

t(8;13)(p12;q12) (updated: old version not available)

Clinics and Pathology

Disease	a myeloproliferative disorder that is frequently associated with T cell, or less commonly, B-cell non Hodgkin lymphoma
Phenotype / cell stem origin	may involve a stem cell involving both myeloid, T lineage, and B-cell lineage
Epidemiology	14 cases are described; median age 43 yrs (range 18-68); sex ratio: 6M/8F
Clinics	aggressive disease; complex picture of myeloid hyperplasia progressing to myelodysplasia and Tor -B- cell lymphoma; enlarged lymph node; blood data: high WBC (median 40 X 10 ⁹ /l); myelemlia; monocytosis and eosinophilia
Evolution	the disease transforms to ANLL, or occasionally ALL, in a median of 6 months
Prognosis	median survival: 12 months

Cytogenetics

Cytogenetics	the same t(8;13) is found both in the bone marrow and in the lymph node, ruling out the hypothesis of a leukemoid reaction caused by a lymphoma; the multilineage involvement suggests the malignant transformation of a primitive hematopoietic stem cell.
Morphological	
Probes	megac Yacs 770-c-2 (1390 kb) and 959-a-4 (1260kb), 856-b-6, 967; 899e2 - (CEPH); BAC 7M15; PAC RPCI 20-G12; FGFR1-specific cosmid 134.8;
Additional anomalies	usually occurs as a single anomaly; duplication of the der(13) was found during disease progression, suggesting that the crucial event might lie on this derivative chromosome; +8, +21 are also recurrently found

Genes involved and Proteins

Gene Name [FGFR1](#)

Location 8p12

Gene Name [ZNF198 \(also called FIM or ID P\)](#)

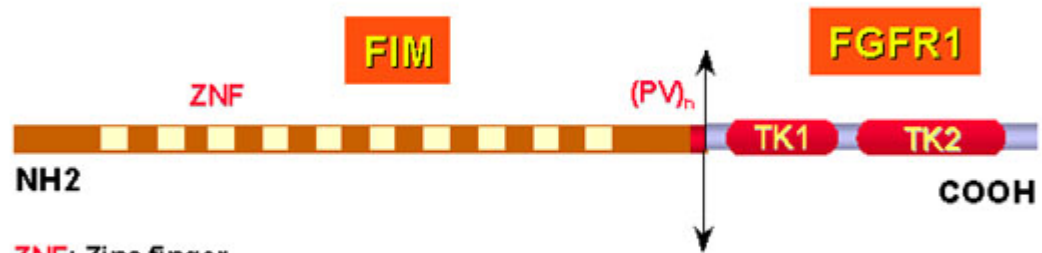
Location 13q12

Protein zinc finger protein (ten repeats in the N-terminal region with the consensus sequence C-X2-C-X18-24-(F/Y)-C-X3-C that corresponds to a novel type of zing finger motifs), a hydrophobic repeat (proline-rich), and potentially two putative nuclear localisation signals

Result of the chromosomal anomaly

Hybrid gene

FIM-FGFR1 fusion protein: Schematic representation
Gene localization: der(13) chromosome



ZNF: Zinc finger

(PV)_n: Proline-Valine repeats

TK1: Tyrosine kinase 1 subdomain

TK2: Tyrosine kinase 2 subdomain

Description
breakpoint in FGFR1 intron 8

Fusion Protein
Description Aberrant tyrosine kinase composed of the N-term two-thirds of FIM (retaining the 10 putative zinc finger motifs), and the FGFR1 intracellular region minus the major part of the juxtamembrane domain (and deleting the N-term immunoglobulin-like and central transmembrane domains of FGFR1)

Oncogenesis through constitutive activation of FGFR1 signal transduction pathways, possibly via dimerization capability mediated by the FIM N-term sequences of the fusion protein

External links

Other database [t\(8;13\)\(p12;q12\)](#) [Mitelman database \(CGAP - NCBI\)](#)

Other database [t\(8;13\)\(p12;q12\)](#) [CancerChromosomes \(NCBI\)](#)

To be noted

Additional cases are needed to delineate the epidemiology of this rare entity:

you are welcome to submit a paper to our new [Case Report](#) section.

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