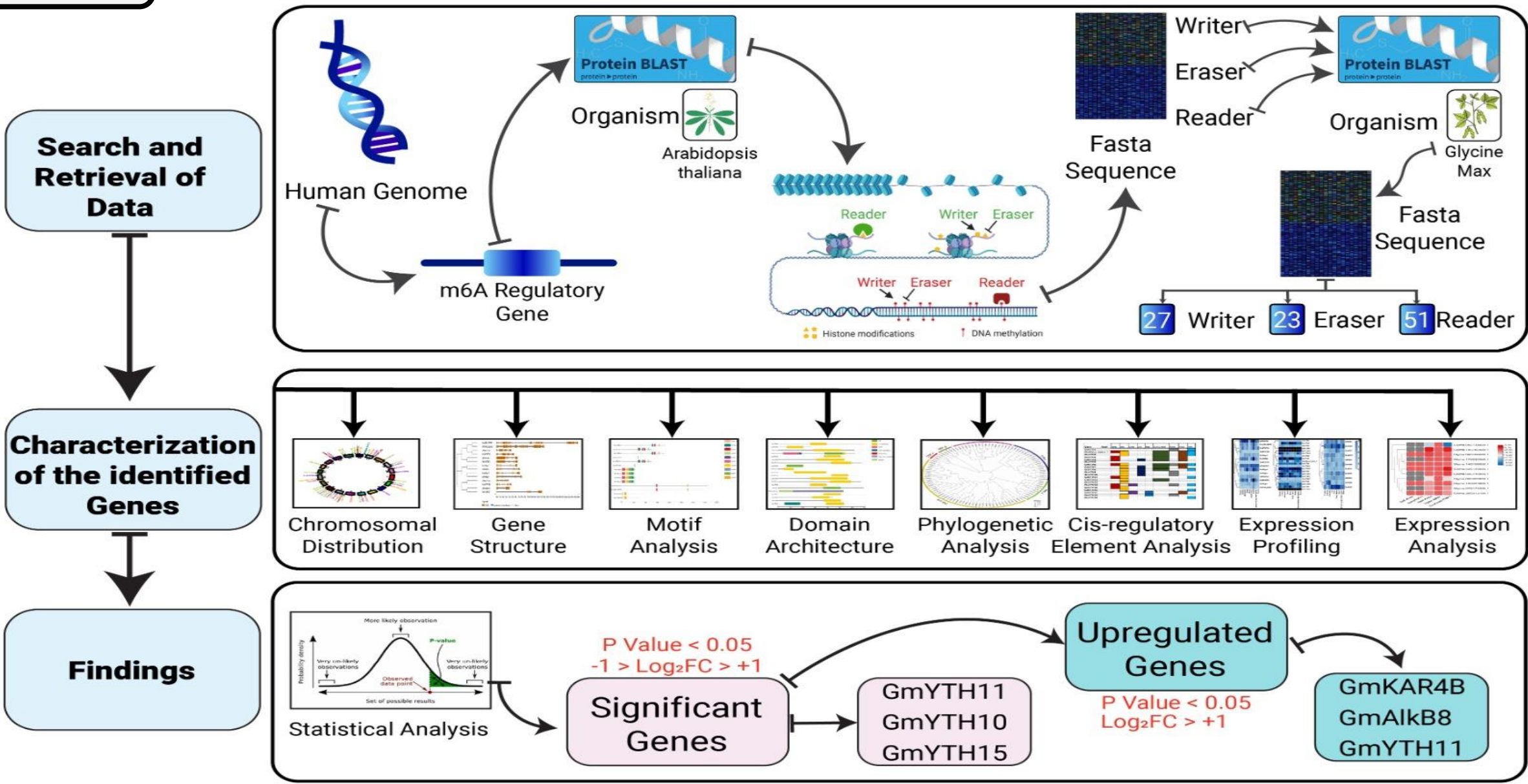




Comprehensive Genome-Wide Identification of Epitranscriptomic Methylation Marker Genes in Glycine Max, and Their Expression Profiling in Various Anatomical Tissues and Perturbation Conditions

