t(7;14)(q21;q32) ERVWE1/IgH

Jean-Loup Huret

Genetics, Dept Medical Information, University of Poitiers, CHU Poitiers Hospital, F-86021 Poitiers, France (JLH)

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Identity

Note
This translocation must not be confused with the t(7;14)(q21;q32) with CDK6/IgH involvement, seen in chronic lymphocytic leukaemia and in splenic marginal zone lymphoma (Corcoran et al., 1999; Hayette et al., 2003). There is also a case of acute myeloid leukaemia with t(7;14)(q21;q32) in a female patient, with no other data (Stephenson et al., 1995).

Clinics and pathology

Disease
Chronic lymphocytic leukaemia (CLL)

Epidemiology
One case to date, a 64-year-old female patient (Wahbi et al., 1997).

Cytogenetics

Cytogenetics morphological
Sole anomaly.

Genes involved and proteins

ERVWE1

Location
7q21.2

Note
Full-length provirus integrated into the human genome.

Protein
ERVWE1 encodes a glycosylated envelope protein, Syncytin-1 with a receptor-binding function; it promotes cell proliferation in the presence of TGF-beta and may exert an anti-apoptotic function (Gimenez and Mallet, 2007).

IGH

Location
14q32.33

Protein
Immunoglobulin heavy chain (see Lefranc, 2003).

Result of the chromosomal anomaly

Hybrid gene

Description
Chromosome junction between the switch region of the C\textsubscript{\textmu} locus of IGH and the 5' upstream the 5' LTR (long terminal repeat) of ERVWE1 (94 bases upstream). However, the CDK6 gene lies 127 kb downstream ERVWE1, and it cannot be excluded that the target of the Immunoglobulin enhancer is CDK6 instead of ERVWE1 (ERVWE1 is from 91 935 631 to 91 945 186, and CDK6 from 92 072 173 to 92 303 877).

Fusion protein

Oncogenesis

There is not yet any clear explanation on the oncogenic process caused by this translocation.

References


This article should be referenced as such: