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Chromosomal abnormalities in lymphoma pathogenesis and their clinical significance

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Chromosomal rearrangements of the immunoglobulin heavy chain (*IGH*) gene with oncogenes, i.e. t(14;18), t(11;14), t(8;14), and t(9;14), have particular impact on the diagnosis and therapeutic management of B-cell lymphoma because of their specificity and causative implications in lymphoma pathogenesis. For example, *BCL2* rearrangement and expression is a possible marker to predict response to rituximab. Chromosome t(14;18)(q32;q21) was present in 56% to 90% of follicular lymphoma, resulting in deregulated transcription of *BCL2* gene. Likewise, t(11;14)(q13;q32) is associated with mantle cell lymphoma, leading to up-regulation of *CCND1* gene. Among these 14q32 translocations, t(14;18), t(8;14), and t(3;14), were concurrently found in leukemia/lymphoma, which was characterized by extremely aggressive clinical course with nodal and/or extranodal involvement, and massive bone marrow infiltration.

Numerical abnormalities of nos. 3, 7, 12, and 18 and t(11;18)(q21;q21) associated with *API2-MALT1* rearrangement are specific to mucosa-associated lymphoid tissue (MALT) lymphomas. Among these abnormalities, t(11;18) is the most important determinant for the selection of treatment in MALT lymphomas, because t(11;18)-positive cases are resistant to *Helicobacter pylori* eradication therapy. Fluorescence in situ hybridization (FISH) directly on paraffin-embedded tissue section is a powerful tool to detect these specific chromosomal abnormalities. In adult T-cell leukemia lymphoma (ATLL) patients and established cell lines, we investigated chromosomal translocations using multicolor spectral karyotyping (SKY), assigning recurrent breakages to 10p11-13, 14q11.2, 14q32, 13q14, 7q22, 8q24, and 17p11.2.