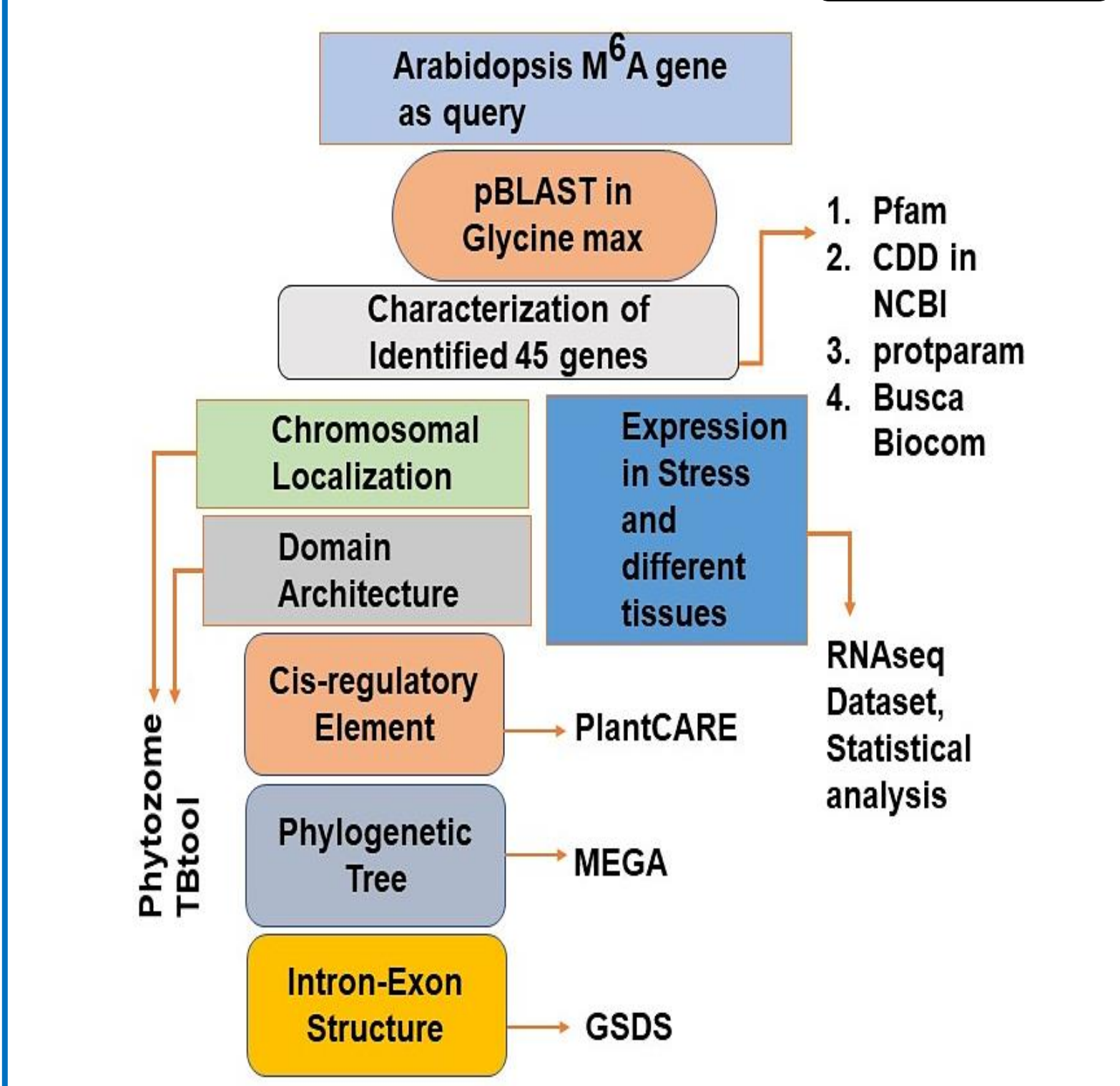
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Abstract



Soybean (*Glycine max*) is one of the major vegetable protein and oil-producing legume plants. various environmental stresses could shorten the flowering and seed-filling periods of soybean, and thus accelerate senescence and reduce productivity. The available soybean genome database prompts us to identify novel stress-modulating genes.

