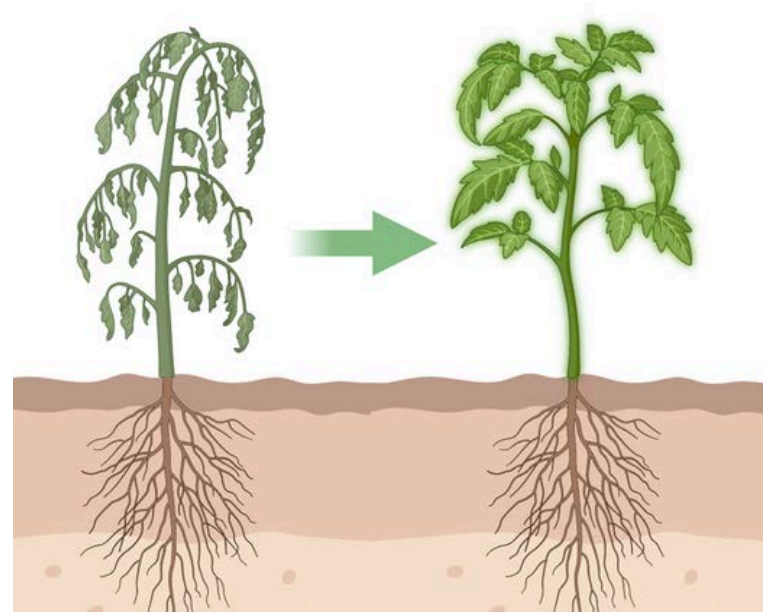


INTRODUCTION

- Water scarcity poses a major challenge to tomato cultivation, as water stress triggers a cascade of physiological disturbances that compromise plant development, yield and fruit quality.



OBJECTIVE

- This research explored physiological and molecular adaptations to water stress in a diverse GWAS panel of 152 tomato accessions.



METHODOLOGY

- Cultivation of Tomato.
- Metabolomics of red ripened fruit (GS-MS and LC-MS).
- Genome Wide Association Studies.
- Functional studies.



