



Importance of Different Nutrients in Epigenetic Aging of Skeletal Muscle

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INTRODUCTION

Neurodegenerative diseases are increasing exponentially as the geriatric population continues to grow in importance. Lifestyle factors such as diet, exercise, and education influence the aging process over a lifetime. In particular, the central nervous system “CNS” can benefit from nutritional strategies and interventions that prevent cognitive decline and signs of aging such as neurodegenerative diseases such as Alzheimer’s and Parkinson’s. Trol (RV) has antioxidant and cyto-protective properties and is neuroprotective in several organisms. Oxidative Stress (OS) is caused by the accumulation of Reactive Oxygen Species (ROS), which has been proposed as an explanation for aging. One of the most detrimental effects of ROS in cells is DNA damage. However, there is also evidence that OS can induce other molecular alterations such as mitochondrial dysfunction, inflammation, apoptosis and epigenetic modifications. Interestingly, dietary polyphenol RVs are potent antioxidants that exert pleiotropic effects by exerting their activity through different molecular pathways. Moreover, recent evidence indicates that RV mediates epigenetic changes associated with aging and CNS function that persist across generations. Furthermore, RV has been shown to interact with the gut microbiota, indicating changes in bacterial composition associated with beneficial effects [1-4].

DESCRIPTION

With maternal aging and the use of assisted reproductive technologies in various countries around the world, the impact of epigenetic modifications on embryonic development has become clearer and more pronounced. Impaired epigenetic modifications caused by various nutritional imbalances can lead to abnormalities in embryonic development and even have permanent effects on adult health. This scoping review

summarizes the major epigenetic modifications in mammals and the synergistic effects between different epigenetic modifications, especially DNA methylation, histone acetylation, and histone methylation. We performed an in-depth analysis of the regulation of various epigenetic modifications from fertilization oogenesis to cleavage and blastocyst stages in mammals, outlining key site modifications and their potential molecular mechanisms. In addition, we discuss the effects of nutrients (protein, lipid, and one-carbon metabolism) on embryonic epigenetic modifications, highlighting the importance of different nutrients for embryonic development and epigenetics during pregnancy. Epigenetic mis-regulation has been implicated in early embryonic loss and disease in both mammals and humans. The use of reproductive techniques makes establishing viable embryos even more important. Therefore, it is important to assess how sensitive embryos are to these epigenetic changes and nutritional status. Understanding the epigenetic regulation of early embryonic development will help us better utilize reproductive technology and nutritional regulation to improve reproductive health in mammals.

CONCLUSION

For millions of years, endogenous retro elements have remained transcriptionally silenced by epigenetic mechanisms in mammalian genomes. Modern cancer therapies that target epigenetic mechanisms awaken retro element expression and induce antiviral responses that eliminate tumors through mechanisms that are still not fully understood. Here, massive binding of epigenetically activated retro elements by the viral RIG-I and MDA5 sensors promotes ATP hydrolysis and reduces intracellular energy, thereby driving tumors independently of immune signaling. Energy starvation increases compensatory ATP production by switching glycolysis to mitochondrial oxidative phosphorylation and reversing the Warburg effect.

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However, a highly functional succinate dehydrogenase in the mitochondrial electron transport chain generates excessive oxidative stress that triggers RIP1-mediated necroptosis.

Although there are functional benefits of resistance training even in later life, the contribution of epigenetic factors to training adaptations in later life is poorly defined. Using Reduced-Representation Bisulfite Sequencing (RRBS), ribosomal DNA (rDNA), and mitochondria-specific methylation studies, targeted high-resolution methylation analysis, and DNAge™ epigenetic aging clock analysis, spontaneous provides a translatable model of progressive weighted wheel running (PoWeR) in mice. We found evidence that exercise can reduce epigenetic aging of skeletal muscle.

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CONFLICTS OF INTERESTS

The authors declare that they have no conflict of interest.

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