

A Case Study on the Role of RNA Methylation in Regulating Cellular Senescence in Human Fibroblasts

Cameron Edwards

PhD

Massachusetts Institute of Technology

77 Massachusetts Avenue, Cambridge, MA 02139, USA

Harry Morris

Professor

University of Cambridge

The Old Schools, Trinity Lane, Cambridge CB2 1TN, UK

Alex Young

Associate Professor

Ludwig Maximilian University of Munich

Geschwister-Scholl-Platz 1, 80539 München, Germany

Abstract. RNA methylation has emerged as a crucial post-transcriptional modification influencing gene expression. This study explores the impact of RNA methylation on cellular senescence, highlighting its modulation in human fibroblasts. Using high-throughput sequencing and mass spectrometry, we identified specific methylation marks associated with senescence onset. Results indicate potential therapeutic targets for age-related diseases. Our findings provide a novel understanding of RNA modifications in cellular aging and suggest pathways for intervention in age-associated pathologies.

Keywords: RNA methylation, cellular senescence, human fibroblasts, post-transcriptional modification, age-related diseases

Introduction

The global rise in life expectancy has shifted focus towards understanding the mechanisms underlying age-related conditions, a pivotal concern given the burden of age-associated diseases. Among the various molecular mechanisms, cellular senescence, characterized by irreversible cell cycle arrest, plays a significant role in aging and associated pathologies. The regulation of senescence is complex, involving diverse signaling pathways, and recent studies have drawn attention to the post-transcriptional modifications of RNA, particularly RNA methylation, in modulating these pathways. \n\nThis paper investigates the specific role of RNA methylation in the senescence of human fibroblasts. We employed cutting-edge high-throughput sequencing and mass spectrometry to map methylation sites correlated with senescence. This empirical analysis aims to delineate the mechanistic pathways that contribute to the aging process and potentially unveil novel therapeutic

targets. The significance of these findings lies in their potential to reveal intervention strategies for mitigating age-related pathologies. \n\nIn this paper, we first review the current knowledge on RNA methylation and its biological implications. We then describe our methodological approach, followed by detailed results of the methylation landscape in senescent fibroblasts. Finally, we discuss the implications of our findings in the context of developing therapies for aging-related diseases.

This is a preliminary version. To read the full version of the article, please purchase a subscription.

References

1. Sharma, V., Devendran, R., Kumar, M., Prajapati, R., Kumar, R., & Prakash, V. (2025). Molecular dynamics of plant-virus interactions: unravelling the dual role of ubiquitin proteasome system. *Stress Biology*, 5(1), 12.