Computational prediction of interactions of long non-coding RNAs and micro RNAs in maize

Yan J.T. [1], Pronozin A.[2,3], Afonnikov D.[1,2,3]*

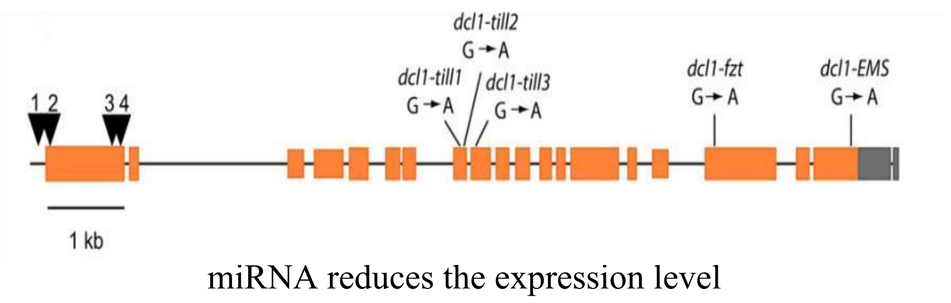
[1] Novosibirsk State University, Novosibirsk, Russia
[2] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
[3] Kurchatov Genomic Center of the Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia

** Corresponding author e-mail: t.yan5@g.nsu.ru*

Motivation and Aim

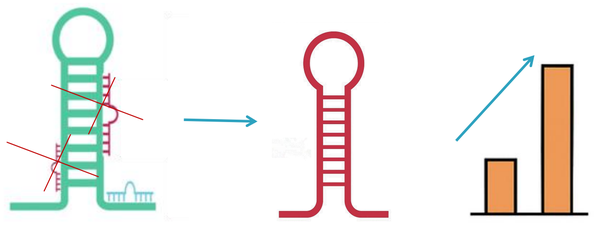
A large portion of the genome consists of non-coding regions, including long non-coding RNAs (lncRNAs) (>200 nt) and microRNAs (miRNAs) (22–24 nt). While miRNA–mRNA interactions have been well studied, miRNA–lncRNA interactions remain largely unexplored in plants. This study analyzed maize transcriptomes with the fuzzy tassel (*fzt*) mutation, which affects the structure of the Dicer-like1 (*DCL1*) gene, a key component of miRNA biogenesis. Compared to the wild type, the mutant plants exhibit reduced expression of certain miRNAs. We hypothesized that the targets of these miRNAs could be lncRNAs with increased expression in the mutant lines.

A deleterious mutation in the *Dicer-like1*

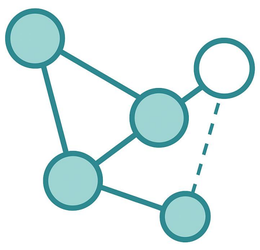


miRNA reduces the expression level

The candidate lncRNAs, predicted as miRNA targets, show elevated expression levels