RESULTS

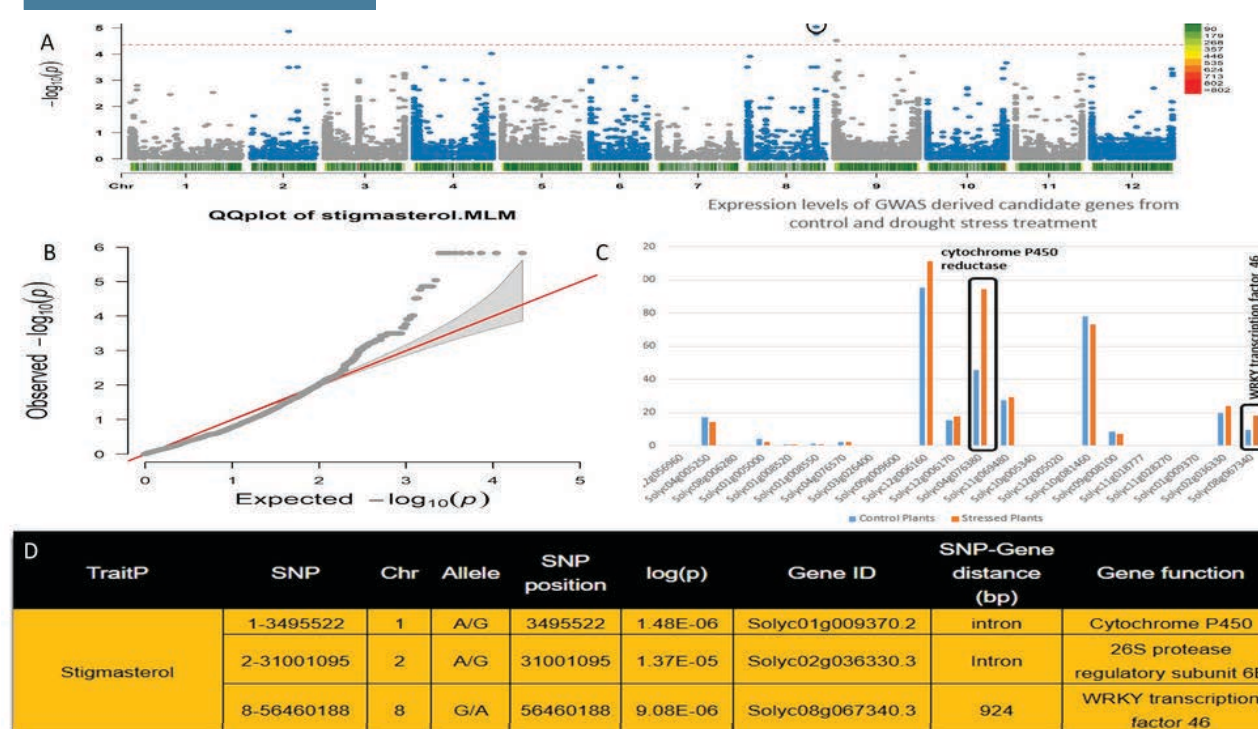


Figure 1 GWAS and Transcriptomics. A, Manhattan plot visualizes SNP associations across the genome. Peaks indicate genomic regions associated with the trait. B, QQ plot compares observed and expected p-values to assess the overall quality of the GWAS results and check for population stratification. C, Bar graph illustrating the expression levels of GWAS-derived candidate genes under control and stress treatment. D, Table summary of SNPs associated with stigmasterol accumulation in tomato.

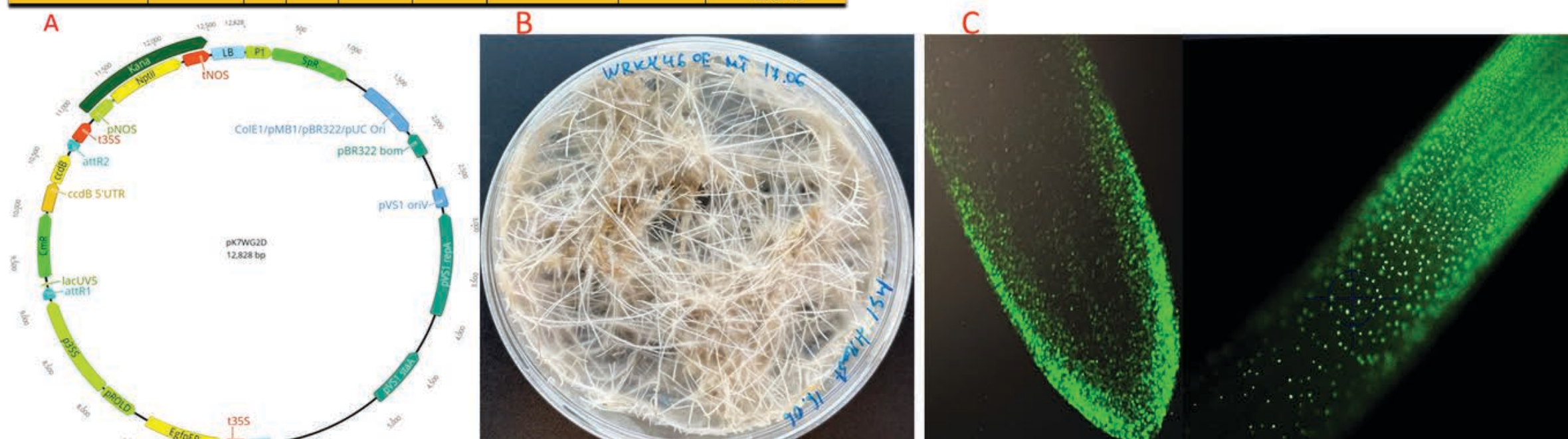


Figure 2. Tomato leaves (money maker) Stable transformation. A, Destination vector pK7WG2D. B, Advanced stage of hairy root formation directed by *Rhizobium rizogenes* 15834. C, Hairy root expressing GFP.

