

Genome-Wide Analysis of Nitrate Transporter (NRT/NPF) Family in Sugarcane *Saccharum spontaneum* L.

Background/objective

Plants take up nitrogen in the form of nitrate, which is vital for plant growth and development. Nitrate can then be absorbed and translocated through transmembrane proteins, primarily in the Nitrate Transporter (NRT)/Peptide Transporter family (NPF). Understanding nitrogen uptake, translocation, and utilization is key to improve nitrogen-use efficiency (NUE) through conventional breeding and genetic engineering strategies. The nitrate transporter family makes for a promising target for improving NUE in sugarcane due to its function in governing nitrogen uptake and distribution in plants.

Approach

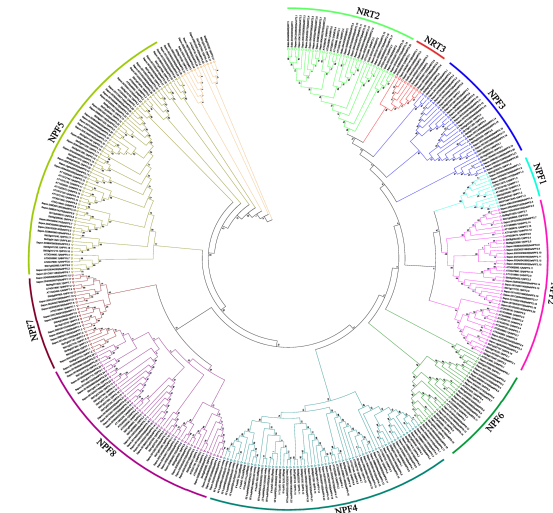
- ❖ Researchers conducted the largest comprehensive analysis to date of NRT/NPF genes at a genome-wide scale in a single plant genome (*S. spontaneum*), which included a BLAST search, phylogenetics, gene structure, protein motif analysis, and RNA-seq data analysis.

Results

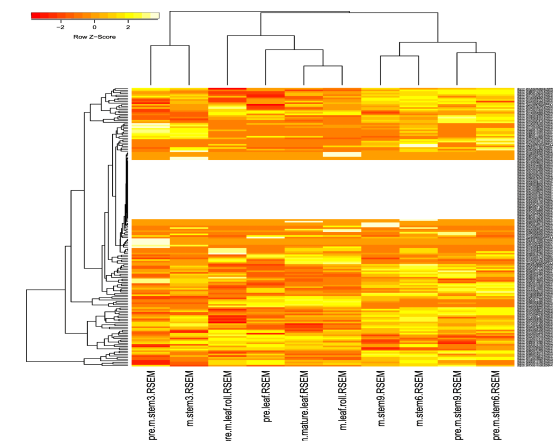
- ❖ The team identified NPF/NRT genes in sugarcane: 178 NPF genes, 20 NRT2 genes, and 6 NRT3 genes.
- ❖ Both SsNPF and SsNRT3 genes showed diversified gene structures and expression patterns, suggesting the possibility to fine-tune the homeostasis of nitrate to cope with the changing environment.

Significance

- ❖ This research provides a genetic foundation for future work in molecular and physiological functions of sugarcane nitrate transporters.
- ❖ The NRT/NPF genes identified provide the basis for further research of nitrate transporter functions in sugarcane to help optimize nitrogen management in bioenergy crops.



Phylogenetic relationship of NRT/NPF proteins among *Arabidopsis*, *Sorghum*, and *Saccharum*.



Heat map of tissue-specific expressions of NRT/NPF genes from *Saccharum*.