Leukaemia Section
Mini Review

t(9;11)(p22;p15)
Cristina Morerio, Claudio Panarello

Dipartimento di Ematologia ed Oncologia Pediatrica, IRCCS Istituto Giannina Gaslini, Largo G. Gaslini 5, 16147 Genova, Italy

Published in Atlas Database: May 2007
Online updated version: http://AtlasGeneticsOncology.org/Anomalies/t0911p22p15ID1232.html
DOI: 10.4267/2042/16966
This work is licensed under a Creative Commons Attribution-Non-commercial-No Derivative Works 2.0 France Licence.
© 2007 Atlas of Genetics and Cytogenetics in Oncology and Haematology

Identity

Note: rare abnormality.

Clinics and pathology

Disease
Acute non lymphoblastic leukemia (ANLL), one case of transformed chronic myeloid leukemia (CML-BC).

Phenotype / cell stem origin
ANLL FAB TYPE M1, M2, M2/M3.

Epidemiology
Five cases reported to date: four adults and one 5-year-old girl.

Prognosis
Unfavorable outcome.

Cytogenetics

Additional anomalies
Sole anomaly in the four ANLL cases, t(9;11) in addition to the t(9;22) in the CML-BC case.

A) Partial Q-banded karyotype showing the t(9;11)(p22;p15); derivative chromosomes are on the right of each pair. B) FISH analysis using PAC 1173K1 (NUP98) and RP11-356J15 (PSIP1) probes (green and red signals, respectively). Arrow and arrowhead indicate the fusion signals on the der(9) and the der(11), respectively.
Genes involved and Proteins

**NUP98**

**Location:** 11p15.5

**Protein**

Nucleoporin 98, a 98 kDa component of the nuclear pore complex involved in nucleo-cytoplasmic transport.

**PSIP1 (PC4 and SFRS1 interacting protein 1)**

**Aliases** LEDGF (lens epithelium-derived growth factor), p75, p52

**Location:** 9p22.3

**Note:** The gene contains at least 15 exons and 14 introns.

**DNA / RNA**

Two alternative splice variants: p75 and p52.

**Protein**

Chromatin-associated protein involved in transcriptional regulation, mRNA splicing and cell survival in vitro. Contains a PWWP domain and AT hook-like motifs.

Results of the chromosomal anomaly

**Hybrid gene**

**Description**

5’NUP98 - 3’PSIP1: The breakpoint in the NUP98 gene is the same in three out of four cases studied (nucleotide 1230), while the breakpoints in PSIP1 are variable.

**Fusion protein**

**Description**

It fuses the GLFG repeat domains of NUP98 to the COOH-terminal of the PSIP1.

References


This article should be referenced as such: