

Austin Dodd

BIOL294

September 30, 2025

Genetics Writing Assignment #4: DNA Methylation and Aging

One of the most important epigenetic processes within the body is DNA methylation. DNA methylation plays a significant role in aging. It is seen as a biomarker of biological age and as a regulator of gene expression that contributes to age related outcomes. The Nature article “How ageing changes our genes huge epigenetic atlas gives clearest picture yet” discusses the function of DNA methylation within the body and its importance in genetics. Additionally, it points out that research into the methylation in organs can help researchers find specific targets within human genetics for antiaging therapies. A growing number of other studies have shown that DNA methylation does in fact exhibit a strong correlation with age. The article continues by stating that an epigenetic marker of ageing was found across different organs and tissues. This is said to be called the epigenetic atlas and could aid researchers in the identification of targets for antiaging treatments and therapies. Other reviews have shown that the faith in this epigenetic biomarker is well placed with its high accuracy. The analysis of DNA methylation can yield patterns that can be interpreted to create aging clocks. An epigenetic clock can be made from the yielded patterns; however, it is not perfect. The problem is whether these clocks are shared across tissue types. The answer, of course, is no. According to “Dynamic DNA methylation During Aging: A ‘Prophet’ of Age-Related Outcomes,” there are two well-known age clocks: Hannum’s clock and Horvath’s clock. The first is suitable for human blood, and the other is used for human tissues and cells.

The Nature article goes into detail about an experiment wherein they conducted an analysis of more than 15,000 samples taken from adults of differing ages. They found that skeletal muscles and lungs experienced a significant amount of loss in methylation with age. This is accurate since methylation acceleration is correlated with poorer lung function in humans during later life. The article also investigates possible biomarkers that span across multiple tissues. These included developmental regulators HDAC4, HOX, MEST, which is associated with diabetes. This is accurate since all can be involved with CpG sites. DNA methylation happens almost exclusively at CpG dinucleotides. This correlation can be seen in the promoters of HDAC4 and HOX genes. Regarding MEST changes in methylation can disrupt normal imprinting and are tied to metabolic disease. It has also been shown in the review article that DNA methylation level across several CpG sites is associated with life expectancy. Meaning an understanding of the mechanisms of ageing in the body can lead to a boost in antiaging therapies. The overall information in this Nature article is accurate; however, the research cited is not peer-reviewed. However, the peer-reviewed article “Dynamic DNA Methylation During Aging: A ‘Prophet’ of Age-Related Outcomes” supports the accuracy of its claims. DNA methylation is a very important part of genetics. Methylation covers how genes are regulated and dives into genomic imprinting as well as aging.

References

- Simms, C. (2025, September 1). How ageing changes our genes — huge epigenetic atlas gives clearest picture yet. *Nature*. <https://www.nature.com/articles/d41586-025-02735-z>.
- Xiao, F.-H., Wang, H.-T. & Kong, Q.-P. Dynamic DNA Methylation During Aging: A “Prophet” of Age-Related Outcomes. *Front. Genet.* **10**, 107 (2019). <https://doi.org/10.3389/fgene.2019.00107>.