2021SandwithSiara-abstract

Abstract

Topologically-associated domains (TADs) are areas of highly associated chromatin that contribute to the overall 3D structure of chromatin. TADs are demarked by boundaries enriched with architectural proteins, which insulate TADs, preventing inter-TAD interactions. TADs are further enriched and insulated by secondary nucleic acid structures known as G-quadruplexes. The major G-quadruplex helicase is DHX36, which has been shown to impact important cellular processes such as replication, transcription, translation, and the stress response. However, it is unknown how the relationship between DHX36 and G-quadruplexes impacts the stability of TAD boundaries. To better understand this dynamic, we knocked out *Dhx36* in mice and performed high throughput chromosome confirmation (Hi-C) technique. This technique will allow us to compare TADs in the knockout versus wild-type mice. We expect to find that knocking out this helicase will improve the stability of G-quadruplexes at TAD boundaries. As a result, we anticipate a greater number of TADs due to stronger insulation at TAD boundaries. If our hypothesis is correct, this will suggest DHX36 influences 3D chromatin structure and gene expression, which will help our understanding in fields such as cancer, aging, and epigenetics.

Honors College
Ball State University
Muncie, IN 47306