Non-canonical RNA tailing and other post-transcriptional regulatory mechanisms in T cell-mediated adaptive immunity.

All living organisms have to fight against various pathogens to maintain their homeostasis. In the vertebrates, an adaptive cell-mediated immune response based on the action of T and B lymphocytes has developed. T lymphocytes are responsible for destroying cells infected by pathogens, activating other cells of the immune system, secreting cytokines, and creating immune "memory". All these functions are strictly regulated at the level of gene expression, which can also take place at the mRNA level. The RNA molecules produced by gene transcription have specially modified ends that increase their stability and their ability to be used as matrices for ribosomes for protein synthesis. The so-called "5' end" has a stable cap structure, while the "3' end" has a so-called poly(A) tail, which is a dynamic sequence of nucleotides (mainly adenosines) that can be elongated and shortened. Moreover, the nitrogenous bases in the RNA also undergo chemical modification, which affects mRNA function and fate in the cell. All these processes result in the formation of many different RNA molecules and proteins from one gene. Our preliminary data indicate that the enzyme involved in the tail elongation of poly(A) can regulate the differentiation and activity of T lymphocytes. In this project, we will attempt to decipher at the molecular level how cytoplasmic polyadenylation of mRNA and other mechanisms of modification of these molecules affect the differentiation and function of T cells. To this end, we will use a modern genomic approach based on the latest nucleic acid sequencing technologies, which we intend to further improve, and other advanced molecular biology methods to gain insight into the processes being studied. This project is expected to contribute to a better understanding of RNA metabolism and its regulatory significance in the immunological response.