## Leukaemia Section

Short Communication

# T-cell/histiocyte-rich large B cell lymphoma 

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## Clinics and pathology

## Disease

T-cell/histiocyte-rich large $B$ cell lymphoma (THRLBCL) is a distinct entity of aggressive lymphoma, recognized by the WHO classification as a separate entity (2008), in which few scattered neoplastic cells (usually <5\%) are surrounded by reactive T-lymphocytes and histiocytes. THRLBCL shares several morphological and immunophenotypic similarities with nodular lymphocyte-predominant Hodgkin's lymphoma (Pittaluga et al., 2010). These two entities may share initial transforming events that occur at germinal center B cell, followed by early divergence in the evolution of the neoplastic process (Franke et al., 2002).

## Phenotype/cell stem origin

The postulated normal counterpart is a germinal centre B cell.
The immunophenotype of the neoplastic component in pan-B positive, BCL6+, CD15-, CD30-.

## Epidemiology

It accounts for a minority of diffuse large B-cell lymphoma (<10\%).

## Clinics

The disease runs an aggressive course and is usually associated with poor outcome in those patients presenting at an advanced stage.

## Pathology

The lymph node section shows scattered large cells surrounded by many lymphocytes and histiocytes. The disease must be distinguished from nodular
lymphocyte-predominant Hodgkin's lymphoma, which has distinct clinical features.

## Treatment

Chemoimmunotherapy using anti CD20 monoclonal antibody rituximab in combination with CHOP or CHOP-like regimens is the standard of care (El Weshi et al., 2007).

## Prognosis

A >80\% overall response rate was obtained by chemoimmunotherapy, with a 5 -year overall survival of approximately $50 \%$ (El Weshi et al., 2007).

## Cytogenetics

## Cytogenetics molecular

Because of the low number of neoplastic cells, there are technical problems in obtaining evaluable metaphase chromosomes in THRLBCL. Tetraploid clones with complex aberrations, including a 14 q 32 translocation, were described in the absence of BCL6, BCL2 or cmyc involvement (La Starza et al., 1996; Wang et al., 2005; de Leval et al., 2006).
The presence of the PAX5/IGH gene rearrangement was demonstrated by fluorescence in situ hybridization (FISH) to represent a recurrent aberration (Poppe et al., 2005).

An average of 4.7 genomic imbalances/case were detected by comparative genomic hybridization in 17 cases of THRLBCL. The most frequently detected imbalances included gain of Xq (59\%, minimal overlapping region Xq12q13), $4 q$ ( $41 \%$, minimal overlapping region $4 q 25 q 26$ ), Xp ( $29 \%$, minimal overlapping region Xp 21 p 11 ), and $18 \mathrm{q}(24 \%$, minimal overlapping region 18q21), as well as loss of 17 p (24\%) (Franke et al., 2002).

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