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Genetic dynamics drive flowering date shortening in wild-cultivated soybean

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The germplasm nursery at the Jianpu Experimental Station of Nanjing Agricultural University, Nanjing, China. Photo by J.X. Qiu.

In China, at the soybean's center of origin, days to flowering (DTF) shortening happened in two evolutionary processes: either annual wild (WA) to farmers' landrace (LR) to released cultivar (RC), or from southern to northern. The genetic dynamics of different evolutionary stages have not been explained, but researchers in China benefit from a complete set of WA, LR, and RC samples for evaluation.

In a new *Crop Science* study, researchers applied a novel genome-wide association analysis (GWAS) to a large representative sample of WA, LR, and RC (1024 accessions) and identified 177 DTF quantitative trait loci (QTLs) with 797 alleles. These alleles were organized into a DTF QTL–allele matrix and its component submatrices.

By comparing DTF QTL-matrices between populations and subpopulations, the scientists found that allele inheritance, emergence, exclusion, and recombination were major genetic drivers of DTF shortening in the WA, LR, and RC evolutionary stages. The researchers found that the LR furthest south was the most primitive, and further DTF shortening can be expected through continuing allele recombination.

Direct comparisons among QTL–allele matrices using an improved GWAS procedure is a novel way of exploring the population evolutionary mechanism.

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Liu, F., He, J., Wang, W., Xing, G., Zhao, J., Li, Y., & Gai, J. (2021). Genetic dynamics of flowering date evolved from later to earlier in annual wild and cultivated soybean in China. *Crop Science*, *61*, 2336–2354. **https://doi.org/10.1002/csc2.20462**

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