

Public Abstract

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Title:LARGE SCALE CpG ISLAND METHYLATION PROFILING OF
SMALL B CELL LYMPHOMA

Non Hodgkins lymphoma (NHL) is a group of malignancies of the immune system with variable clinical behaviors and diverse molecular features. Each year 56,000 new cases of NHL are diagnosed in the United States with Small B cell Lymphoma (SBCL) comprising roughly one third of all cases. Unfortunately, the incidence of NHL has increased over past decades, for unknown reasons, and is one of only two cancers increasing in incidence. The SBCLs includes B-cell chronic lymphocytic leukemia (CLL), mantle cell lymphoma (MCL) and low grade follicular lymphoma (FL). Current classification systems are based on clinical staging, chromosomal abnormalities and cell surface antigen, and offer important diagnostic information. However, there is still considerable overlap in biology, clinical behavior, genetic and epigenetic alterations among the SBCLs. DNA methylation plays an important role in cancers by silencing a broad spectrum of genes including tumor suppressor and DNA repair genes. In this study, we used a high throughput approach to classify SBCL based on similarities in DNA methylation. Our data revealed that there is diversity in DNA methylation among different SBCL subtypes, and some genes were preferentially methylated in a subset -related manner. These differentially methylated genes might have diagnostic and prognostic implications. This study provides the first insight into the global methylome of B-cell lymphomas.