Determining the mechanism of LINE-1 ribonucleoprotein particle assembly and inhibition by nucleoside reverse transcriptase inhibitors.

Jocelyn C Newton^{*}, Gerwald Jogl[#], John M Sedivy[#]

Graduate Program in Pathobiology and [#]Department of Molecular Biology, Cell Biology, and Biochemistry, Brown University, Providence, RI 02912

Mobile genetic elements are sequences of DNA capable of altering their genomic location, resulting in host DNA damage and genomic instability. In humans, Long Interspersed Nuclear Element-1 (LINE-1) is the only autonomously replicating element, accounting for 17% of the genome¹. Age-associated changes in the chromatin landscape and immune function are correlated with the transcriptional derepression of the LINE-1 element during cellular senescence. Two open reading frames produce a chaperone ORF1 protein and a catalytic ORF2 protein which assemble onto its native transcript to form a ribonucleoprotein (RNP) particle. The ORF2 protein consists of endonuclease, reverse transcriptase (RT), and nucleic acid binding domains whose functions are required for successful retrotransposition. After assembly, the LINE-1 RNP particle enters the nucleus and integrates into new genomic locations via a 'copy-and-paste' mechanism using its RNA-intermediate. Through comparative homology modeling²⁻³, various constructs isolating the functional LINE-1 RT domain were designed, expressed, and purified from Escherichia coli. Nucleoside reverse transcriptase inhibitors (NRTIs) originally developed for treating human immunodeficiency virus (HIV)⁴ also inhibit LINE-1 RT activity. Therefore, we are using complementary techniques in biochemistry and structural biology to elucidate both the mechanisms of LINE-1 RNA binding and inhibition by NRTIs to explore the LINE-1 RT as a potential drug target in age-associated diseases.

¹Lander, ES et al. Initial sequencing and analysis of the human genome. *Nature* 409:860-921 (2001).

²Song Y et al. High resolution comparative modeling with RosettaCM. *Structure* (2013).

³Xu D et al. FFAS-3D: Improving fold recognition by including optimized structural features and template reranking. *Bioinformatics* (2013).

⁴Dia L et al. Effect of reverse transcriptase inhibitors on LINE-1 and Ty1 reverse trancriptase activities and on LINE-1 retrotranposition. *BMC Biochemistry* 12(18):(2011).