Dynamic epigenetic modifications occur during lineage development in the hematopoietic system (1). A broad epigenetic programming has recently been described to occur during B-Cell maturation and there is a prominent loss of methylation (hypomethylation) with increasing maturity (2) (3). CLL cases showed methylation changes at specific CpG sites associated with time to progression (4). We collected the datasets of differential CpGs during disease progression and the genes associated with those CpGs. The dataset consists of 27 patients. DNA methylation data was collected from these patients both at the time of diagnosis and after clinical progression, but before treatment. 4,752 CpG altered during disease progression and were co-located near 2,670 genes. Using those genes, we will identify the pathways critical for CLL pathogenesis. It is vital to know which genes are druggable to block the pathways. In this study we aim to identify CpGs involved in disease progression and to propose the known drugs to block the critical pathways in CLL.

Themes:

Check (highlight) the most applicable theme according to the abstract.

| Innovation and Technology | Health and Wellness | Culture and Society | Sustainability and Conservation |

Comments:

Given that MURC is a generalist conference, your abstract should be accessible and understood by a broad audience. Avoid jargon or explain abbreviations/terms that you use. What is the significance of your study/why is it important?