



Integrative Genomic and Metabolomic Analysis Reveals Key Loci for Tomato Fruit Quality under Water Stress

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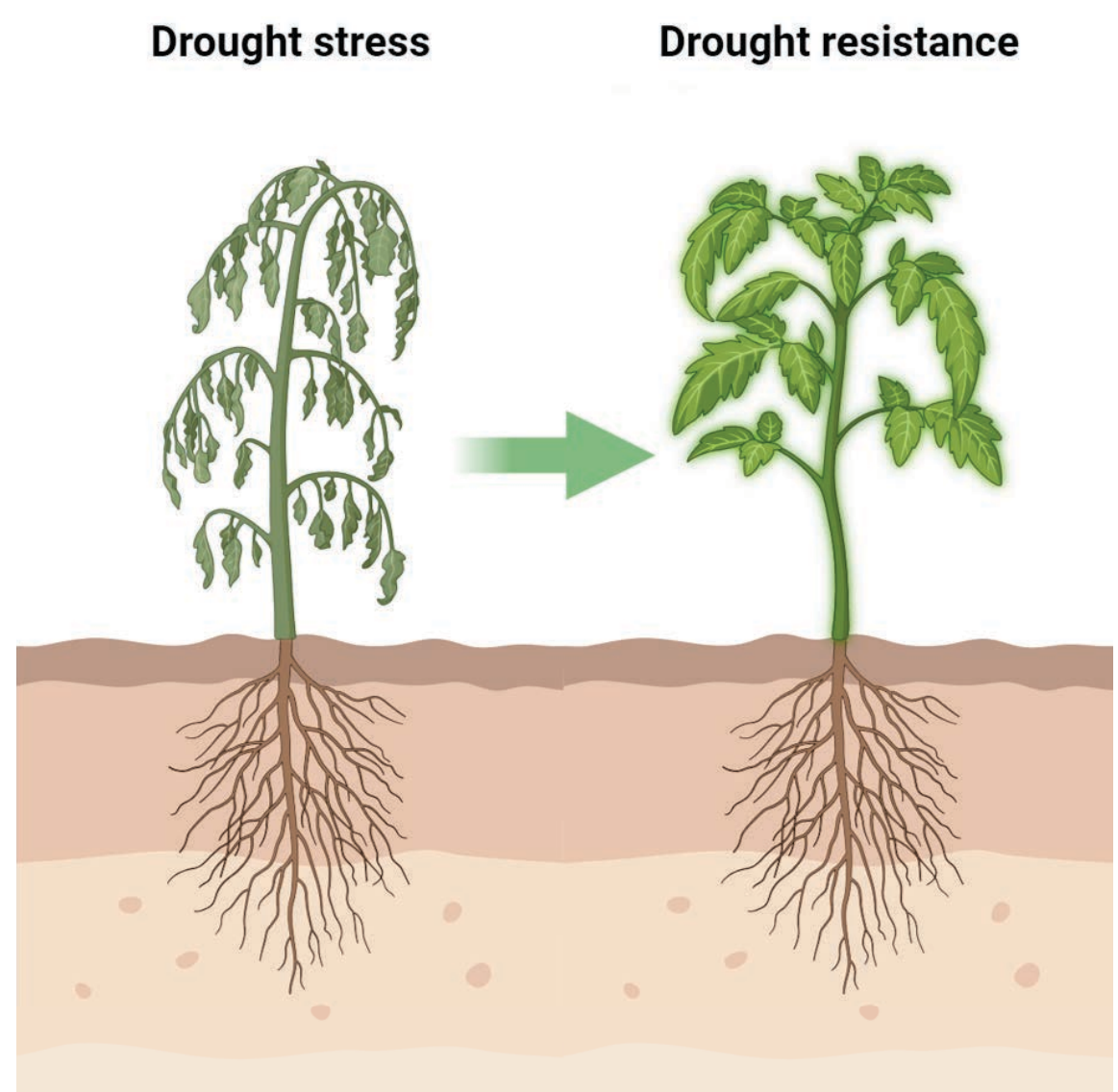
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INTRODUCTION

✓ *Solanum lycopersicum* (tomato) is one of the most important horticultural plants commonly consumed in the human diet

✓ Water stress disrupts critical physiological processes such as photosynthesis, respiration, and stomatal regulation thereby limiting plant growth and productivity



OBJECTIVES

✓ In this study, we evaluated a diverse panel of 152 tomato accessions grown under well-watered and water stress conditions to elucidate the genetic basis of metabolic reprogramming associated with fruit quality.

