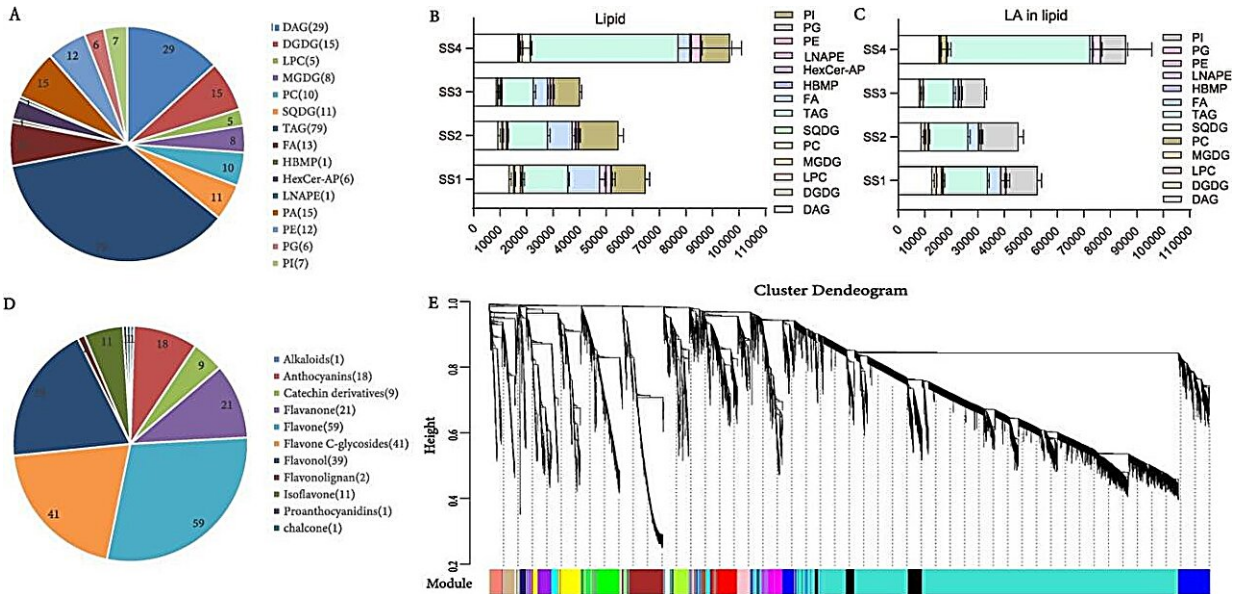


Unveiling the genetic blueprint of safflower

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Metabolites of lipid and flavonoids and the transcriptome profile analysis. A Lipid composition and the parentheses refer to the number of this ingredient. B Lipid composition of seeds at four developmental stages. C LA content in each kind of lipid. D Flavonoid composition and related numbers. E Co-expression network analysis on all the transcriptome data of safflower using WGCNA and 20 modules, including 15, 769 genes. Credit: The authors

A research team has completed a high-quality chromosome-scale assembly of the Chuanhonghua 1 safflower genome. This work sheds light on the genetic underpinnings of crucial traits like linoleic acid (LA) and hydroxysafflor yellow A (HSYA) production. It sets a new precedent for crop improvement and functional genomics studies.

Safflower (*Carthamus tinctorius* L.), a plant known for its vibrant flowers and nutrient-rich seeds, has been cultivated for thousands of years in the fertile crescent region. It is highly regarded for its oil, rich in LA; and its flowers, which contain HSYA, substances with wide-ranging industrial and medicinal applications. Despite its value, [genetic research](#) on safflower has been constrained by the limited understanding of its genome.

