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Dissection of the network underlying agronomic traits in soybean

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Many agronomically important traits exhibit modularity and tend to be tightly integrated. The understanding of how traits become associated or correlated is essential in the improvement of complex traits. Soybean (*Glycine max* L Merr) is a major crop of agronomic importance as the predominant source of animal feed protein and cooking oil, which was domesticated from wild soybean (G. soja Sieb & Zucc) in China 5,000 years ago. Understanding soybean domestication and improvement and a comprehensive dissection of the genetic basis of agronomic traits is important for soybean improvement. By analysis of several hundred re-sequenced wild, landrace and improved soybean accessions, we detected 230 selective sweeps and 162 selected copy number variants. Combined with previous quantitative trait loci (QTL) information, we find that, of the 230 selected regions, 96 correlate with reported oil QTLs and 21 contain fatty acid biosynthesis genes, 96 of which correlate with reported oil QTLs. Moreover, we detected more than two thousands association signals via a comprehensive GWAS for dozens of agronomic traits. Through modeling analysis, we find that amount of association sites are tightly linked and form a complex network to regulate the modularity of different complex traits. This study provides valuable resources for genomics-enabled improvements in soybean molecular breeding.

Biography

Zhixi Tian has completed his PhD from Institute of Genetics and Developmental Biology, Chinese Academy of Sciences and Postdoctoral studies from Purdue University, USA. He is a Principle Investigator of Institute of Genetics and Developmental Biology. His research interests focus on functional genomics and genetics of soybean. He has published more than 27 papers in reputed journals.

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