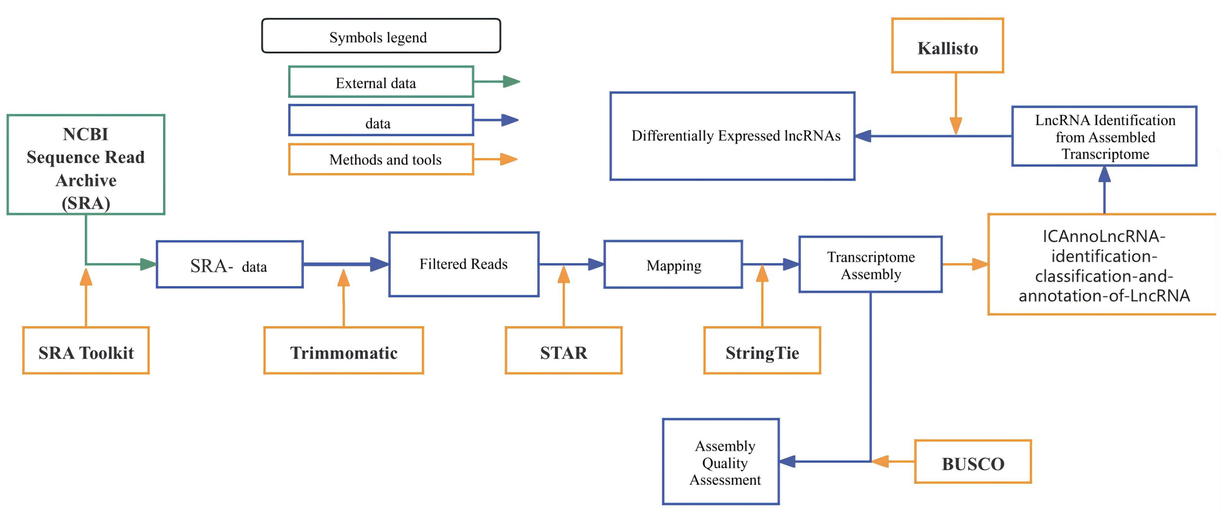


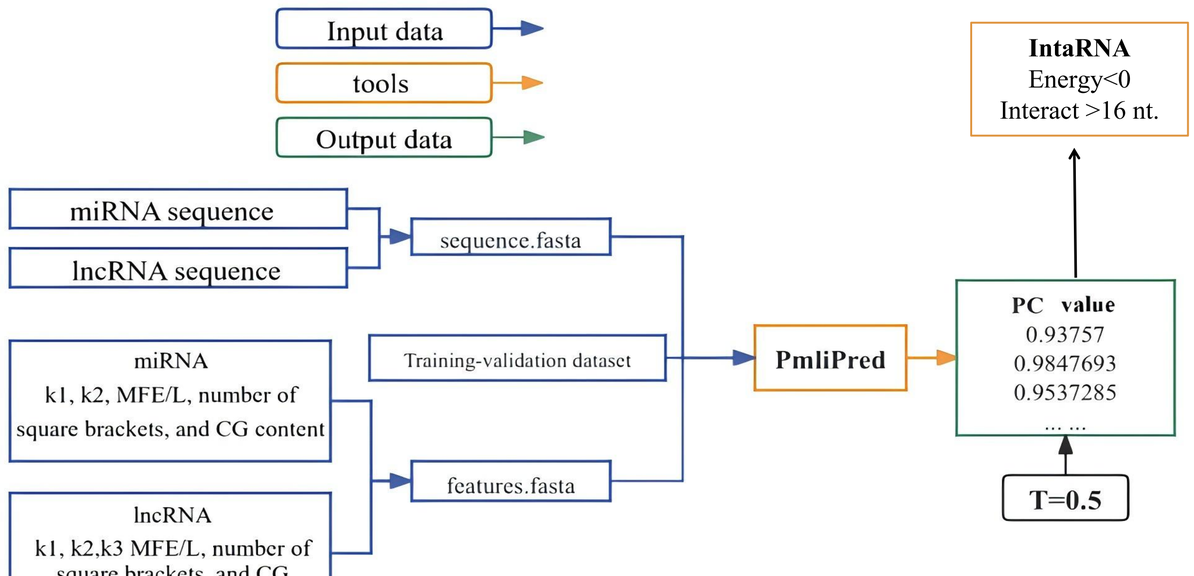
Prediction of miRNA–lncRNA interactions for candidate molecules allows for the evaluation of regulatory networks and interaction mechanisms.



Methods and Algorithms

This study developed a comprehensive bioinformatics analysis pipeline that integrates transcriptome assembly, lncRNA identification and classification, differential expression analysis, miRNA–lncRNA interaction prediction, result visualization, and interaction network construction, systematically uncovering the potential regulatory relationships between lncRNAs and miRNAs in maize.

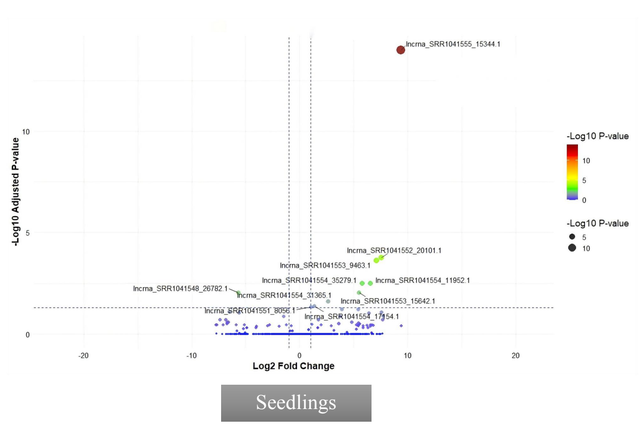




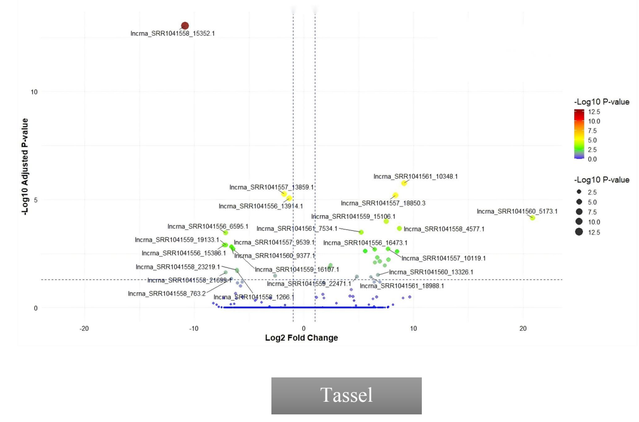
Results and Conclusions

By comparing shoot and tassel transcriptomes between wild-type and fzt mutant lines, we identified 9 and 20 lncRNAs, respectively, that showed increased expression in the mutant plants. Using computational methods, we predicted interactions between 14 lncRNAs and miRNAs with reduced expression in the mutants, and reconstructed an interaction network. Among these, we found that 9 lncRNAs interact with multiple miRNAs, indicating their potential role as competing endogenous RNAs (ceRNAs or “sponges”).

