

The utilization of advanced RNA sequencing technologies to investigate post-transcriptional mechanisms involved in the regulation of gene expression.

Abstract

Antagonistic mechanisms, such as deadenylation and polyadenylation, play critical roles in post-transcriptional regulation of gene expression and transcriptome remodeling in eukaryotic cells. This work explores cytoplasmic mRNA deadenylation and decay in yeast and the role of non-canonical poly(A) polymerases in murine gametogenesis. The dissertation consists of three multiauthor publications in which I was primarily responsible for bioinformatic analysis. Utilizing Nanopore RNA Sequencing (DRS) data, we modeled yeast mRNA deadenylation rates in vivo and identified transcript-specific decay dynamics under normal and stress conditions. In murine studies, TENT5 poly(A) polymerases were shown to regulate the stability of key transcripts governing oocyte and spermatocyte maturation. Analyses also revealed unique poly(A) tail compositions in testes and ovaries transcriptomes. The enrichment of non-canonical nucleotides in poly(A) tails of transcripts crucial for germ cell development opens new avenues for future research into the regulatory mechanisms of gametogenesis.