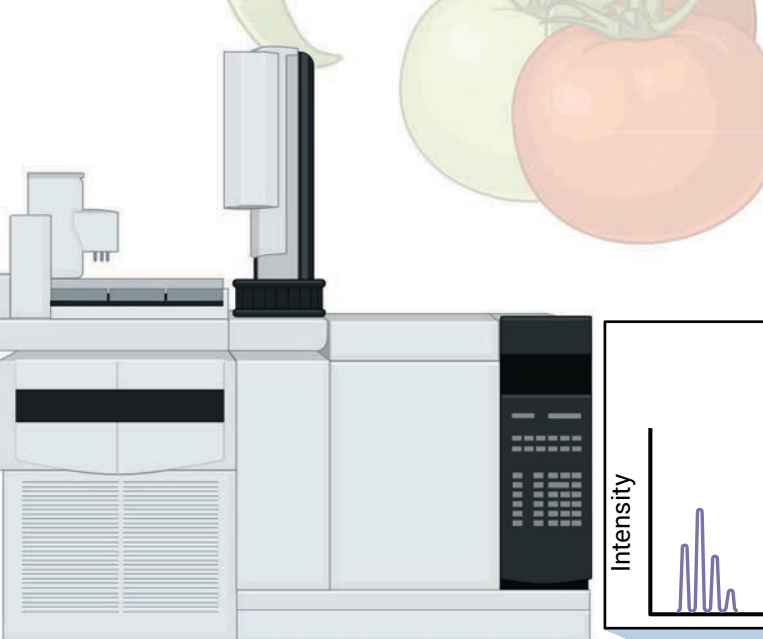
METHODS

Water Stress

I. Tomato cultivation, physiological parameters and phenotyping



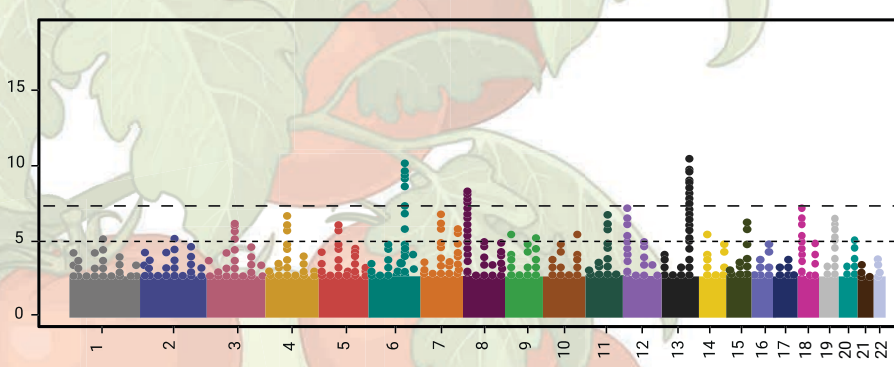
II. Metabolomics: Metabolite extraction from fruits, GC-MS, and LC-MS



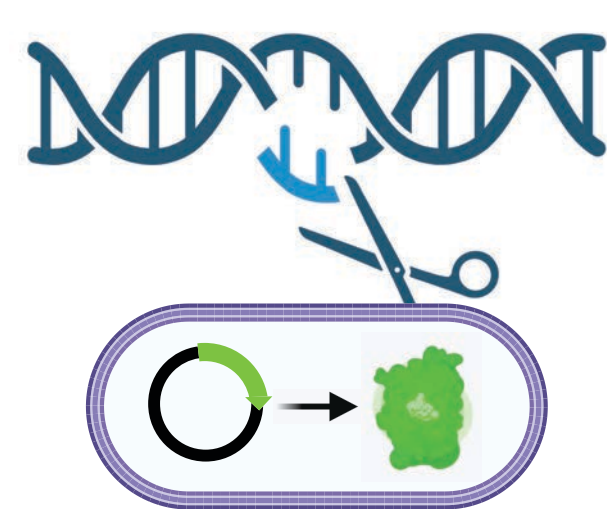
III. GWAS analysis

✓ Genotyping: SNP arrays or NGS for genome-wide genotyping

✓ Analysis: Statistical models (MLM, CMLM, GLM) for genotype-phenotype associations.