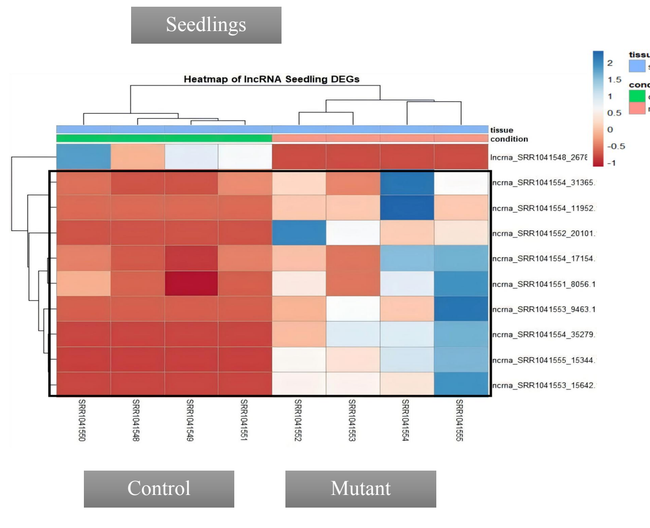
Differential expression of lncRNAs in maize tissues



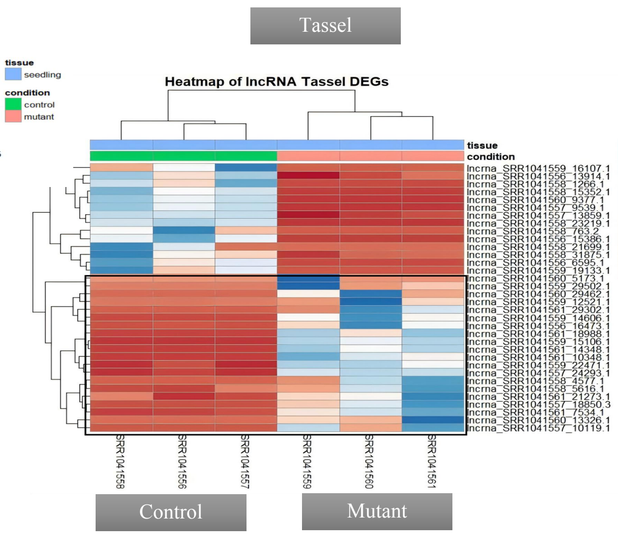
Seedlings



Tassel



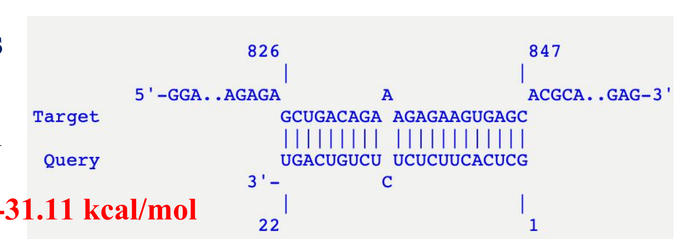
Control Mutant



Control Mutant

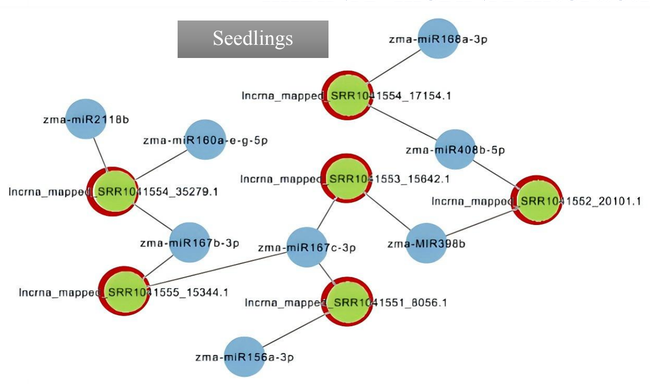
Examples of miRNA-lncRNA interactions predicted by the IntaRNA program

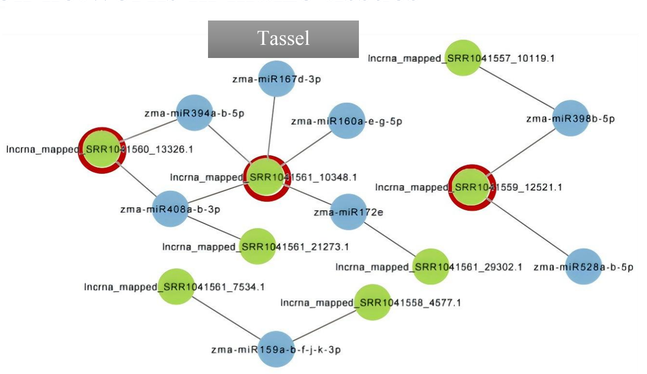
lncRNA: lncrna_mapped_SRR1041551_8056.1
miRNA: zma-miR156a-3p



Energy -31.11 kcal/mol

miRNA–lncRNA interaction networks in maize tissues





This work was supported by the state budget project No. FWNR-2022-0020