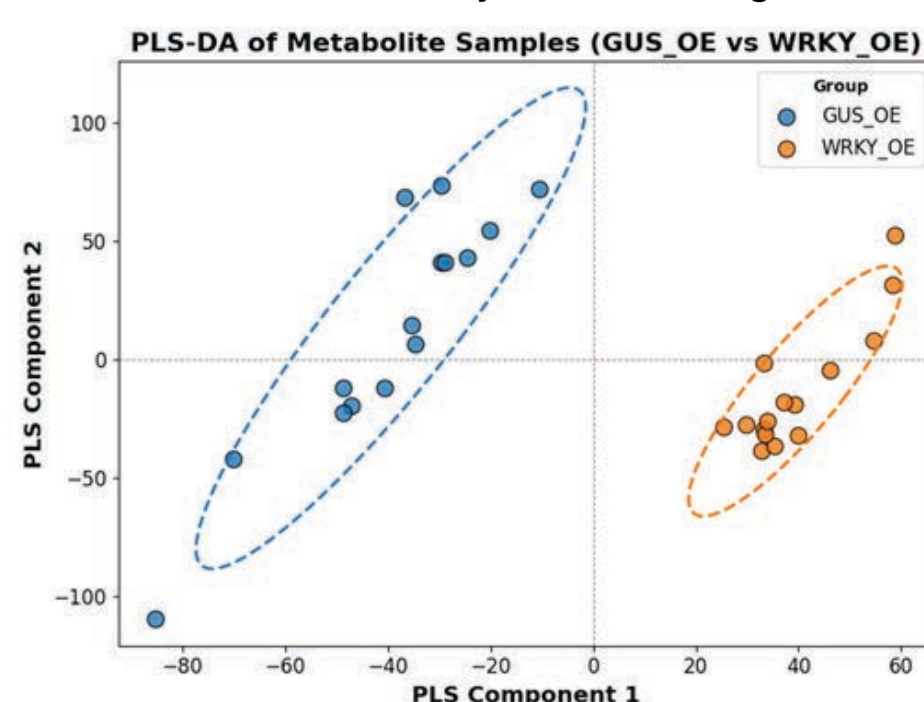
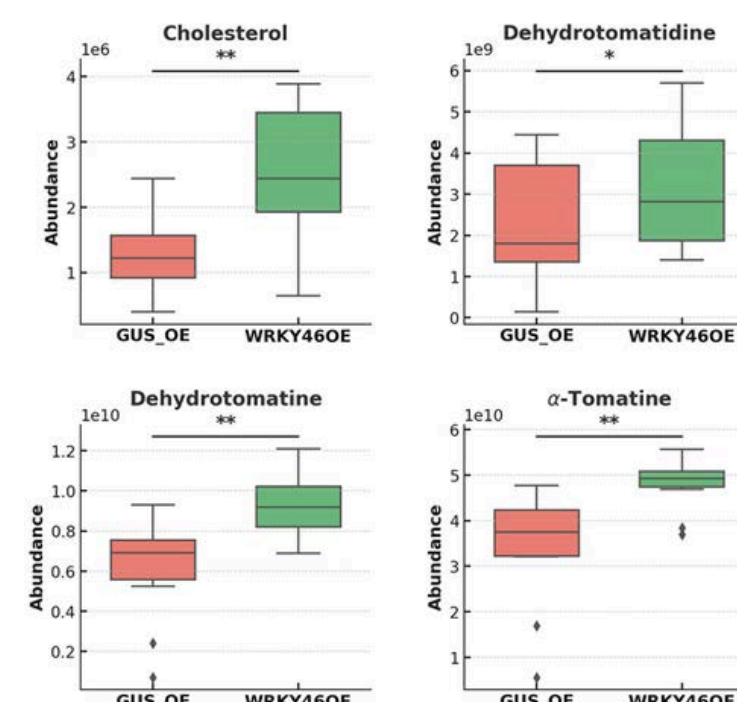


Figure 3. PLS-DA of LC-MS profiles from GUS-OE (blue) against SIWRKY46-OE (orange) tomato hairy-root lines

Figure 4. Boxplot graph comparing four SGA (steroidal glycoalkaloid) biosynthetic pathway components in GUS-OE against SIWRKY46-OE hairy roots



CONCLUSION

This study provides a comprehensive, multi-layered analysis of the tomato's response to water stress, integrating metabolic, and genetic data to uncover the molecular architecture of drought tolerance. A pivotal finding was the identification and functional validation of the transcription factor *SIWRKY46* in relation to water stress.

ACKNOWLEDGEMENTS

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