

Research Paper

Clinical Significance of *BCL2*, *C-MYC*, and *BCL6* Genetic Abnormalities, Epstein-Barr Virus Infection, CD5 Protein Expression, Germinal Center B Cell/Non-Germinal Center B-Cell Subtypes, Co-expression of *MYC/BCL2* Proteins and Co-expression of *MYC/BCL2/BCL6* Proteins in Diffuse Large B-Cell Lymphoma: A Clinical and Pathological Correlation Study of 120 Patients

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Abstract

Background: Clinical significance of germinal center B-cell (GCB) and non-GCB sub-categorization, expression of *MYC*, *BCL2*, *BCL6*, *CD5* proteins and Epstein Barr virus encoded RNA (EBER) positivity in diffuse large B-cell lymphoma (DLBCL) remain controversial. Could these biomarkers accurately identify high risk DLBCL patients? Are *MYC*, *BCL2* and *BCL6* proteins expression feasible as baseline testing to predict *c-Myc*, *BCL2* or *BCL6* gene rearrangements?

Aims: To investigate prognostic values of GCB/non-GCB sub-categorization, Double Protein Expression Lymphoma (DPL), Triple Protein Expression Lymphoma (TPL), positivity of *CD5* protein and EBER in patients with DLBCL disease. To evaluate correlation between *BCL2*, *c-Myc* and *BCL6* gene rearrangements with *BCL2*, *MYC* and *BCL6* proteins expression.

Methods: Diagnostic tissue samples of 120 DLBCL patients between January 2012 to December 2013 from four major hospitals in Malaysia were selected. Samples were subjected to immunohistochemical staining, fluorescent in-situ hybridization (FISH) testing, and central pathological review. Pathological data were correlated with clinical characteristics and treatment outcome.

Results: A total of 120 cases were analysed. Mean age of diagnosis was 54.1 years \pm 14.6, 64 were males, 56 were females, mean follow up period was 25 months (ranged from 1 to 36 months). Of the 120 cases, 74.2% were non-GCB whereas 25.8% were GCB, 6.7% were EBER positive, 6.7% expressed *CD5* protein, 13.3% were DPL and 40% were TPL. The prevalence of *c-Myc*, *BCL2*, *BCL6* gene rearrangements were 5.8%, 5.8%, and 14.2%, respectively; and 1.6% were Double Hit Lymphoma (DHL). EBER positivity, DPL, TPL, *c-Myc* gene rearrangement, *BCL2* gene rearrangement, extra copies of *BCL2* gene and *BCL6* gene rearrangement were associated with shorter median overall survival ($P < 0.05$). IPI score was the significant determinants of median overall survival in DPL and TPL ($P < 0.05$). *CD5* protein expression and GCB/non-GCB sub-categorization did not affect treatment outcome ($P > 0.05$). Overall, *c-Myc*, *BCL2* and *BCL6* gene rearrangements showed weak correlation with expression of *MYC*, *BCL2* and *BCL6* proteins ($P > 0.05$). Fluorescent *in situ* hybridization is the preferred technique for prediction of treatment outcome in DLBCL patients.

Conclusion: *c-Myc*, *BCL2*, and *BCL6* gene rearrangements, EBER expression, DHL, TPL and IPI score are reliable risk stratification tools. *MYC*, *BCL2* and *BCL6* proteins expression are not applicable as baseline biomarkers to predict *c-Myc*, *BCL2*, and *BCL6* gene rearrangements.

Key words: diffuse large B-cell lymphoma, *c-Myc*, *BCL2* and *BCL6* gene rearrangements, diffuse large B-cell lymphoma with *CD5* protein expression, diffuse large B-cell lymphoma with positive EBER expression, non-germinal center B-cell subtype, Asia