Cell Biology: Research & Therapy

Opinion Article A SCITECHNOL JOURNAL

Telomeres and Epigenetics: Relationship between DNA Methylation and Telomere Length

Jehna Lerea*

Department of Genetics, Cell Biology and Development, University of Minnesota, Minneapolis, USA

***Corresponding author:** Jehna Lerea, Department of Genetics, Cell Biology and Development, University of Minnesota, Minneapolis, USA; E-mail: lereaj@uom.edu

Received date: 21 February, 2023, Manuscript No. CBRT-23-95185;

Editor assigned date: 23 February, 2023, Pre QC No. CBRT-23-95185(PQ);

Reviewed date: 07 March, 2023, QC No. CBRT-23-95185;

Revised date: 14 March, 2023, Manuscript No. CBRT-23-95185(R);

Published date: 24 March, 2023, DOI: 10.4172/2324-9293.1000173

Description

Telomeres are the protective caps located at the end of chromosomes, which shorten with each round of cell division. These structures play an important role in maintaining genome stability, and their length is associated with cellular aging, cancer, and other diseases. Recently, it has been discovered that telomere length is regulated by a complex interplay between genetic and epigenetic factors. It will explore the connection between telomeres and epigenetics, with a focus on the interplay between DNA methylation and telomere length [1].

Epigenetics refers to the study of changes in gene expression that occur without any alteration in the underlying DNA sequence. These changes can be induced by various factors, including environmental exposures, lifestyle choices, and aging. One of the most widely studied epigenetic modifications is DNA methylation, which involves the addition of a methyl group to the cytosine residue in the DNA molecule.DNA methylation has been shown to play an important role in gene expression regulation and is involved in numerous biological processes, including cell differentiation, development, and disease [2].

In recent years, several studies have shown that DNA methylation can also impact telomere length. For example, a study published in the journal in 2017 found that DNA methylation levels at specific sites in the genome were associated with telomere length in white blood cells. Specifically, the study showed that DNA methylation levels at a site on chromosome 10 were strongly associated with the telomere length, suggesting that this site may plays an important role in telomere length regulation [3-5].

Another study published in the journal in 2018 found that DNA methylation of a gene called TERT, which encodes with the catalytic subunit of telomerase, was associated with telomere length in the breast cancer cells. The study showed that the higher levels of TERT DNA methylation were associated with shorter telomeres in these cells [6].

These studies and others like them suggest that DNA methylation plays an important role in telomere length regulation, but the exact mechanisms underlying this relationship are not yet fully understood. One hypothesis is that DNA methylation may impact telomere length by regulating the expression of telomere-related genes. For example, DNA methylation of the TERT gene has been shown to regulate telomerase activity, which is involved in telomere lengthening. Another hypothesis is that DNA methylation may impact telomere length by directly regulating telomere structure and function [7].

One of the challenges in studying the relationship between telomeres and epigenetics is that telomere length and DNA methylation are both dynamic processes that can be influenced by a variety of factors. For example, exposure to environmental toxins or stressors can lead to changes in DNA methylation patterns, which in turn can impact telomere length. Similarly, lifestyle choices, such as diet and exercise, have been shown to impact both telomere length and DNA methylation levels [8].

Despite these challenges, recent advances in technology have allowed researchers to study the relationship between telomeres and epigenetics in more detail. For example, the development of high-throughput sequencing techniques has enabled researchers to profile DNA methylation patterns at a genome-wide level, which has led to the discovery of new telomere-related genes and pathways. Similarly, advances in telomere measurement techniques, such as qPCR and flow-FISH, have allowed researchers to more accurately measure telomere length in various cell types and tissues [9,10].

Conclusion

Continued research into the interplay between telomeres and epigenetics is important for a better understanding of the fundamental processes underlying aging, disease, and cellular function. This knowledge could have significant implications for the development of new therapies for diseases such as cancer, as well as for the development of strategies to promote healthy aging. As technology continues to advance, it is likely that our understanding of the complex relationship between telomeres and epigenetics will continue to grow, providing new insights into the mechanisms underlying cellular function and disease.

References

1. Lin-Goerke JL, Robbins DJ, Burczak JD (1997) PCR-based random mutagenesis using manganese and reduced dNTP concentration. Biotechniques 23: 409-412.
2. Goldberg AA, Richard VR, Kyryakov P, Bourque SD, Beach A, et al. (2010) Chemical genetic screen identifies lithocholic acid as an anti-aging compound that extends yeast chronological life span in a TOR-independent manner, by modulating housekeeping longevity assurance processes. Aging 2: 393-414. [
3. Swinnen E, Wilms T, Idkowiak-Baldys J, Smets B, De Snijder P, et al. (2014) The protein kinase Sch9 is a key regulator of sphingolipid metabolism in Saccharomyces cerevisiae. Mol Biol Cell 1: 196-211.
4. Joshua IM, Höfken T (2017) From Lipid Homeostasis to Differentiation: Old and New Functions of the Zinc Cluster Proteins Ecm22, Upc2, Sut1 and Sut2. Int J Mol Sci 18: pii: E772.
5. Wellinger RJ, Zakian VA (2012) Everything you ever wanted to know about Saccharomyces cerevisiae telomeres: beginning to end. Genetics 191: 1073- 1105.
6. Noda T. (2017) Regulation of Autophagy through TORC1 and mTORC1. Biomolecules 7:E52.

7. Smith JJ, Marelli M, Christmas RH, Vizeacoumar FJ, Dilworth DJ, et al. (2002) Transcriptome profiling to identify genes involved in peroxisome assembly and function. J Cell Biol. 158:259-271.
8. Allen D, Seo J (2018) ER Stress Activates the TOR Pathway through Atf6. J Mol Signal 13: 1.
9. Yorimitsu T, Zaman S, Broach JR, Klionsky DJ (2007) Protein Kinase A and Sch9 Cooperatively Regulate Induction of Autophagy in Saccharomyces cerevisiae. Mol Biol Cell 18: 4180-4189.
10. Chen J, Zheng XF, Brown EJ, Schreiber SL (1995) Identification of an 11-kDa FKBP12-rapamycin-binding domain within the 289-kDa FKBP12-rapamycinassociated protein and characterization of a critical serine residue. Proc Natl Acad Sci USA 92:4947-4951.