A new diagnostic classifier for Burkitt and Diffuse Large B-Cell Lymphoma predicts outcome

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Burkitt lymphoma (BL) and diffuse large B-cell lymphoma (DLBCL) represent distinct entities among aggressive B-cell non-Hodgkin lymphomas (BCL), each with important clinical and therapeutic consequences. However, there is increased recognition of DLBCLs which share features with BL but deviate with respect to one or more findings and are currently classified in a provisional intermediate group in the WHO classification 2008. To overcome the poor diagnostic reproducibility of this category, we analyzed 242 cytogenetically defined (BCL2, BCL6, MYC translocations) BCL for differential protein expression of selected markers, based on recent transcriptional and gene-expression profile studies. By analyzing primary lymphomas on a tissue microarray, we identified expression of CSE1L and ID3 as being associated with the diagnosis of BL ($p < 0.05$), whereas STAT3 was over-expressed in DLBCL. All three markers were associated with favourable prognosis in DLBCL. Most interestingly, machine learning techniques for classification showed that only the combination of CSE1L, STAT3 and MYC translocation, subsumed under the algorithm called “new FISH classifier”, was able to identify patients, initially classified as intermediate between BL/DLBCL, who profited from intensive, BL-like regimens. We present a promising diagnostic algorithm for BCL with additional prognostic and predictive values.

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