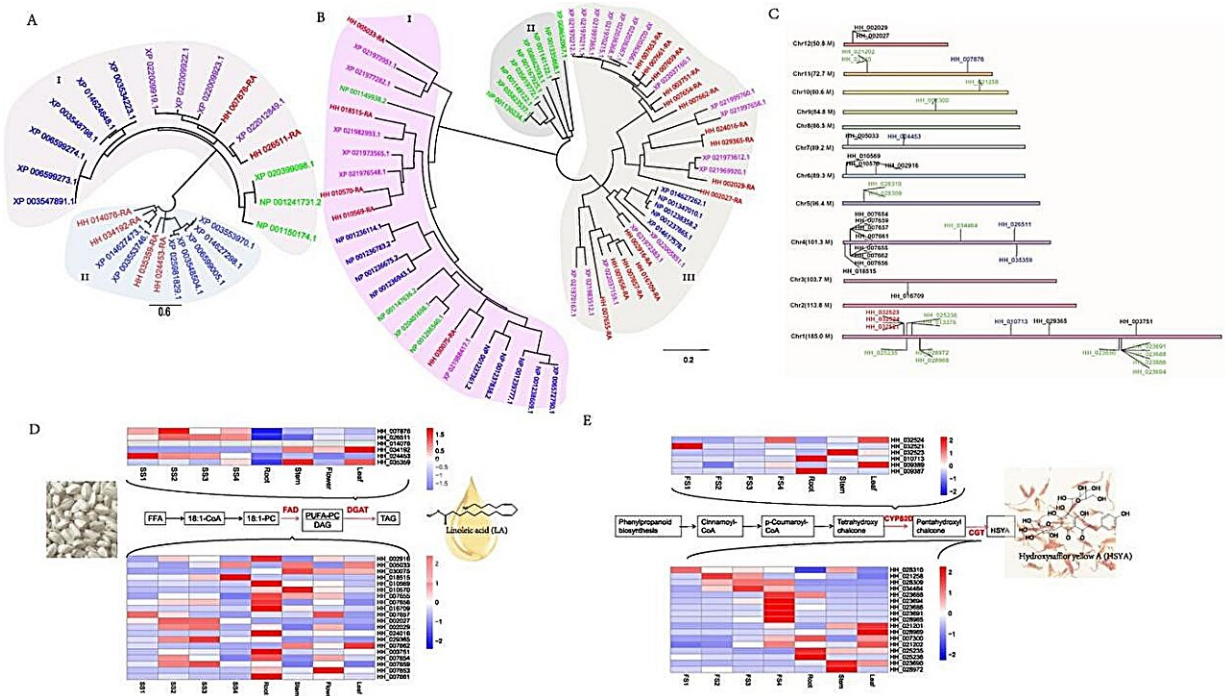
A study [appearing](#) in *Horticulture Research* elucidates the genetic underpinnings of safflower, thus paving the way for targeted breeding strategies.

The research team employed an integrated sequencing strategy combining Illumina, Oxford Nanopore, and Hi-C technologies to achieve a high-quality genome assembly of 1.17 Gb with contigs assigned to 12 chromosomes, reflecting about 100-fold coverage relative to the estimated genome size. This assembly facilitated the identification of a recent whole-genome duplication event, underpinning the extensive genomic rearrangements and evolutionary history of safflower, corroborated by [phylogenetic analysis](#) using 274 single-copy genes across 12 species, and a detailed examination of gene family expansion and contraction.

Metabolomic and transcriptomic profiling across different developmental stages of seeds and flowers revealed a comprehensive lipidome with a predominant presence of triacylglycerols (TAGs) and a diverse flavonoid metabolite spectrum, respectively, highlighting the biosynthetic pathways of key compounds such as LA and HSYA. Through genomic analysis, the researchers predicted 39,809 [protein-coding genes](#), with substantial annotation against public databases, and identified specific gene families—diacylglycerol acyltransferase (DGAT) and fatty acid desaturases (FADs) for LA biosynthesis, and CYP and CGT for HSYA biosynthesis—indicating their pivotal roles in

these metabolic pathways.

Notably, the re-sequencing of 220 safflower lines yielded 7,402,693 high-quality SNPs, facilitating a [genome-wide association study](#) (GWAS) that pinpointed significant SNPs associated with agronomic traits, particularly oil content and flower color. This GWAS analysis, along with the functional verification of the candidate gene HH_034464 (CtCGT1), implicated in HSYA biosynthesis, underscored the potential of molecular markers in enhancing breeding programs for desired traits. The functional assays confirmed CtCGT1's role in the glycosylation of flavonoids, crucial for HSYA production, thereby shedding light on the genetic underpinnings of key metabolic traits in safflower.



Genetic and expression analysis of the genes for LA and HSYA biosynthesis. A Phylogenetic analysis of DGATs. I represents subfamilies of DGAT2. II represents subfamilies of DGAT1. Green color indicates DAGTs from *Z. mays*. Blue indicates DGATs from soybean. Purple indicates DGATs from *H. annuus*.

Red indicates DGATs from safflower. B Phylogenetic analysis of FAD2. Colors have the same meanings as for DGATs. C Chromosome distribution of candidate genes. Green indicates genes for CGTs, red for CYPs, blue for DAGTs, and black for FAD2. D Gene expression for DGATs. E Gene expression for FAD2. F Gene expression for CYPs. G Gene expression for CGTs. Credit: The authors

Dr. John Smith, an expert in plant genomics, praised the achievement, stating, "This comprehensive genome assembly is a milestone in safflower research. It not only enhances our understanding of plant evolution but also provides a rich resource for identifying genes responsible for key agricultural and medicinal traits."

By providing a foundation for the molecular breeding of safflower, this research offers the potential to enhance crop resilience, nutritional content, and therapeutic efficacy. Looking forward, the challenge lies in leveraging this vast genomic resource to develop superior safflower varieties that meet the demands of a changing global climate and growing population.

The chromosome-scale genome assembly of the Chuanhonghua 1 safflower represents a critical step forward in the genetic exploration of this valuable crop. This research not only opens new avenues for safflower functional gene mining and breeding but also has broader implications for the agricultural and pharmaceutical industries.

More information: Jiang Chen et al, Whole-genome and genome-wide association studies improve key agricultural traits of safflower for industrial and medicinal use, *Horticulture Research* (2023). [DOI:](#)

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