ABSTRACT

Diffuse large B-cell lymphoma (DLBCL) is the most common type of non-Hodgkin lymphoma. It is a molecular and prognostic heterogeneous disease. Three main genetic subtypes are called germinal center-like DLBCL (GC-like DLBCL), non-germinal center-like DLBCL (nonGC-like DLBCL) and primary mediastinal B-cell lymphoma (PMBL). These subtypes can be reliably distinguished only with usage of gene expression profiling (GEP). The GEP method can be applied only when fresh frozen tissue is available. The method is technically difficult and expensive. Thus, it is not used routinely. Since the DLBCL subtypes differ in prognosis, it is extremely important to be able to distinguish them.

The presented thesis is focused on distinguishing of PMBL diagnosis in the group of DLBCL. Easily stored formalin-fixed, paraffin-embedded tissue (FFPE) and gene expression analysis using real-time quantitative polymerase chain reaction (RTqPCR) are used.

In the first step, PMBL and DLBCL cases were distinguished with an internationally accepted clinical-pathological method. The agreement between clinical-pathological diagnosis and GEP is only 76%. In the presented text a genetic algorithm for PMBL/DLBCL distinguishing is suggested. It uses three carefully chosen genes and their expression is measured with RTqPCR. Both, the clinical-pathologic and genetic algorithms are compared with help of clinical data. The genetic one seems to be closer to the GEP method than the clinical-pathologic one.

The text describes the establishment of the gene expression analysis from FFPE tissue using RTqPCR method. Clinical data are analyzed with respect to both the algorithm described above.