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# Leukaemia Section

**Short Communication** 

# t(11;22)(q13;q13) HRASLS5/PHF21B

Nathalie Douet-Guilbert, Etienne De Braekeleer, Corinne Tous, Nadia Guéganic, Audrey Basinko, Marie-Josée Le Bris, Frédéric Morel, Marc De Braekeleer

Cytogenetics Laboratory, Faculty of Medicine, University of Brest, France / marc.debraekeleer@univbrest.fr

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# Abstract

Review on t(11;22)(q13;q13), with data on clinics, and the genes involved.

#### Keywords

Acute myeloid leukemia; t(11;22)(q13;q13); HRASLS5; PHF21B

# **Clinics and pathology**

# Disease

Myeloid hemopathies

# Epidemiology

Five cases of myeloid hemopathies (myelodysplastic syndrome, acute promyelocytic leukemia, chronic myeloid leukemia, acute erythroleukemia, and acute monoblastic leukemia (FAB type M5b) in an unpublished case herein described) with t(11;22)(q13;q13). No molecular characterization was performed in four cases (Gibbons et al., 1994; Jennings et al., 1998; Mauritzson et al., 2001; Ramkumar et al., 2008).

# Clinics

A 52-year-old woman seen because of fever and asthenia (present case, and 2 male and 2 female patients, aged 48, 69, 73).

# Cytology

Bone marrow aspirate showing 23.5% of blasts CD33+, MPO+, CD117+, CD11c+ (present case).

# Evolution

Complete remission was not achieved by

chemotherapy. She received allogeneic hematopoietic stem cell transplantation 6 months following diagnosis and remained in complete remission 10 months after transplantation.

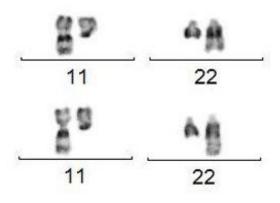
# Cytogenetics

#### Note

A normal 46,XX karyotype was found at diagnosis in the present case.

The t(11;22)(q13;q13) was identified during evolution (6 months after diagnosis but before stem cell transplantation).

It involves the HRASLS5 and PHF21B genes that have never been shown to form a fusion gene.



RHG banding showing chromosomes 11 and 22 and the derivatives der(11) and der(22).

# Cytogenetics morphological

t(11;22)(q13;q13) is identified by banding cytogenetics.

# Cytogenetics molecular

To determine the position of the breakpoints on chromosomes 11 and 22, BAC clones located in the bands of interest were used as probes in FISH experiments. Analysis with RP11-449A4, located at 11q13.1, showed a split signal while RP11-660B16 was translocated on chromosome 22. The breakpoint was mapped between positions 63184796 and 63242850, in a 58 kb region that contains 14kb of the HRASLS5 (HRAS-like suppressor family, member 5) gene [UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly]. Analysis with RP11-367O12, located at 22q13.31, showed a split signal that hybridized to both der(11) and der(22). This BAC clone contains the PHF21B (PHD finger protein 21B) gene.

# Genes involved and proteins

# HRASLS5

Location

# 11q13.2

DNA/RNA

The HRASLS5 gene contains 6 coding exons, spanning 29.8 kb. It is predominantly expressed in testis (Jin et al., 2009).

#### Protein

The protein has 279 amino acids and catalyzes the N-acylation of phosphatidylethanolamine (PE) to generate N-acylphosphatidylethanolamine (NAPE), a precursor of bioactive N-acylethanolamines. Mutagenesis studies suggested a possible role of the N-terminal domain in membrane association or protein-protein interaction (Jin et al., 2009). However, its function(s) remain(s) largely unknown. Whether HRASLS5 is a tumor suppressor involved in the control of cell proliferation as other members, notably HRASLS2, belonging to the same family, remains to be determined (Hughes et al., 2000; Shyu et al., 2008; Uyama et al., 2009).

#### PHF21B

Location

22q13.31

#### DNA/RNA

The PHF21B gene contains 13 coding exons, spanning 127.8 kb, according to the UCSC Genome Browser, but 16 according to the National Center for Biotechnology Information (NCBI). There are 8 probable alternative promoters and transcription

produces 13 alternatively spliced mRNAs (http://www.ncbi.nlm.nih.gov/IEB/Research/Acem bly/av.cgi?db=humanq=PHF21B).

#### Protein

The protein has 531 amino acids. It contains one PHD (homeodomain) type zinc finger domain (amino acids 313-357), found in nuclear proteins thought to be involved in chromatin-mediated transcriptional regulation, and a transcription initiation factor TFIIIB, Bdp1 subunit (amino acids 137-267), involved in regulating transcription from RNA polymerase III promoters (http://www.ncbi.nlm.nih.gov/gene/112885).

However, its function(s) remain(s) largely unknown.

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