

Dissection of genetic network underlying important agronomic traits accelerates modern breeding in soybean

With the support by the National Natural Science Foundation of China and the “Strategic Priority Research Program” of the Chinese Academy of Sciences, a collaborative study by the research groups led by Professors Tian Zhixi (田志喜), Wang Guodong (王国栋), and Zhu Baoge (朱保葛) from the Institute of Genetics and Developmental Biology, Chinese Academy of Sciences and Zhang Zhiwu from Washington State University, deeply dissected the genetic network undergoing 84 agronomic traits, which was published in *Genome Biology* (2017, 18: 161).

Correlations among different traits and genetic interactions among genes that affect a single trait pose a challenge to modern breeding. Traits associated with yield and quality are usually regulated by a complicated network composed of multiple loci. As a result, many complex traits exhibit intimate correlation and tend to be tightly integrated, resulting in heritable covariation, which adds the complexity for breeding. Therefore, an understanding of traits co-variation is essential for the genetic improvement of multiple complex traits.

Soybean is a major crop of agronomic importance as a predominant source of protein and oil. A highly efficient molecular design system will significantly facilitate the breeding of high yield and quality soybean varieties. To understand the genetic networks underlying phenotypic correlations, 809 soybean accessions were collected from all over the world and phenotyped for two years at three locations for 84 agronomic traits related to growth period, architecture, color, seed development, oil content, or protein content. The researchers identified 245 significant genetic loci through genome-wide association studies and further confirmed that 95 genetically interacted with other loci among these identified loci.

The team determined that 14 oil synthesis-related genes are responsible for fatty acid accumulation in soybean, which will allow the development of a soybean variety with higher oil content. They also demonstrated that 51 traits could be linked through the linkage disequilibrium of 115 associated loci and these links reflect phenotypic correlations. Meanwhile, they revealed that 23 loci have pleiotropic effects on different traits.

This study established a genetic network of loci associated with phenotypes, providing insights into the genetic correlation among complex traits. These findings will facilitate future soybean functional studies and modern breeding in soybean through molecular design.

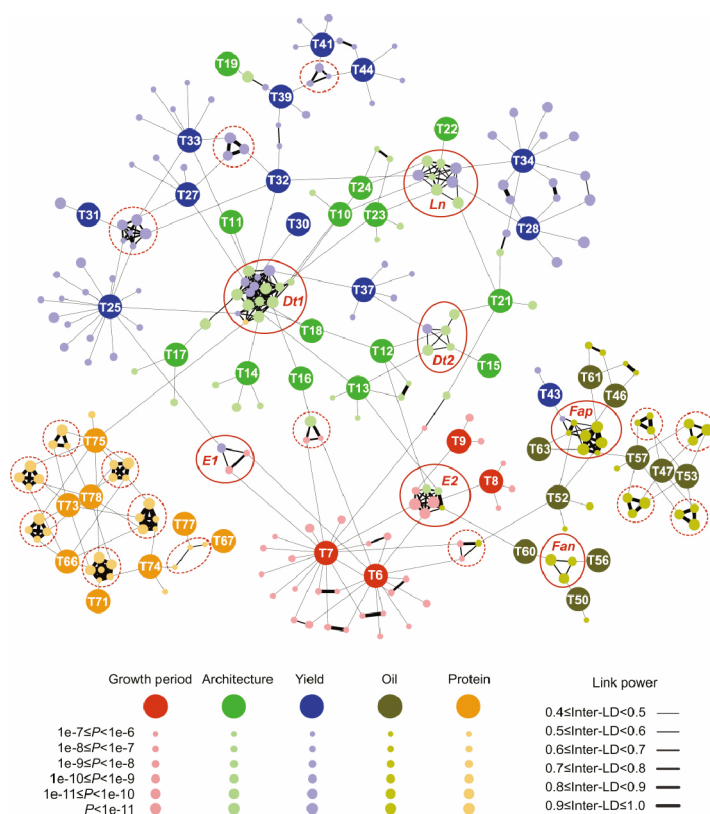


Figure Association networks across different traits in soybean.