1; found with, del(20),+mar in 1 and in a sideline with del(20)(q11) in 1. The majority of remaining patients had complex and highly complex aberrations with monosomy 5/del(5q) and less frequently chromosome 7 abnormalities or their combination.

AML: Sole anomaly in 6, in 4 of them found in a sideline. Rarely detected with well-known primary chromosome translocations; found in association with 4 t(9;22)(q34;q11) in 4, t(8;21)(q22;q22) in 2, inv(16)(p13q22)/t(16;16) in 2 and t(1;22)(p13;q13) in 3 AML-M7 patients. Mainly found as a part of complex and highly complex karyotypes and unstable clones with frequent chromosome 5 and/or 7 abnormalities or both abnormalities together (about 2/3 of patients) and with commonly observed chromosomal abnormalities characteristic for myeloid malignancies such as +8 and 12p, 13q and 17p deletions and loss of a sex chromosome.

ALL: Sole anomaly in 19 pediatric and 4 adult B-ALL patients; about half of patients presented with hyperdiploid (about 200 patients), polyploid (10 patients) or hypodiploid (about 50 patients) karyotypes. The remaining patients presented mainly with complex karyotypes, with relative low frequency of primary anomalies, being t(9;22)(q34;q11) the most frequent, that has been detected in 35 B-ALL patients. Among them, -20 was detected as a sole additional anomaly to t(9;22) in 4 patients. Other primary anomalies were less frequent, the t(1;19)(q23;p13) has been detected only in 5 and t(4;11) in 2 patients.

BAL: Found as part of complex karyotypes in association with t(9;22)(q34;q11) in 2 and with -5/del(5q) and/or -7/del(7q) in 4 out of 9 patients.

Result of the chromosomal anomaly

Fusion protein

Oncogenesis

Monosomy 20 is a non-random chromosome abnormality that has been reported in a variety of hematological neoplasms, including myelodysplastic syndromes, acute myeloid leukemia, Philadelphia chromosome-negative myeloproliferative neoplasms and acute lymphoblastic leukemia. Monosomy 20 results in haploinsufficiency of genes leading to a loss of expression, which may contribute to the development of malignancy. While the pathogenesis remains unknown, monosomy 20 is presumed to remove tumor suppressors at 20q12, the common deleted region of the well-known 20q deletion. Such candidate tumor suppressors may include L3MBTL1 and SGK2 and their repression may contribute to the development of malignancy by inducing replicative stress, DNA damage, and genomic instability. Isolated monosomy 20 could be an early event, although additional events need to accumulate for cancer development, while in complex karyotypes it is associated with unstable clones reflecting disease evolution.

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