NATHAN SHOCK CENTERS
OF EXCELLENCE IN THE
BASIC BIOLOGY OF AGING

PILOT AWARDEE SPOTLIGHT

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Development of the first epigenetic clock in tooth tissues. Towards a better understanding of tooth aging

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How did you become interested in aging?
To be totally honest, it was by chance. I did my PhD in biomedical sciences focused on the application of antioxidants to cancer treatment. During my postdoctoral tenure my research switched to improving age-at-death estimation of human remains based on biochemical techniques. It was when I started to work with human teeth and learnt more about the hallmarks of aging. I realized that there is a gap of knowledge on tooth aging, which increased my curiosity and my willingness to devote my research to this field.

Briefly describe your project in non-scientific terms. What questions are you trying to answer?
DNA methylation refers to the addition of a methyl group, “a label”, to one of the letters of the DNA, cytosine. These labels can alter how to read the letters of the DNA, and as a result, change the transcription and at the end the production of the proteins. With aging, depending on the type of tissue and the genes, there is an increase or decrease of these labels. My project studies these labels on the most internal layers of the tooth, dentin and pulp. The idea is to identify which genes have more or less labels with aging and if there are differences between these two tissues, leading to a better understanding of tooth aging.

What previous research or experience informed the development of this proposal?
I published two studies analyzing these label changes in dentin and pulp. Both of them were carried out with pyrosequencing, which limited the number of samples and genes to test. The genes I assessed were based on previous works developed on other tissues, not tooth specific. Despite of that, it was possible, for some of the genes, to find a correlation between methylation changes and aging in both dentin and pulp, finding differences between these two tissues.

What’s exciting about your project’s potential impact?
The methodological approach is different respect to my previous publications. The samples are analyzed with the Illumina Methylation Array, which interrogates several genes and methylation sites at the same time. This will provide us a better understanding of the methylation changes with aging in dentin and pulp, and also, point out the differences between these two tissues. The final goal is to develop the first epigenetic clock in tooth tissues.

If your project is successful, what is the next step?
The next step will be to increase the number of samples and age ranges to confirm these results. Additionally, on these same samples we would analyze the transcriptome and proteome to correlate methylation changes with expression changes during aging.

How has support from and collaboration with the Nathan Shock Centers helped further this project and/or your research overall?
Since I started to work on methylation I wanted to do the Illumina Array to interrogate several genes and methylation sites to have a clear picture of the epigenetic changes with aging in human teeth. The award from Nathan Shock Centers has been crucial to provide the resources and support to achieve this goal and the generation of preliminary data to hopefully apply for extramural funding to expand this project and pursue the next steps. Moreover, I appreciate the mentoring support from Dr. Christy Carter (UAB Nathan Shock Center) and Dr. Willard Freeman (Oklahoma Nathan Shock Center), as someone relatively new in the aging field their advice and guidance are really helpful.