Genome-wide analysis of long non-coding RNAs responsive to multiple nutrient stresses in *Arabidopsis thaliana*

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Motivation and Aim: Nutrient stress is a most important environmental stress that limits plant growth and development. Although recent evidence highlights the vital functions of long non-coding RNAs (lncRNA) in response to single nutrient stress in some model plants, a comprehensive investigation of the effect of lncRNAs in response to nutrient stress has not been performed in *A. thaliana*. So we presented the identification and characterization of lncRNAs under seven nutrient stress conditions.

Methods and Algorithms: Raw data from previously RNA-seq datasets were downloaded from NCBI SRA, including 14 nutrient stress samples and 12 untreated control ("normal") samples. After processing these raw data, we identify lncRNAs, construct ceRNA network based on the crosstalk of miRNAs and their target, built a stress-related co-expression network based on 14 stress samples.

Results: The expression pattern analysis revealed that aberrant expression of lncRNAs is a stress-specific manner under nutrient stress conditions, and that lncRNAs are more sensitive to nutrient stress than protein coding genes (PCGs). Moreover, competing endogenous RNA (ceRNA) network and lncRNA-mRNA co-expression network (CEN) were constructed to explore the potential function of these lncRNAs under nutrient stress conditions. We further combined different expressed lncRNAs with ceRNA network and CEN to selected key lncRNAs in response to nutrient stress.

Conclusion: Our results suggest that lncRNAs play a significant role in the response of nutrient stress in *A. thaliana*. The integrative analysis of ceRNA network and CEN may provide important information for further insights into the role of lncRNAs in response to stress in plants.