**Toward soybean molecular design breeding**

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Soybean (*Glycine max* [L.] Merr.) is a major crop of agronomic importance as a predominant source of protein and oil. To meet the needs of the rapidly increasing human population, soybean breeders are challenged with finding a high-efficiency breeding strategy for developing soybean varieties with higher yield and improved quality. Molecular breeding has been proposed to be a powerful and effective approach for crop breeding, but requires a better understanding of the genetic architecture and networks underlying agronomical traits.

To develop molecular design breeding in soybean, we first comprehensively investigated the genetic information and evolution of large number of representative soybean accessions from worldwide, including individual de novo genome assemblies for 27 representative soybeans that were selected from 2,898 deeply sequenced accessions, and investigation the genetic variation, epigenetic variation, and 3D-genomic variations among the accessions. Meanwhile, we developed an integrating method to identified the causal genes conferring important agrominic traits based on population genetics and multi-omics data, and identified a number of genes. Through systematic genome-wide association analysis and genetic network construction, we established multi-trait genetic regulatory coupling network, and bred some elite cultivars by molecular design breeding.

***References:***

[1] Liu Y. et al, Pan-genome of wild and cultivated soybeans. Cell 2020, 182: 162-176.

[2] Wang M. et al, Parallel selection on a dormancy gene during domestication of crops from multiple families. Nature Genetics 2018, 50: 1435-1441.