Epigenetic Factors Impacting Type 2 Diabetes in American Indians

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Alejandra Salazar Gonzalez and Shelley Cole, Ph.D.

Abstract

American Indians have been found to be at higher risk of type 2 diabetes (T2D) than any other ethnic or racial groups in the United States, with an estimated prevalence rate of 33%. Given that T2D prevalence rates amongst the American Indian population are so high, studying the complex factors that contribute to T2D is crucial. Of particular importance to this study is identifying heritable effects involved in development of T2D. Epigenetic effects, heritable changes to DNA that affect gene expression such as DNA methylation (DNAm), have been shown to be associated with T2D phenotypes.

Studies in other subpopulations have previously identified differential DNAm at the ABCG1 gene as being associated with T2D. ABCG1 plays a significant role in promoting cholesterol efflux, and it has been associated with T2D and related traits. As such, we sought to determine whether those results generalized to American Indians by assaying DNAm at ABCG1 within a sample population of 285 American Indian participants in the Strong Heart Study (SHS). In verifying whether there is a significant association between DNAm levels and T2D, we hypothesize that individuals diagnosed with T2D will have higher rates of DNAm at loci in ABCG1 than individuals who do not have T2D. Ultimately, we hope the results of this experiment can provide more insight on the role that differential DNAm has to play in the risk and development of T2D.

KEYWORDS: Type 2 diabetes; American Indians; Epigenetics; DNA methylation; ABCG1

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Studies in other subpopulations have previously identified differential DNAm at the *ABCG1* gene as being associated with T2D. *ABCG1* plays a significant role in promoting cholesterol efflux, and it has been associated with T2D and related traits. As such, we sought to determine whether those results generalized to American Indians by assaying DNAm at *ABCG1* within a sample population of 285 American Indian participants in the Strong Heart Study (SHS). In verifying whether there is a significant association between DNAm levels and T2D, we hypothesize that individuals diagnosed with T2D will have higher rates of DNAm at loci in *ABCG1* than individuals who do not have T2D. Ultimately, we hope the results of this experiment can provide more insight on the role that differential DNAm has to play in the risk and development of T2D.

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