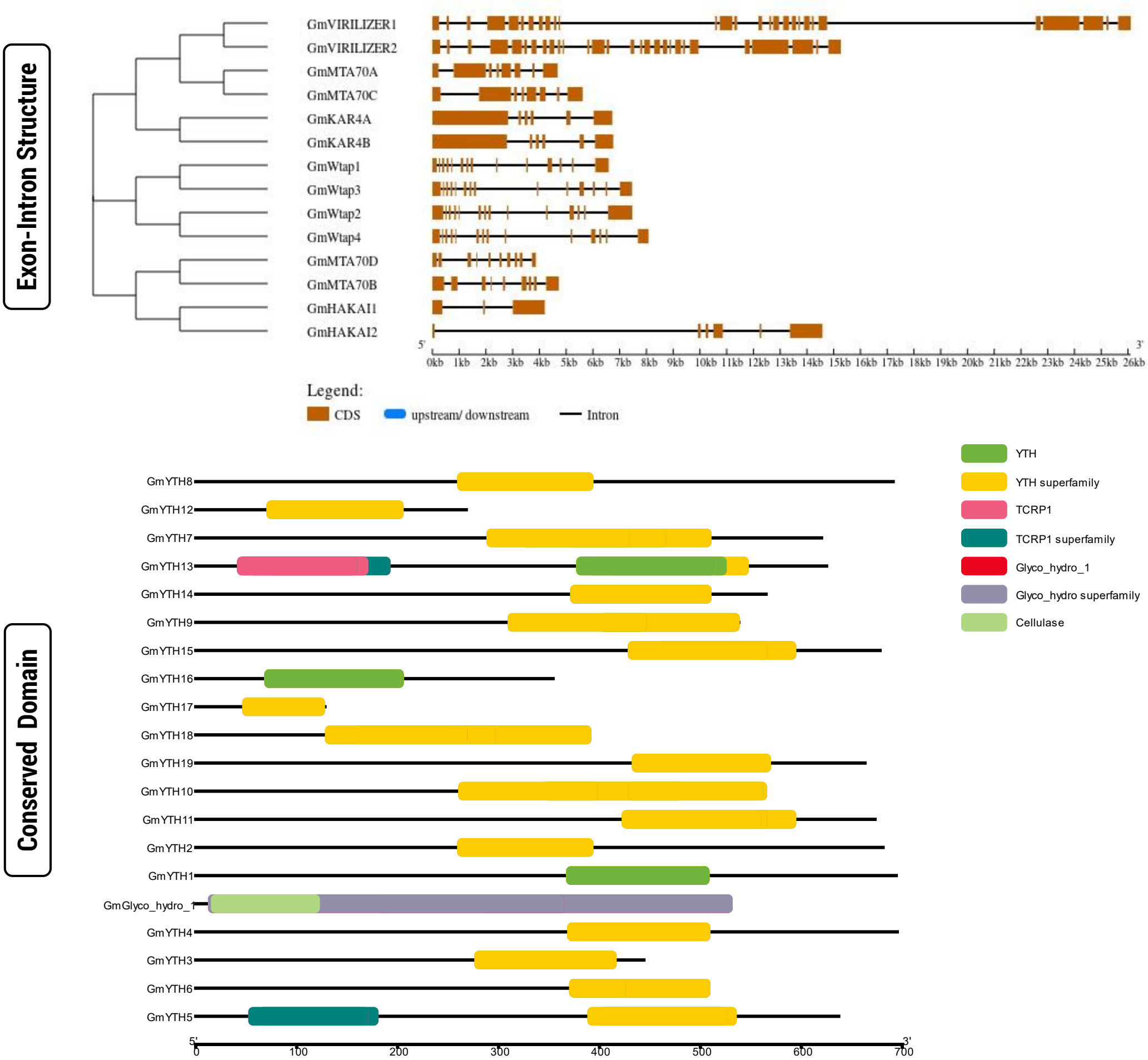
Method



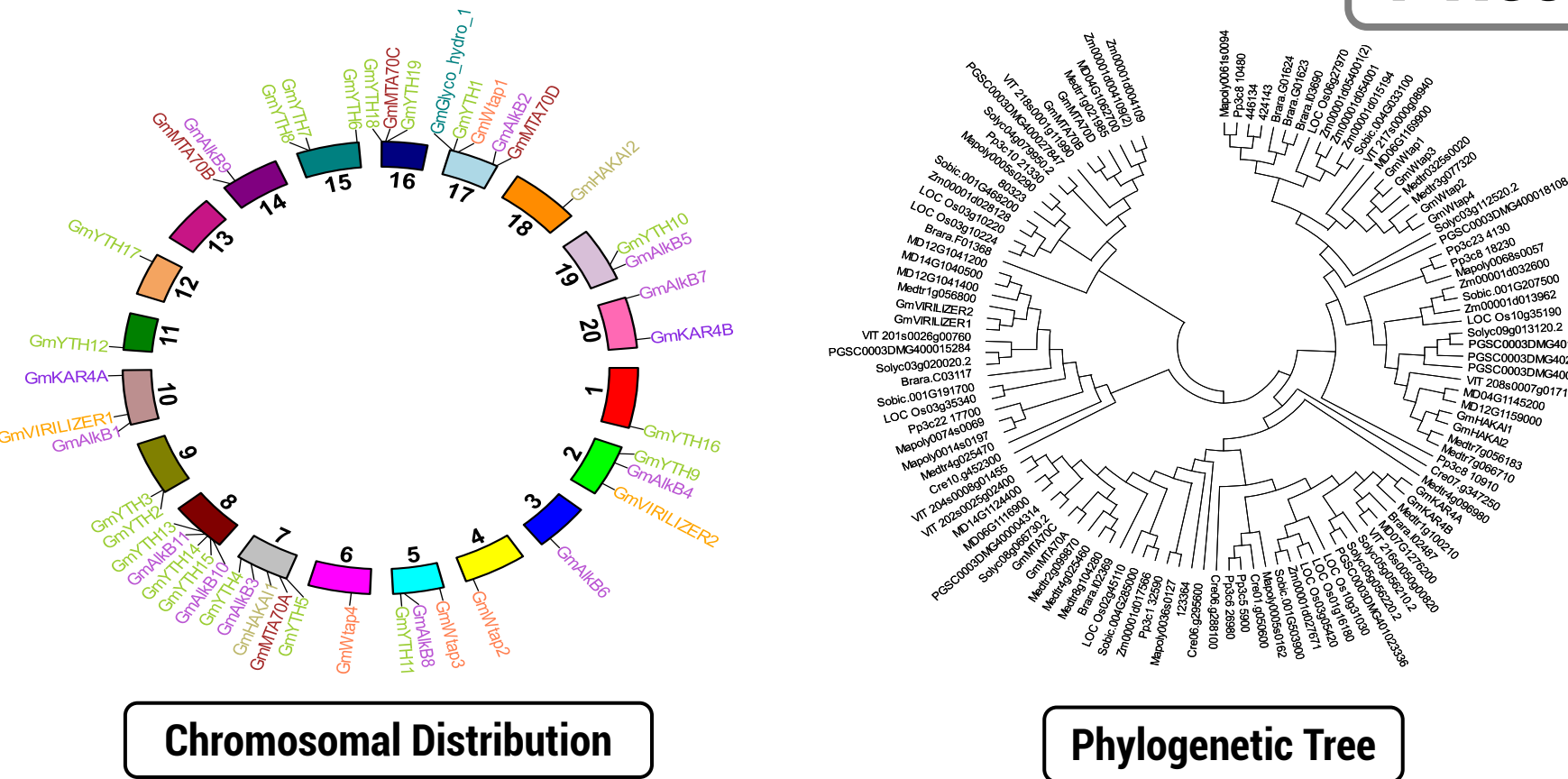
Study Objectives

This present study aims to identify m6A regulatory genes in Soybeans and their correlation with stress conditions.

