

## **Single-molecule analysis on the interaction between translation, poly(A) tail, and diverse sequence context**

Han Seungbeom

An RNA molecule engages in several interactions with numerous molecules within the cytoplasm, and it exists in diverse states. A notable attribute of cytoplasmic RNA is its ability to facilitate translation initiation by interacting between its poly(A) tail and the 5' terminal. Contrary to expectations based on this closed-loop hypothesis, several studies indicate that genes with short tails do not always include a large quantity of ribosomes. This trend, however, might be caused by the aggregation of tail length and ribosome load at the gene level, which obscures the positive correlation between the length of the poly(A) tail and the amount of ribosomes bound to RNA. We employed polysome fractionation and direct RNA sequencing techniques to examine translation and poly(A) tail length in a comprehensive transcriptome consisting of individual, full-length molecules. We discovered numerous sequence characteristics related with the number of ribosomes on an RNA molecule by resolving isoform-level differences. In addition, in our study we observed a positive correlation between the length of the poly(A) tail and the accumulation of ribosomes at the single-molecule level. Yet, we also discovered that the increase in ribosome loading did not consistently rise with longer poly(A) tail lengths. The link between poly(A) tail length and ribosome accumulation was found to be correlated with many sequence features related to translation and RNA stability.