**Tailing in the regulation of microRNA and mRNA**

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**Abstract**

More than 100 types of RNA modifications have been described thus far, yet their regulatory functions remain largely unexplored. Recent developments revealed that at least some of the modifications are considerably abundant and widely conserved. In this presentation, I will discuss our recent findings which uncovered the importance of RNA 3’ end modifications (or “tails”) in the microRNA and mRNA pathways. Terminal nucleotidyl transferases add untemplated nucleotides to the 3’ end of RNAs and their precursors, and thereby affect processing, stability, and activity of RNAs. MicroRNAs are subject to uridylation and adenylation. Uridylation controls the biogenesis of let-7 microRNAs, and plays a key role in developmental and tumorigenic transitions. Adenylation of microRNA occurs pervasively in activated oocytes and early embryos, and results in microRNA clearance during maternal-to-zygotic transition. Tailing is not restricted to the microRNA pathway. To understand the function of RNA tailing beyond the miRNA pathway, we have developed a new method termed TAIL-seq which determines poly(A) tail length and 3’ end modifications simultaneously. Using this method, we found widespread uridylation on deadenylated mRNAs in mammal, fish and frog. TUTases play an integral role in mRNA turnover by generating an oligo(U) tail which serves as a general mark for mRNA decay. I will present our recent results from functional analyses of various tails and tailing enzymes in the microRNA and mRNA pathways.