t(3;21)(q26;q22) in treatment related leukemia

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Identity

Note: This data is extracted from a very large study from an International Workshop on treatment related leukemias - restricted to balanced chromosome aberrations (i.e.: -5/del(5q) and -7/del(7q) not taken into account per see), published in Genes, Chromosomes and Cancer in 2002.

\[ t(3;21)(q26;q22) \] G- banding - Courtesy Melanie Zenger and Claudia Haferlach.
**Clinics and pathology**

**Disease**

Treatment related myelodysplasia (t-MDS) or acute non lymphocytic leukemias (t-ANLL).

**Note**

The study included 16 cases; t-MDS without progression to ANLL accounted for 38%, t-MDS progressing to ANLL for 25%, t-ANLL for the remaining 38% (to be compared with the 80% of t-ANLL in cases with t(8;21)); no case of acute lymphoblastic leukaemia.

**Epidemiology**

t(3;21)(q26;q22) was found in 3% of t-MDS/t-ANLL; sex ratio: 5M/11F.

**Clinics**

Age at diagnosis of the primary disease 49 yrs (range 14-72); age at diagnosis of the t-MDS/t-ANLL: 53 yrs (range 19-73). Median interval was 36 mths, range: 17-139). Primary disease was a solid tumor in 56% of cases and a hematologic malignancy in 44%. Treatment included topoisomerase II inhibitors in 81% of cases).

**Prognosis**

Median survival was 8 mths. Outcome was worse than the outcome of patients with t(8;21)(q22;q22), t(15;17) or inv(16) treatment related leukemias, and similar to the outcome of patients with 11q23 rearrangement.

**Cytogenetics**

**Additional anomalies**

The t(3;21) was found solely in 31% of cases; additional anomaly was: -7/del(7q) in 31% of cases, +8 was not observed. A complex karyotype was found in 25% of cases.

**Result of the chromosomal anomaly**

**Hybrid gene**

Description

5' AML1 - 3' MDS1-EVI1; breakpoint is most often in the AML1 intron 6.

**References**


This article should be referenced as such: