

**Project Title: Differential Gene Expression in CLL Cells**

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**Abstract**

Chronic Lymphocytic Leukemia or CLL is the most common adult leukemia in the western world with a heterogenous clinical outcome. Despite years of research, there remains no curative treatment. CLL consists of an abnormal expansion of malignant B cells in the bone marrow, lymph nodes, and blood. Recently, there have been a number of advances that have led to the identification of several factors that predict the rate of tumor progression, treatment response, and overall survival. Most studies of CLL have involved CLL cells isolated from the blood since these cells are a readily accessible homogeneous population of tumor cells. Despite the identification of different prognostic groups, the molecular basis for these differences remains unknown. One possible explanation is that tumor cells isolated from the blood may represent more differentiated or mature B cells that share many of the same properties regardless of the overall aggressiveness of the disease. In this proposal, we hypothesize that the CLL cells in the lymph nodes clustered together in groups called pseudofollicles, or CLL cells in the bone marrow, may play a significant role in determining the aggressiveness of a leukemia in a given patient. Therefore, we will compare the gene expression of CLL cells in the bone marrow/lymph nodes with CLL cells in the blood from the same patients. Thus, the results of these studies might provide us with data that will help us better predict the clinical outcome in CLL patients.