DESCRIPTION FOR THE GENERAL PUBLIC (IN ENGLISH)


Transfer RNAs are mainly known for their canonical function as essential components of the translational machinery, where they are responsible for delivering correct amino acid in the process of protein synthesis. For decades, this undisputed role of tRNAs has been considered their only function in the cell, until 2009 when first small RNAs, derived from tRNAs (tRFs) were observed by Cole and colleagues. Further studies followed and have since implicated the tRFs in various diseases such as cancer, HIV infections and Lou Gehrig's disease (ALS). The field of tRF research is still young and full of unanswered questions but there is published evidence from animal, yeast and bacterial studies linking these small molecules to regulation of gene expression by direct targeting of messenger RNA transcripts.

As there is very little information about tRFs in plants, in part due to the lack of proper analytical tools, we propose **two main objectives** for this research project: **1) development of a computational methodology pipeline** which will allow for: functional analysis of plant small non-coding RNAs, discovery and analysis of their target mRNAs, and deciphering the mechanism of sRNA-mRNA binding. **2) employing the proposed pipeline for functional analysis of candidate regulatory RNAs derived from tRNAs and their targets in the plant *Arabidopsis thaliana***.


In our research we are asking the following questions: "**are small RNAs, derived from tRNAs capable of silencing other genes in plants and if so, which genes do they target?**" In order to answer these questions, we first need to design a multi-step computational method that will help us decipher the details of this mRNA targeting mechanism and allow for identification of candidate genes to undergo silencing. This method will rely on programs that we plan to develop in house, as well as take advantage of existing open source software and will be put together in an easy to use package.


The results of this study will provide insight into the so far unexplored functionality of tRNA-derived fragments in plants by deciphering their targeting mechanism. Moreover, the methodology developed for this project will allow for further exploration of small non-coding RNAs in plants which utilize an alternative pathway of targeting than the one utilized by currently available analytical tools. There is no doubt that the demand for such techniques is strong, therefore the development of this method will be of immense impact to the plant sRNA community. It will also benefit the agricultural research in establishing protocols for production of crops with desired agronomic traits. The software created as part of the project will be provided free of charge under open source licenses and will benefit both academic and commercial users.