IV. Functional Studies



RESULTS

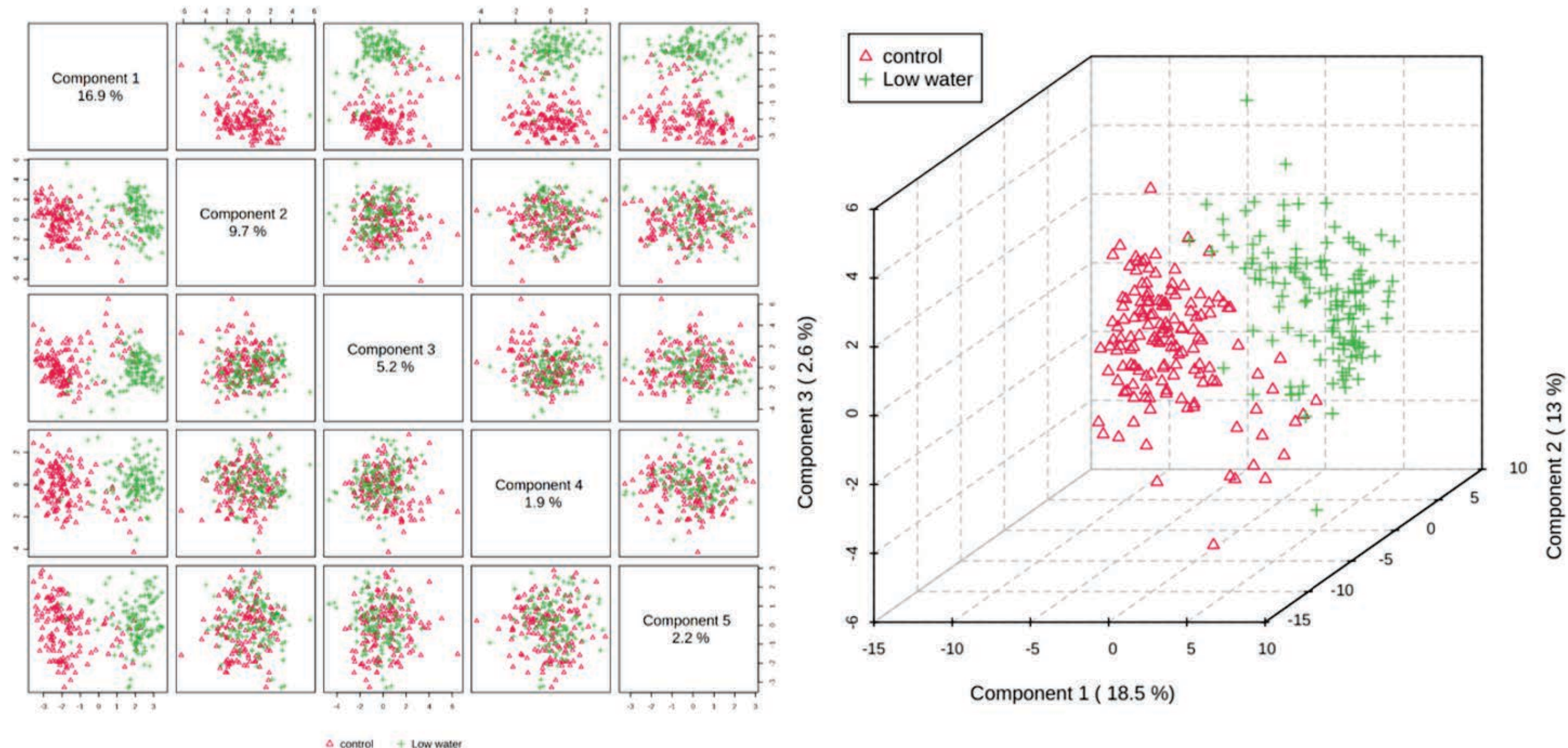


Figure 1. Metabolite profiling of the tomato fruits at red ripe stage of the 152 GWAS accessions under control and low water stress was performed by GC-MS analysis. PLS-DA (partial least squared discriminant analysis) revealed significant accumulation of stress-specific metabolites

