# Characterization of Ty1 genomic RNA structure in the in vitro state and on the particular steps of its replication in yeast cells

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Abstract

Ty1 is a retroelement that naturally occurs in the genome of the yeast *Saccharomyces cerevisiae.* It resembles simple retroviruses but replicates without leaving the host cells. Ty1 replicates via RNA intermediate, which is 5652nt long and fulfill a dual role: template for proteins synthesis and gRNA that is packed in dimeric form into VLPs, where Ty1 gRNA is reverse transcribed to a cDNA copy that later integrates into host dsDNA. Unlike viral gRNA for which complete *in vitro*, *in virio*, *ex virio* and also *in vivo* structures are increasingly presented, little is known about gRNA structures of LTR retrotransposons. Also, it remains unexplored how structures of viral and retrotransposons gRNA change during their replication inside the cellular compartments.

The research undertaken as a part of this doctoral dissertation allowed for investigation of Ty1 gRNA secondary structure model in the *in vitro* condition as well as on the particular steps of its replication in yeast cells. Using SHAPE probing I explored structure model of the entire Ty1 gRNA under defined *in vitro* conditions (Andrzejewska, Zawadzka et al. *NAR,* 2021). I indicated that this structure differ significantly from Ty1 gRNA structure in vivo and is more stable and structurally homogenous. Next, I characterized structural alterations of Ty1 gRNA during its replication cycle inside the cell (Zawadzka et al. *Viruses*, 2022). Using SHAPE probing, I obtained the first, nuclear structure of LTR retrotransposon gRNA. Through a detailed comparison with the Ty1 gRNA structures established in the cytoplasm, VLPs and those synthetized *in vitro* I detected that LTR retrotransposon gRNA undergoes a significant structural rearrangements, and its architecture is closely dependent on the local environment of cellular compartments. To better understand RNA folding in distinct biological states, together with the team, we prepared the comprehensive review in which we summarize the up-to-date knowledge about the RNA structure to function correlation inside the cell (Andrzejewska, Zawadzka et.al. *IJMS*,2020)