

Prof. Norman Chiu

*Department of Chemistry and Biochemistry,
University of North Carolina Greensboro, USA*



Towards Standard-free Quantitative Profiling of RNA Modifications Using Mass Spectrometry

ABSTRACT

Although selected RNA modifications have been extensively studied, the functions of many other modifications within the epitranscriptome remain largely unknown. This is partly due to the limited availability and high cost of RNA standards, which hinder the development of robust analytical methods for comprehensive and quantitative profiling. Theoretically, the interplay among different RNA modifications can influence RNA functions, thus highlighting the importance of accurate profiling for biomarker discovery. Using mass spectrometry as a universal platform, recent advances have enabled untargeted analysis of RNA modifications. In our study, using the glioblastoma epitranscriptome as a model system, we introduce a practical approach to address the lack of standards and correct the bias in the electrospray ionization of different ribonucleosides. Our developed method has shown to improve quantitative accuracy and reproducibility. With the ability to determine the accurate quantity of each RNA modification, we extended our study on the chemical stability of modified nucleosides under various experimental conditions. If unaddressed, these factors can introduce significant bias and lead to erroneous conclusions in quantitative studies of epitranscriptomes.