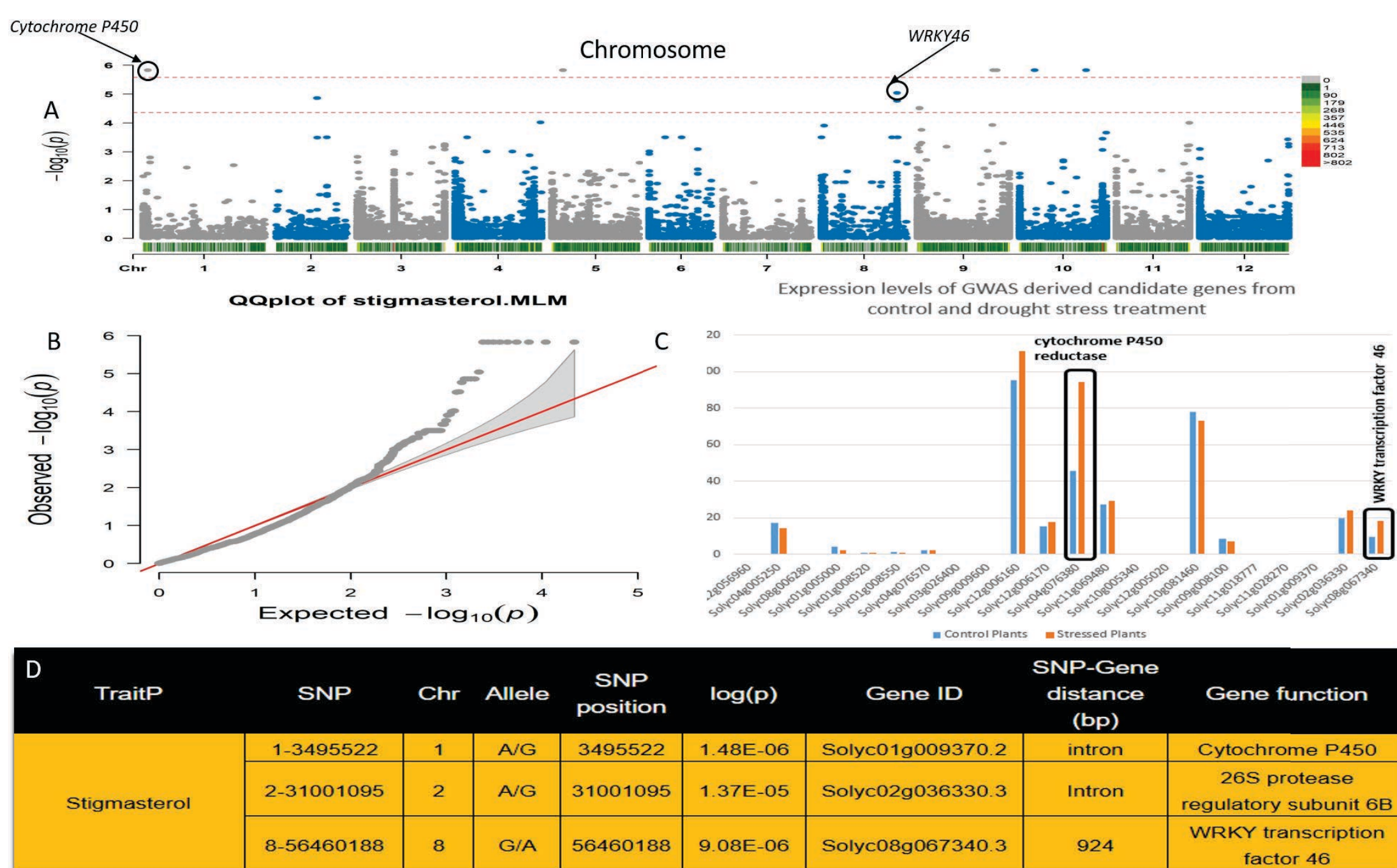


Figure 3. GWAS and Transcriptomics. A, Manhattan plot visualizes SNP associations across the genome. Peaks indicate genomic regions associated with the trait. B, QQ plot compares observed and expected p-values to assess the overall quality of the GWAS results and check for population stratification. C, Bar graph illustrating the expression levels of GWAS-derived candidate genes under control and stress treatment. D, Table summary of SNP associated with stigmasteryl accumulation in tomato.

CONCLUSION

✓ Our integrative approach combining association mapping, transcript profiling, and functional validation provides a robust framework for unraveling the molecular mechanisms underlying metabolic adjustments in tomato under water limited conditions.

✓ Our findings present promising targets for marker-assisted selection and metabolic engineering, contributing valuable insights toward sustainable crop improvement strategies under challenging environmental conditions.

