Research Strategy

Significance:

All cells in the body share the same genetic code, yet different cell types with specific functions exist in different environments. Genes are regulated in different tissue types by several mechanisms in the epigenome. How these different epigenetic landscapes are formed during differentiation is a central question of biology. The process of hematopoiesis allows us to study the change in epigenetics as progenitor cells differentiate into terminal cell types. The genome is wrapped out histones into discrete packages called nucleosomes, and the proteins of these histones can be marked with certain modifications that allow regulation of gene expression. However, genes cannot be transcribed while wrapped in nucleosomes, and so the DNA code must be unwrapped and made accessible before transcription can occur. ATAC-seq allows us to find unwrapped sections of DNA, and we can measure the accessibility of DNA during differentiation in sections of the genome that are marked by histone modifications. We can measure at which step in the differentiation process that these common sections of marked chromatin become accessible, and through motif analysis we can identify which transcription factors are the initial factors that are present during these crucial differentiation stages.

This F31 application seeks to validate my hypothesis that