

Long terminal repeat (LTR)-retrotransposons are widespread in eukaryotic genomes and play an essential role in their functioning. These mobile genetic elements may be beneficial to their hosts by providing new regulatory sequences, but their activity can also be a source of genomic rearrangements, lead to mutations and diverse genetic diseases. The Ty3/Gypsy (*Metaviridae*) is one of the most important and representative families of LTR-retrotransposons in eukaryotes. The Ty3 retrotransposons have pronounced structural and functional similarities to retroviruses, like HIV-1, but they are not infectious and do not leave the host cell. The yeast Ty3 retrotransposon is one of the most completely characterized LTR-retroelements. It replicates via an RNA intermediate, which is reverse transcribed in virus-like particles, and resulting cDNA can integrate into the host genome, thereby duplicating the element. During the replication cycle, Ty3 genomic RNA (gRNA) serves as a template for protein synthesis as well as for reverse transcription. Although yeast Ty3 retrotransposon is broadly utilized as an informative model to understand the biology of LTR-retroelements, the structure of its RNA genome remains unknown.

The knowledge of the native structure of retrotransposon RNA genomes exposed to the cellular environment is necessary to reach a comprehensive view of how genome architecture influences the retrotransposition process. The main goal of this project is to provide the first secondary structure model of the entire RNA genome (5.2 kb) of the Ty3 retrotransposon in yeast and establish its remodeling determinants in the cellular environment. For this purpose, I will use the recent technological advances, coupling RNA structure chemical mapping with next-generation sequencing, enabling the delivery of high-quality RNA structural models. To determine the impact of the cellular factors on the Ty3 genome folding, I will compare the Ty3 gRNA structure determined *in vivo* with that obtained in cell-free conditions. Moreover, I will analyze the structure of the Ty3 RNA genome in cells subjected to different environmental changes to establish the role of translation and other energy-dependent processes in retrotransposon RNA folding.