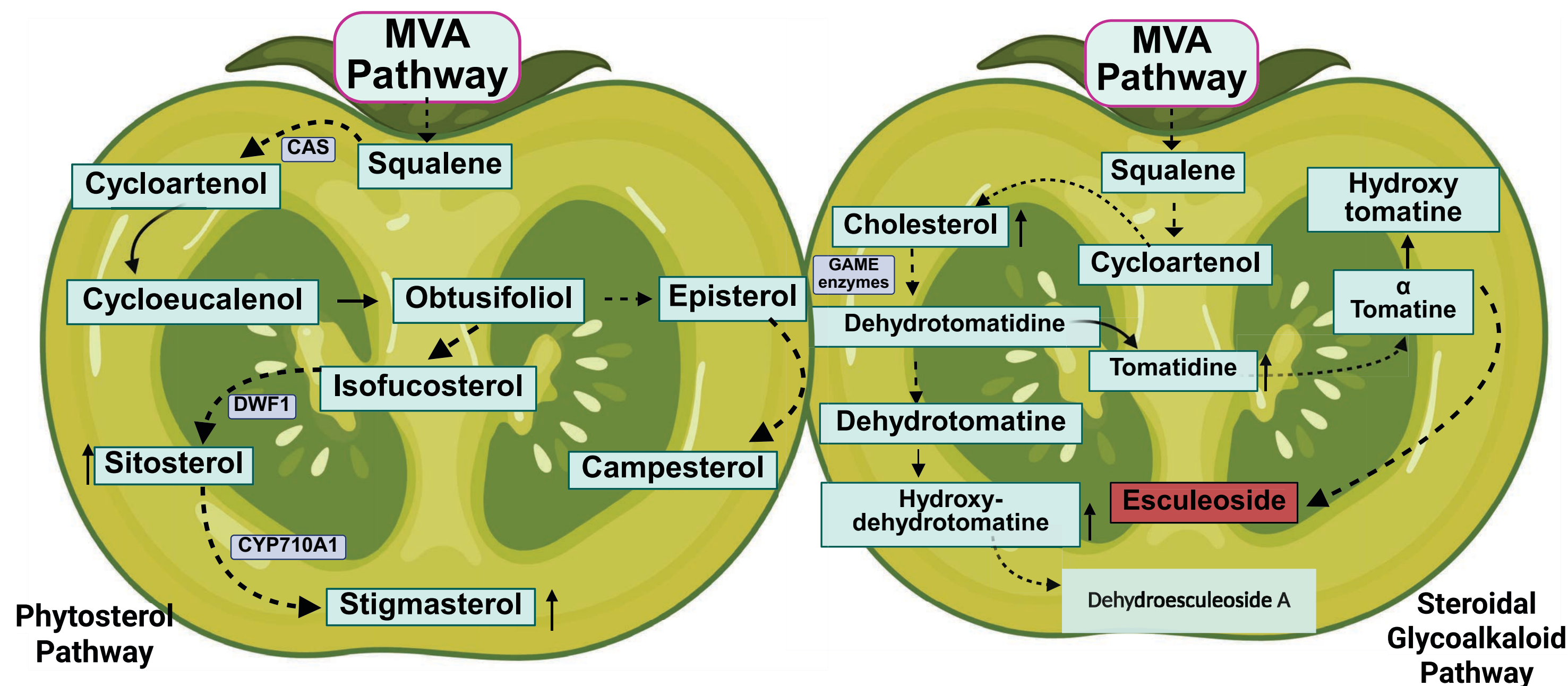


Figure 2. Simplified representation of phytosterol and steroidal glycoalkaloid pathways.

Genome-wide association mapping using 122,222 single nucleotide polymorphisms identified robust associations between metabolic variation and candidate genes, notably *WRKY46* and a *cytochrome P450 monooxygenase*. Transcript analysis confirmed a significant upregulation of both *WRKY46* and the *cytochrome P450* gene in response to water stress, highlighting their active involvement in sterol biosynthetic pathway during stress conditions.

