t(1;3)(p36;q21)

Jay L Hess

Department of Pathology, The University of Michigan, M5240 Medical Science I, 1301 Catherine Avenue, Ann Arbor, MI 48109-0602, USA (JLH)

Published in Atlas Database: May 2002
Online updated version: http://AtlasGeneticsOncology.org/Anomalies/t0103.html
DOI: 10.4267/2042/37878
This article is an update of:
This work is licensed under a Creative Commons Attribution-Noncommercial-No Derivative Works 2.0 France Licence. © 2002 Atlas of Genetics and Cytogenetics in Oncology and Haematology

Identity

Disease
Myeloid lineage (MDS, ANLL, therapy related ANLL, CML, MPD); features similar to those of the 3q21q26 syndrome including normal or elevated platelet count at diagnosis, megakaryocytic hyperplasia and dysplasia. Very rarely in lymphoid lineage.

Phenotype/cell stem origin
Of 39 cases, there were: 22 myelodysplastic syndromes (MDS) (17/22 transformed into refractory acute non lymphoblastic leukemia (ANLL) of -M1 or -M4 type), 8 de novo ANLL, 3 therapy-related MDS, 2 polycythemia vera, 1 essential thrombocytopenia, 1 chronic myelogenous leukemia (CML), 1 multiple myeloma, 1 waldenstrom's macroglobulinemia.

Epidemiology
Patients are aged: 30-80 yrs.

Clinics
Roughly 50% of patients present with MDS, another 10% with therapy associated MDS, 25% with de novo AML, and the remainder with a range of other
myeloproliferative disorders. The majority of MDS patients transform into AML with a short preleukemic phase. Blood data: frequent thrombocytosis or normal platelet count.

**Cytology**

Frequently characterized by dysmegakaryocytepoiesis.

**Pathology**

The pathology is typical of MDS, often with a prominent monocytic component. Trilineage dysplasia.

**Treatment**

Patients are treated with conventional chemotherapy for AML.

**Prognosis**

Very poor so far: from 16 cases, median survival was 6 mths in ANLL, 20 mths in MDS.

**Cytogenetics**

Note

Other rearrangements showing similar clinical features include inv(3)(q21q26), t(3;3)(q21;q26), t(3;5)(q21;q31), t(3;8)(q21;q24), and t(3;21)(q26;q22). The breakpoints in 3q21 cluster in a 50 kb region centromeric to the breakpoint in inv(3)(q21q26) and the ribophorin gene (RPN1). The breakpoints at 1p36 are clustered in a 90 kb region at 1p36.3.

**Additional anomalies**

del (5q) in 5 of 20 cases (1/4).

**Genes involved and proteins**

Note

Mechanisms of oncogenesis: the available data suggest that transcription of MEL1 (MDS1/EVI1-like gene) is activated as a result of translocation bringing the gene just 3' to RPN1 gene at 3q21. MEL1 is a 1257 amino acid protein that is homologous (63% similar in amino acid sequence) to EVI. The mechanism of activation of MEL1 is similar to EVI1 that is activated by juxtaposition 3’ to RPN1 in the t(3;3)(q21;q26) and 5’ to RPN1 in the inv(3)(q21q26). It appears that MEL1 is normally expressed in uterus and kidney and not in normal hematopoietic cells or in leukemias that lack the t(1;3)(p36;q31). The MEL1 protein contains 2 DNA binding domains (7 C2H2 zinc finger repeats at the amino terminus and 3 zinc finger repeats at the carboxyl terminus). The amino terminal domain of MEL1 contains a PRD domain, a motif also found in the same location in the MDS1/EVI1 protein but not in MDS1. This is of interest because this domain is also found in RIZ, PRDI-BF1, and egl-43 and is homologous to the SET (Suvar3-9, Enhancer of zeste, Trithorax) domain that present in MLL. Inclusion of this domain in EVI1 appears to convert EVI1 from a transcriptional repressor to an activator. Therefore MEL1 may be a transcriptional activator. The target genes of MEL1 have not been identified.

**References**


Bitter MA, Neilly ME, Le Beau MM, Pearson MG, Rowley JD. Rearrangements of chromosome 3 involving bands 3q21 and 3q26 are associated with normal or elevated platelet counts in acute nonlymphocytic leukemia. Blood. 1985 Dec;66(6):1362-70


Marsden KA, Pearse AM, Collins GG, Ford DS, Heard S, Kimber RL. Acute leukemia with t(1;3)(p36;q21), evolution to t(1;3)(p36;q21), t(14;17)(q32;q21), and loss of red cell A and Le(b) antigens. Cancer Genet Cytogenet. 1992 Nov;64(1):80-5


Mochizuki N, Shimizu S, Nagasawa T, Tanaka H, Tanikawa M, Yokota J, Morishita K. A novel gene, MEL1, is highly homologous to the MDS1/EVI1 gene and is transcriptionally activated in t(1;3)(p36;q21)-positive leukemia cells. Blood. 2000 Nov 1;96(9):3209-14


This article should be referenced as such:

Hess JL. t(1;3)(p36;q21). Atlas Genet Cytogenet Oncol Haematol. 2002; 6(3)