

Project Title: Identification of potential G-quadruplex forming sequences in the archaeon *Halobacterium salinarum*

Company/Lab Webpage: South Dakota School of Mines and Technology

<http://www.sdsmt.edu/>

Department of Chemistry and Applied Biological Sciences

<http://www.sdsmt.edu/Academics/Departments/Chemistry-and-Applied-Biological-Sciences/Chemistry-and-Applied-Biological-Sciences/>

Background information:

G-quadruplexes are stable alternative DNA structures formed by sequences rich in guanine nucleotides. These sequences associate through Hoogsteen hydrogen bonds, and may be intramolecular or intermolecular. These structures have been associated with telomeres, where they are thought to decrease the activity of telomerase and promote telomere shortening. They have also been found in the promoter region of many genes, including several proto-oncogenes. It has been speculated that these regions play a regulatory role, and may be involved in transcriptional regulation.

Recently, a genome-wide search of several prokaryotic genome sequences found that potential G-quadruplex forming sequences grouped by gene function {Beaume, 2013 #3564}.

Interestingly, genes for radioresistance in three organisms contained potential G-quadruplex forming sequences. The formation of G-quadruplex structures can be chemically attenuated by certain compounds; one such compound was found to decrease the radiation resistance of *D. radiodurans* by 60%.

Haloarchaeons are also known to be extremely radiation resistant. The genomes of these organisms are also high in GC content, which would suggest a high potential for G-quadruplex formation.

Project goal:

The goal of this project is to identify potential G-quadruplex forming sequences in the promoters (or the genes) of the archaeon *Halobacterium salinarum*, and determine if the sequences group by function (hopefully radiation resistance, or DNA maintenance).

Specific Objectives:

- Develop an algorithm for high GC content genomes, or modify an existing one, to screen for potential G-quadruplex forming sequences in the haloarchaea
- Employ the algorithm to screen the *H. salinarum* genome (and possibly also *H. volcanii*)
- Identify the functions of the genes associated with the potential G-quadruplex forming sequences