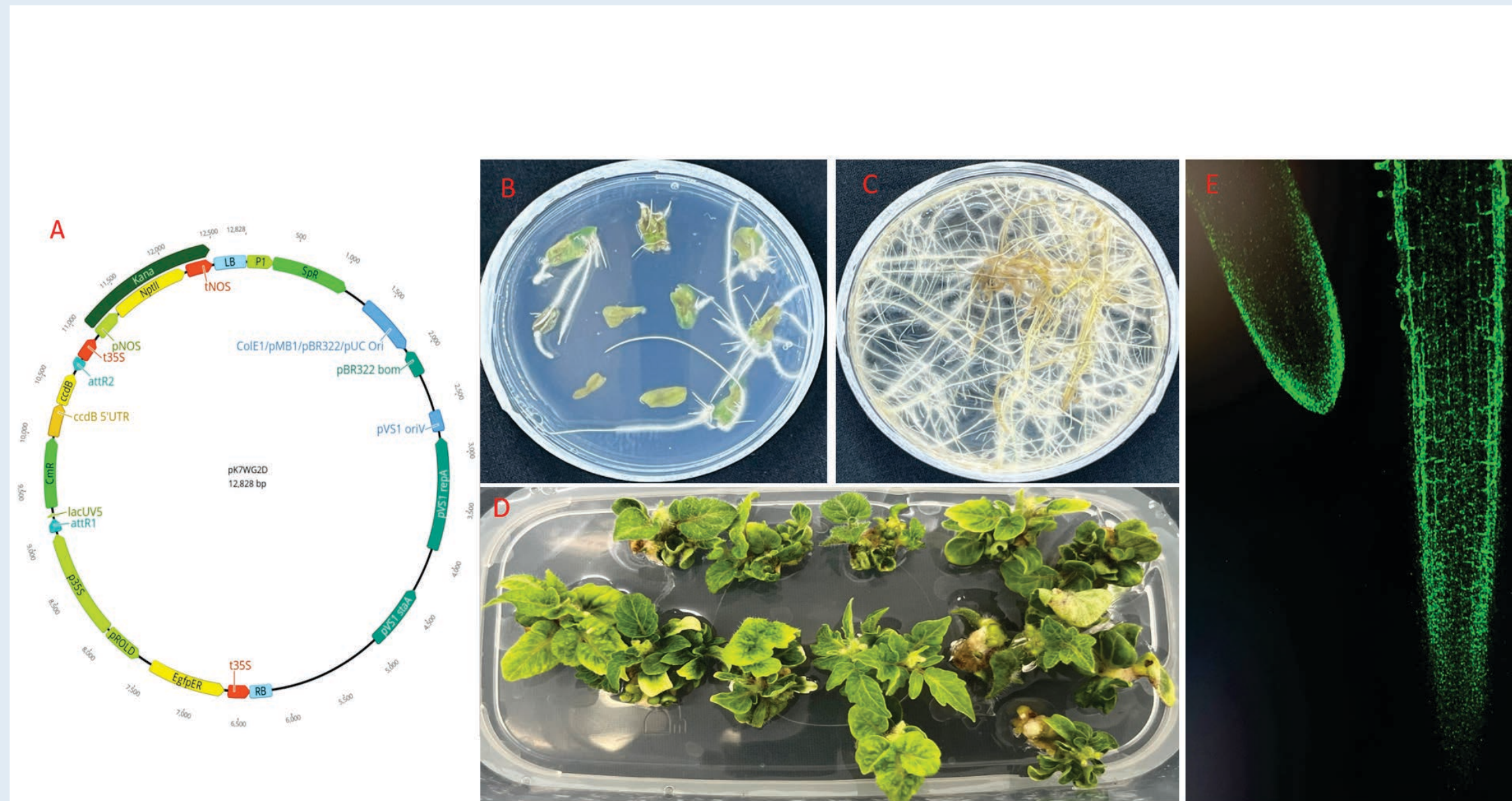


Figure 4. Tomato leaves (money maker) Stable transformation. A, Destination vector pK7WG2D. B, initial transformation with *Rizobium rizogenes 15834*. C, Advanced stage of hairy root formation directed by *Rizobium rizogenes 15834*. D, Stable transformation with *Agrobacterium tumefaciens GV3101*. E, Hairy root expressing GFP.

Drought stress can lead to change in the metabolic pathways related to phytosterols and steroidal glycoalkaloids. This changes can significantly affect the flavour, quality and the nutritional value of tomato fruits

Although hairy root overexpression lines of *WRKY46* in tomato cultivar 'Moneymaker' provide a rapid and generally reliable system for functional validation, the results were not reproducible for metabolite quantification. Consequently, stable transgenic lines overexpressing *WRKY46* were subsequently generated to enable more comprehensive and heritable analysis of metabolic traits.

ACKNOWLEDGEMENTS

This work was funded by project NatGenCrop, Grant agreement N° 101087091, and the European Regional Development Fund through Programme Research Innovation and Digitalisation for Smart Transformation, Grant agreement N° BG16RFPR002-1.014-0003-C01