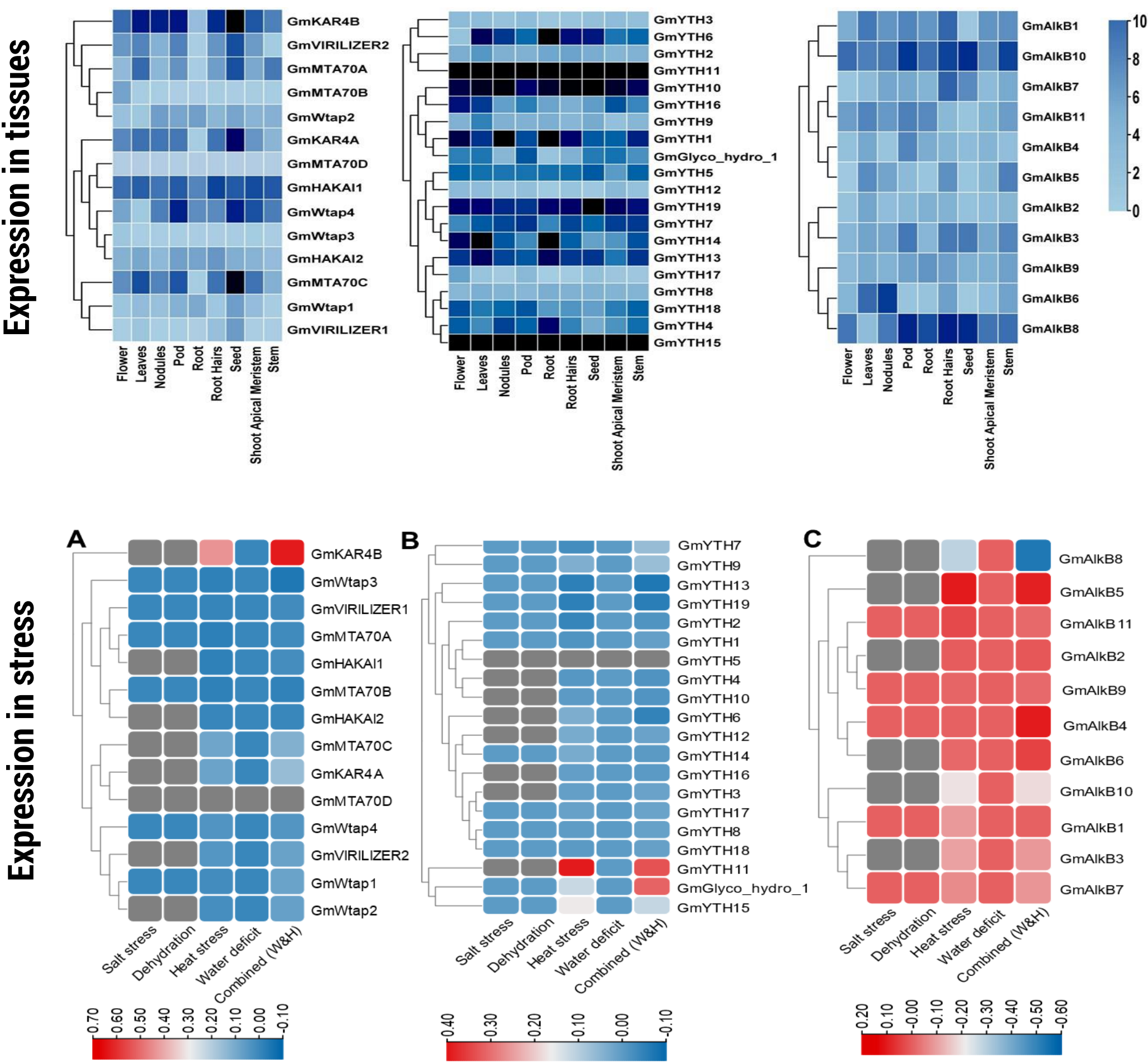
2.Results



1.Results



3.Results



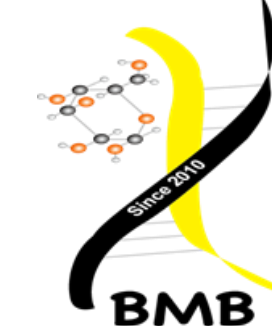
Conclusion

1. A genome-wide identification of m6A regulatory genes has been conducted in the soybean.
2. Detailed analysis of the identification genes, chromosomal location, phylogenic relationship, and presence of cis-regulatory elements have been performed.
3. Expression profiling in different anatomy has revealed the regular RNA methylation pattern in various plant tissues.
4. Glycine max's stress tolerance pathway could be explored for molecular and functional characterization.

Future Aspects

This study will encourage researchers to functionally validate and elucidate the molecular mechanism of plants utilizing RNA methylation in stress tolerance, thus, facilitating crop engineering.

Acknowledgment



Related Articles

Nishat, Z. S., Hasan, M. S., Islam, M. S., Hossain, T., & Ghosh, A. (2022). Identification of epitranscriptomic methylation marker genes in Arabidopsis and their expression profiling in response to developmental, anatomical, and environmental modulations. *Current Plant Biology*, 30(March), 100247. <https://doi.org/10.1016/j.cpb.2022.100247>