Christopher Lessard, PhD

Sjögren's Syndrome Foundation Research Grant

LAY ABSTRACT

The Lay Abstract is for publicity purposes and should use simple language summarizing the proposed research and its significance.

The human genome contains ~22,000 genes that are expressed as the result of very complex mechanisms involving both proteins and thousands of non-coding regulatory RNA molecules. Recent work by the ENCODE project has found that ~80% of the human genome is functional and actively transcribed into RNA, but only 3-5% contains sequences that code for proteins. Our preliminary studies have found active regions of the genome that do not code for proteins, called long non-coding RNAs (lncRNAs), which are dysregulated and may contribute to the risk of developing Sjögren's syndrome. Their precise function is currently unexplored. In other diseases, including breast and prostate cancers, lncRNAs have been shown to be important diagnostic markers and potential targets for therapeutic interventions. The goal of this project is to characterize the lncRNAs that are implicated in SS and to evaluate their potential as diagnostic markers and therapeutic targets.

SCIENTIFIC ABSTRACT

The Scientific Abstract is written for SSF reviewers and a professional audience.

The human genome contains ~22,000 genes that are expressed as the result of very complex mechanisms that involve both proteins (such as transcription factors) and thousands of non-coding regulatory RNAs. Recent work by the ENCODE project has found that ~80% of the human genome is biochemically active while only 3-5% contains protein-coding sequences. In several diseases, such as prostate and breast cancer, lncRNAs have recently been shown to be important diagnostic markers, prognostic indicators, and targets for successful therapeutic interventions. Our preliminary RNAsequencing studies using whole blood from Sjögren's syndrome (SS) patients have found a substantial number of dysregulated long non-coding RNAs (lncRNAs). We propose to validate these candidates in disease relevant cell types and test potential functional mechanisms. Understanding the role of lncRNAs in SS has significant potential to open completely novel lines of investigation and significantly impact diagnosis and treatment.