Combination of Phenomics, Genomics and Transcriptomics to Dissect Genetic Basis of Soybean Compact Plant Architecture

Li D 1, Qin C 1, Tian Y 1, Bai D 1, Schnable J 2, Jin X 1, Liu B 1, Li Y 1, Qiu L 1

E-mail of corresponding author: [liyinghui@caas.cn](mailto:liyinghui@caas.cn), [qiulijuan@caas.cn](mailto:qiulijuan@caas.cn)

1 Institute of Crop Science, Chinese Academy ofAgricultural Sciences, Beijing 100081, China

2 Department of Agronomy and Horticulture, University of Nebraska‐Lincoln, Lincoln, Nebraska 68583, USA

Planting soybeans (*Glycine max* (L.) Merr.) at high densities has been shown to significantly enhance crop yields. To achieve this, we harnessed omics-based solutions to pinpoint genes that facilitate successful high-density planting practices. Our study began by collecting time-series phenotypic data using an unmanned aircraft system, focusing on canopy coverage variation in a diverse panel of soybean varieties. Through a genome-wide association study (GWAS), we identified 35 loci that displayed dynamic associations with canopy coverage across developmental stages. Among them were 10 known QTL related to flowering time and plant height, as well as novel QTL influencing canopy coverage. One of these novel loci named *GmARF1* showed evidence of adaptive selection during domestication, with a low canopy coverage haplotype favored in high-density planting within high latitude regions. Furthermore, we conducted GWAS and a transcriptome-wide association study (TWAS) on plant height, leading to the identification of *GmPH13*, which encodes a WD30 protein. A 5.5kb transposon insertion responsible for a truncated GmPH13 protein results with reduced plant height and improved lodging resistance, making it suitable for high-density planting. Confirmation of these findings was achieved through gene editing mutants of *GmPH13*, which exhibited reduced height, while over-expression of *GmPH13* led to increased plant height. Furthermore, we identified 57 soybean varieties harboring favorable haplotypes for both *GmARF11* and *GmPH13*. In summary, our research not only provided valuable insights into genes but also furnished a collection of materials with an expanded genetic basis for soybean cultivation under high-density planting conditions, ultimately enhancing crop productivity.

***References:***

[1] Qin et al. 2023, Nat Commun, vol. 14, p. 6813

[2] Li et al. 2023, J Integr Plant Biol, vol. 65, p. 117–132