Researchers uncover genetic module regulating soybean seed traits

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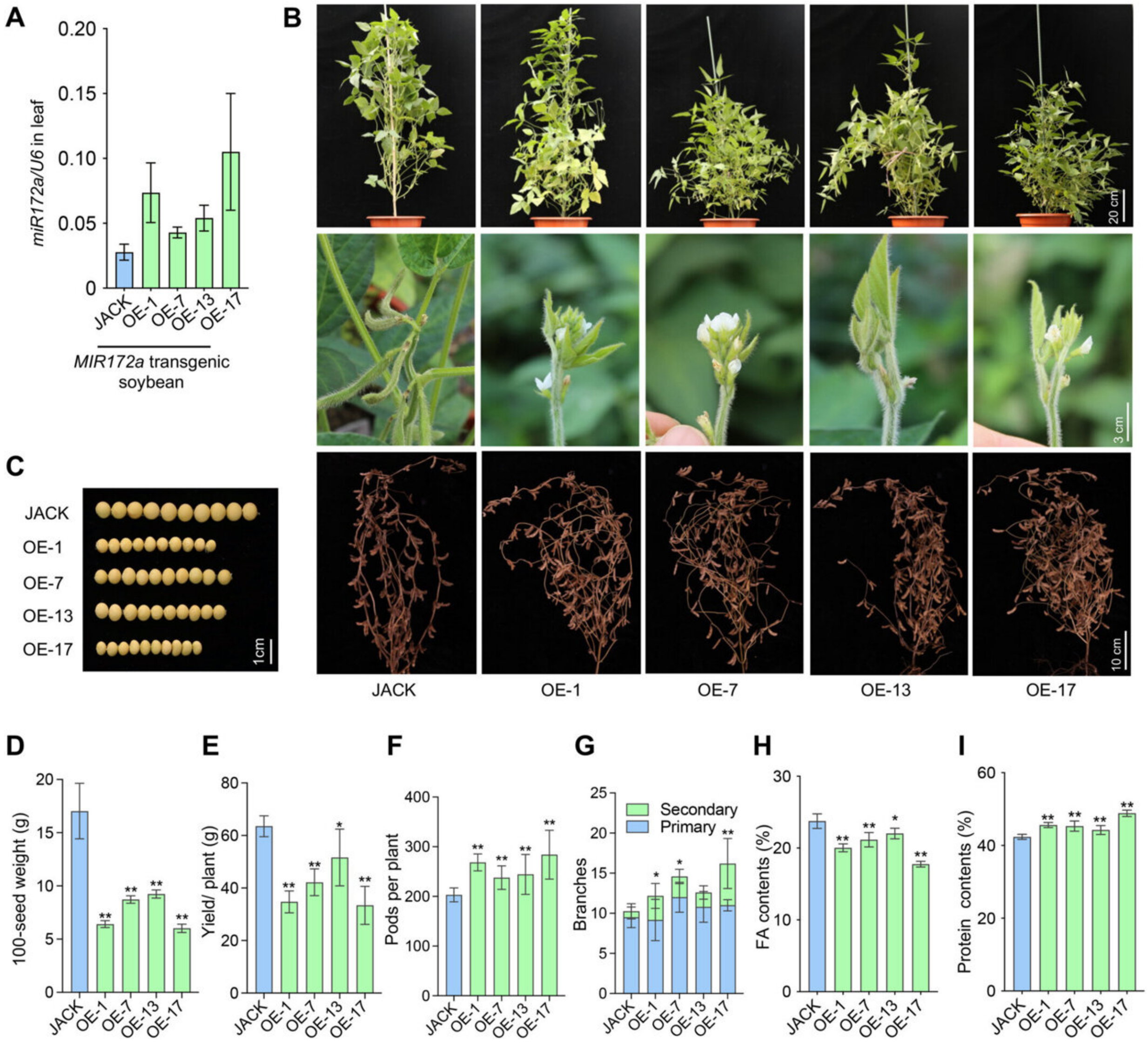

Seeds and other agronomic traits of MIR172a transgenic soybean plants. Credit: *Journal of Integrative Plant Biology* (2025). DOI: 10.1111/jipb.70015

Soybeans (Glycine max) are a vital global source of plant protein and oil, used in food, feed, and industry. Increasing soybean yields is critical for ensuring food security and promoting sustainable agriculture. However, the molecular mechanisms that shape seed size, weight, and composition still remain unclear.

A research team led by Prof. Zhang Jinsong from the Institute of Genetics and Developmental Biology of the Chinese Academy of Sciences has discovered a crucial genetic module that controls soybean seed characteristics, providing new insights for crop improvement.

Their study, published in the *Journal of Integrative Plant Biology* on August 14, reveals how miR172a and its target genes ERF416/413 influence seed size, weight, oil and protein content.

MiR172a was found to directly impact seed morphology and composition. Overexpression of MIR172a made seeds significantly smaller and lighter. It also altered fatty acid profiles, reducing palmitic, stearic, oleic, and linoleic acids while increasing linolenic acid, accompanied by a simultaneous rise in protein content.

Molecular experiments confirmed that miR172a triggers the cleavage of mRNAs from two target genes, ERF416 and ERF413. Gene editing experiments further clarified their roles. ERF416/413 mutants produced smaller seeds with reduced 100-seed weight.

Surprisingly, however, they had up to 31.8% higher yield per plant and increased oil content (especially oleic acid), though protein levels declined. Conversely, overexpression of ERF416 resulted in larger, heavier seeds (with up to 13% higher 100-seed weight), but had no effect on total yield and decreased oil content.

The researchers also mapped the downstream regulatory pathways of ERF416/413, which directly bind to the promoters of other genes like GmKIX8-1 (involved in seed size control) and GmSWEET10a (responsible for sugar transport), thereby influencing seed development.

Analysis of 289 soybean accessions showed three major haplotypes of ERF416. Hap1 was linked to larger seeds but lower oil content, while Hap3 correlated with higher oil content—making Hap3 a promising allele for breeding high-oil soybean varieties.

"This work identifies the miR172a–ERF416/413 module as a central regulator of soybean seed development," said Prof. Zhang. It provides valuable genetic resources and molecular targets for breeding soybeans with optimized yield and quality, balancing seed size, protein, and oil content.

More information: Meng Jin et al, The miR172a-ERF416/413 module regulates soybean seed traits, *Journal of Integrative Plant Biology* (2025). DOI: 10.1111/jipb.70015

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