Diffuse large B-cell lymphoma (DLBCL). DLBCL is a molecularly heterogeneous type of aggressive lymphoma, accounting for approximately 40% of all B-cell non-Hodgkin lymphomas (NHL) of the Western world. Translocations involving the chromosomal region 15q11-13 also have been identified in nonlymphoid tumors.

**Phenotype/cell stem origin**

B-cell. The chromosomal translocation t(14;15)(q32;q11-13) can activate BCL8 gene expression in lymphoid tissues, whereas BCL8 expression is not normally found in hematopoietic tissues.

**Epidemiology**

Translocations affecting 15q11-13 and various chromosomal partners occur in about 3-4% of DLBCL.

**Clinics**

At present, it is not yet clear whether chromosomal translocation t(14;15) identifies a homogeneous.

**Pathology**

Clinico-pathologic subtype of DLBCL.

**Prognosis**

The effect of BCL8 expression on the prognosis of patients has yet to be investigated.

**Cytogenetics**

**Additional anomalies**

DLBCL is a heterogeneous disease with respect to karyotypic abnormalities. t(14;15)(q32;q11-13) is a rare chromosomal translocation restricted to 4-5% DLBCL. The most frequent cytogenetic abnormalities detected in DLBCL involve BCL6 t(3;V)(q27;V), BCL2 t(14;18)(q32;q21), and myc t(8;14)(q24;q32), and occur in 25%, 20% and 10% of DLBCL, respectively.

**Variants**

In addition to IGHV gene translocation, other translocations of the chromosomal region 15q11-13 involve additional chromosomal sites, including 22q11 (IGLV), 9p13, 1p32, 7p13, 12q24, and 15q22.

**Genes involved and proteins**

**IgH**

**Location**

14q32

**DNA/RNA**

IgH gene is composed of V (variable), D (diversity), J (joining), and C (constant) segments. During B cell development, a recombination event at the DNA level creates a rearranged IGHV-D-J gene.

**Protein**

Proteins encoded by the IgH gene are the immunoglobulin heavy chains.
**BCL8**

**Location**  
15q11-q13

**DNA/RNA**  
3 exons. The 5’ part of exon 1 and the 3’ part of exon 3 are non-coding. Two alternative transcripts: a major transcript of 2.6 kb, and a less expressed transcript of 4.5 kb, due to differential polyadenylation.

**Protein**  
100 amino acids, predicted molecular weight of 19 kDa; predicted: similar to protein neurobeachin (Lysosomal trafficking regulator 2). Truncated polypeptides with uncertain function are also produced.

**Result of the chromosomal anomaly**

**Hybrid gene**

**Description**  
The translocation t(14;15)(q32;q11-13) leaves the coding region of BCL8 gene intact, and does not lead to the formation of a hybrid gene. BCL8 is adjacent to the chromosomal breakpoint, that is located upstream of a rearranged VH segment. BCL8 is a part of a large duplicated region within 15q11 containing several pseudogenes, including orphan IGH copies of V and D segments and it’s possible that this V/D segments can rearrange with D/J segments on chromosome 14.

**Fusion protein**

**Description**  
The chromosomal translocation does not lead to the formation of a fusion protein.

**Oncogenesis**  
t(14;15)(q32;q11-13) causes activation of the BCL8 proto-oncogene by deregulated expression of BCL8. This chromosomal translocation may contribute to lymphomagenesis by altered expression level of BCL8.

**References**


This article should be referenced as such: