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The Effect of NHERF1 on MicroRNA Alterations in Aging Mouse Kidneys

Kutrupiya Hashemia*

Department of Biochemistry and Molecular Genetics, Assiut University, Assiut 71516, Egypt

Introduction

As organisms age, they undergo numerous physiological changes that can impact organ function and overall health. The kidneys, essential for maintaining fluid and electrolyte balance, are particularly susceptible to age-related alterations, which can lead to impaired renal function and increased susceptibility to diseases. Recent research has identified microRNAs (miRNAs) as critical regulators of gene expression that play significant roles in various biological processes, including aging and disease. These small non-coding RNAs modulate gene expression post-transcriptionally and can influence cellular processes such as inflammation, fibrosis, and cellular senescence [1]. The sodium-hydrogen exchanger regulatory factor 1 (NHERF1) is a scaffolding protein known for its role in regulating various signaling pathways and its involvement in cellular processes such as cell adhesion and transport. Emerging evidence suggests that NHERF1 might also influence the miRNA landscape within cells, potentially affecting how miRNAs regulate gene expression in the context of aging. Understanding the role of NHERF1 in modulating miRNA profiles in aging kidneys could provide insights into the mechanisms underlying age-related renal dysfunction and identify potential therapeutic targets for preserving kidney function in the elderly [2].

Description

To investigate the role of NHERF1 in the miRNA landscape of aging mouse kidneys, we conducted a series of experiments involving both genetic and molecular analyses. We utilized aging mouse models with varying levels of NHERF1 expression, including wild-type and NHERF1 knockout mice, to assess how NHERF1 influences miRNA expression in the kidneys. Initially, we performed a comprehensive miRNA profiling using high-throughput sequencing techniques to identify and quantify miRNAs in the kidneys of aging mice. We compared the miRNA profiles between NHERF1-deficient and wild-type mice to determine how the absence of NHERF1 affects the expression and regulation of specific miRNAs [3].

In parallel, we analyzed kidney tissues for signs of age-related changes, such as fibrosis, inflammation, and cellular senescence, to correlate these changes with alterations in miRNA expression. We also performed functional assays to assess kidney function and integrity, including measures of glomerular filtration rate and tubular function. To further understand the relationship between NHERF1 and miRNAs, we conducted luciferase reporter assays and gene expression studies to validate the targets of differentially expressed miRNAs. These assays helped us identify key gene targets regulated by miRNAs that are influenced by NHERF1 and elucidate the potential pathways through which NHERF1 affects kidney aging. Overall, this multi-faceted approach allowed us to create a detailed picture of how NHERF1 modulates the miRNA landscape in aging kidneys and to explore the implications for kidney function and aging [4,5].

Conclusion

The study has provided significant insights into the role of NHERF1 in modulating the miRNA landscape in aging mouse kidneys. Our findings indicate that NHERF1 influences the expression of specific miRNAs that are critical for maintaining renal function and managing age-related changes. The differential expression of these miRNAs in NHERF1-deficient mice suggests that NHERF1 plays a crucial role in regulating miRNA profiles that impact kidney aging and function. By identifying specific miRNAs and their gene targets that are affected by NHERF1, this research uncovers potential mechanisms through which NHERF1 influences renal aging processes. These insights could lead to new strategies for targeting miRNA pathways to mitigate age-related renal dysfunction and preserve kidney health in the elderly. Future research should continue to explore the functional roles of these miRNAs and their targets in the context of kidney aging and investigate how NHERF1-mediated regulation of miRNAs can be leveraged for therapeutic interventions. Overall, this study contributes to a deeper understanding of the molecular mechanisms underlying kidney aging and highlights the importance of NHERF1 in shaping the miRNA landscape and its implications for renal health.

Acknowledgement

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Conflict of Interest

None.

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***Address for Correspondence:** Kutrupiya Hashemia, Department of Biochemistry and Molecular Genetics, Assiut University, Assiut 71516, Egypt; E-mail: kutrupiyahashemia@gmail.com*

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