

Comprehensive Analysis of the T2T Genome of the Soybean cv. Zhonghuang 13

CHINA, December 2, 2023 /EINPresswire.com/ -- A comprehensive analysis of the soybean genome can help develop improved varieties of soybean by identifying crucial genes linked to desirable traits. Unfortunately, previous soybean genomic data have resulted in the persistence of over 1000 gaps. Recently, a joint team of researchers from China undertook a novel, comprehensive analysis of the soybean cultivar known as Zhonghuang 13 (ZH13), which occupied the largest planting area in the first two decades of 21st century in China, and delivered



Cv. Zhonghuang 13.

the complete T2T genomic data, enhancing our understanding of soybean genetics and evolution.

Soybean (Glycine max) is one of the most crucial oil and protein crops, and contribute to more than a quarter of the protein utilized in both food and animal feed. It is widely acknowledged that cultivated soybean emerged through the domestication of its annual ancestor in the Yellow River basin. Therefore, the exploration of genetic resources within the origin region bears immense significance in advancing the global frontiers of soybean breeding.

In comparison to the cultivar of Williams 82, ZH13 boasts higher genetic diversity and ecological type of origin reign. Furthermore, ZH13 is an ideal variety in the breeding strategy called "Potalaization", which allows breeding of novel widely adapted soybean varieties through the use of multiple molecular tools in existing elite widely adapted varieties. To date, however, soybean genome analyses are incomplete and contain many gaps, which have so far limited in-depth investigations into its properties.

To address this, a joint team of researchers from China, including senior author and cocorresponding author Dr. Yadong Wang from the Center for Bioinformatics, School of Computer Science and Technology at the Harbin Institute of Technology, and co-corresponding author Dr. Tianfu Han from the Institute of Crop Sciences at the Chinese Academy of Agricultural Sciences, conducted a telomere-to-telomere (T2T) assembly of the Chinese soybean cultivar Zhonghuang 13 (ZH13), termed ZH13-T2T. The study was published in The Crop Journal.

"Imagine you have a giant jigsaw puzzle, but it's missing some pieces. This puzzle is like the genetic code, or the "recipe," of ZH13. The missing pieces are like gaps in our understanding of this recipe," explained by Dr. Yang Hu, co-corresponding author of the study. "In this effort, we used a super-advanced and precise method to find and fit in all those missing pieces. With this powerful tool, we could see everything—even the tricky parts that were hidden before".

The researchers used a multi-assembler approach to minimize biases and enhance assembly accuracy. Their assembly spanned 1,015,024,879 base pairs (bp), effectively filling in all the gaps from the previous analyses. In the process, they identified over 50,000 protein-coding genes, of which 707 are novel. ZH13-T2T was found to have longer chromosomes, 421 not-aligned regions (NARs), 112 structure variations (SVs), and a significant expansion of repetitive elements compared to earlier analyses.

"We've delivered the first complete Chinese soybean cultivar T2T genome," said Dr. Bo Liu, the other co-corresponding author. The complete, accurate genome sequence of the ZH13 cultivar can now be used to identify crucial genes, and genetic variants linked to desirable traits."

This information would also contribute to accelerating soybean breeding programs to develop new cultivars with specific enhanced traits, crop yields, improved resistance to pests and diseases, and adaptability to different regions and climates.

"For instance, researchers can use the genomic information to manipulate specific genes that encode improvements in soybean traits, such as photothermal adaptability, oil content, protein quality, or tolerance to abiotic and biotic stressors," concluded by Baiquan Sun, an author of the study.

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