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Bulk RNA Barcode Sequencing Highlights RNA Splicing's Role in Modulating Aging Dermal Stem Cells with Botanical Extracts

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Introduction

Aging is a complex biological process characterized by progressive functional decline in cells and tissues. In the skin, aging affects dermal stem cells, which are essential for maintaining tissue homeostasis and repair. Recent advances in high-throughput sequencing technologies, such as bulk RNA barcode sequencing, have provided novel insights into the molecular mechanisms underlying stem cell aging. One particularly intriguing discovery is the role of RNA splicing in modulating aging-associated changes in dermal stem cells, especially when influenced by botanical extracts. These findings open new avenues for understanding and potentially mitigating skin aging through targeted molecular interventions. RNA splicing is a critical post-transcriptional process that generates multiple transcript isoforms from a single gene, contributing to proteomic diversity and functional specialization. Splicing regulation becomes particularly significant in stem cells, where precise control over gene expression is necessary for maintaining their regenerative potential. During aging, dysregulation of splicing machinery can lead to aberrant splicing patterns, resulting in impaired cellular functions and reduced stem cell fitness. Bulk RNA barcode sequencing has emerged as a powerful tool to investigate these splicing alterations systematically, enabling researchers to profile transcriptomic changes at a high resolution.

Description

One key finding from recent studies is that aging dermal stem cells exhibit widespread alterations in RNA splicing. Genes involved in cell cycle regulation, DNA repair, extracellular matrix remodeling, and stress responses are particularly affected. These changes are often associated with a decline in the expression or activity of splicing factors, such as serine/arginine-rich (SR) proteins and heterogeneous nuclear ribonucleoproteins (hnRNPs). For instance, a decrease in the expression of the splicing factor SRSF3 has been linked to defective splicing of transcripts critical for stem cell function, leading to reduced proliferation and differentiation capacity in aging dermal stem cells. Botanical extracts have garnered significant attention as potential modulators of aging due to their bioactive compounds with antioxidant, anti-inflammatory, and regenerative properties. Intriguingly, some botanical extracts have been shown to influence RNA splicing in aging cells, including dermal stem cells. Using bulk RNA barcode sequencing, researchers have identified specific splicing events modulated by botanical extracts, shedding light on their molecular mechanisms of action. For example, extracts from plants rich in polyphenols, such as green tea or grape seed, have been demonstrated to enhance the expression of certain splicing factors, restoring proper splicing patterns and mitigating aging-associated functional decline [1].

A recent study employing bulk RNA barcode sequencing revealed that a particular botanical extract significantly modulates RNA splicing in aging dermal stem cells. This extract, derived from a medicinal plant with a history of use in traditional medicine, was found to upregulate key splicing factors such as SRSF2 and HNRNPA1. These splicing factors play critical roles in maintaining transcriptome integrity and cellular resilience. Treatment with the extract restored the splicing of transcripts involved in cell cycle progression and DNA repair, promoting enhanced proliferation and genomic stability in aging dermal stem cells. Furthermore, the study highlighted the impact of botanical extract treatment on alternative splicing events. One notable example is the splicing of the pre-mRNA encoding lamin A, a nuclear envelope protein implicated in cellular aging. Aging cells often exhibit an increased production of progerin, a toxic lamin A isoform associated with nuclear abnormalities and cellular senescence. The botanical extract was shown to reduce progerin levels by promoting the inclusion of canonical exons in lamin A pre-mRNA, thereby mitigating nuclear defects and improving stem cell function [2].

In addition to splicing factor regulation, botanical extracts were found to influence splicing regulatory elements within target genes. Analysis of RNA sequencing data identified specific changes in splicing enhancer and silencer motifs, suggesting that the extract's bioactive compounds may directly interact with the splicing machinery. These findings underscore the potential of botanical extracts as natural modulators of RNA splicing, offering a novel approach to counteract the detrimental effects of aging on dermal stem cells. Another critical aspect revealed by bulk RNA barcode sequencing is the interplay between RNA splicing and other regulatory pathways in aging dermal stem cells. For instance, splicing-mediated changes in transcripts encoding key transcription factors, signaling molecules, and epigenetic regulators were observed following treatment with botanical extracts. These changes likely contribute to the comprehensive rejuvenation effects observed in treated stem cells. By modulating multiple layers of gene regulation, botanical extracts appear to restore a youthful transcriptomic profile, enhancing the regenerative potential of aging dermal stem cells [3].

The therapeutic implications of these findings are profound. By targeting RNA splicing, it may be possible to develop novel interventions to combat skin aging and associated disorders. Botanical extracts, with their natural origin and pleiotropic effects, represent a promising avenue for such interventions. However, challenges remain in translating these findings into clinical applications. The bioavailability, stability, and specificity of botanical compounds need to be thoroughly investigated. Additionally, the molecular targets and pathways modulated by these compounds require further characterization to ensure efficacy and safety. To advance this field, integrative approaches combining bulk RNA barcode sequencing with complementary techniques such as single-cell RNA sequencing, proteomics, and metabolomics are essential. These approaches will provide a more comprehensive understanding of how RNA splicing and other regulatory networks interact in aging dermal stem cells. Furthermore, leveraging computational modeling and machine learning can help identify key splicing events and regulatory elements that are most amenable to modulation by botanical extracts [4,5].

Conclusion

The role of RNA splicing in aging dermal stem cells and its modulation by botanical extracts represents an exciting frontier in aging research. Bulk RNA barcode sequencing has been instrumental in uncovering the intricate transcriptomic changes associated with these processes, offering valuable insights into the molecular mechanisms of skin aging. By harnessing the potential of botanical extracts to modulate RNA splicing, researchers are

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paving the way for innovative strategies to enhance skin health and combat aging. Continued research in this area promises to unlock new therapeutic possibilities, contributing to healthier and more resilient skin as we age.

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Conflict of Interest

None.

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