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Evolutionary differentiation among maturity and geographic groups of world soybeans based on population QTL-allele constitution of growth date traits

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Soybean is a photoperiod-sensitive crop and extremely diverse in flowering and maturity dates, which have a direct impact on its adaptability. About 10 genes conferring flowering and maturity dates have been reported and cloned. Whether these genes composes the whole genetic system of the traits is to be exhausted. To dissect the genome-wide QTL(quantitative trait loci)-allele constitution of flowering and maturity dates, a sample with 371 varieties covering 13 maturity groups (MGs) and 13 geographic regions was organized and phenotyped in two years. The restricted two-stage multi-locus model genome-wide association study (RTM-GWAS) was conducted with 20,701 SNP linkage disequilibrium blocks (SNPLDBs) as markers. A total of 52 and 59 QTL for flowering and maturity dates were detected, which explained 84.8% and 74.4% of their phenotypic variation, respectively. A total of 241 alleles of flowering date and 246 alleles of maturity date with their respective allele effects were organized into a QTL-allele matrix, respectively, which showed the genetic structure of flowering and maturity dates of the world soybeans. The detected QTL for flowering and maturity dates covered the most of those reported in SoyBase with about one-third of them have not been reported yet. There appeared specific-present alleles only in primary MGs (MGI-MGVII) but not in newly developed MG000–MG0 and MGVIII-MGX. Thus the emergence of these new MGs are due to the QTL-allele recombination rather than new mutants. Among the geographic regions, specific-present alleles were found in both the centers and non-centers in old continents as well as some in new continents. Thus these new mutant alleles might occur before new MGs came out. From the detected QTL, 110 and 99 candidate genes for flowering and maturity dates relate to 9 biological processes, respectively. The optimal crosses for shortening and extending growth periods were predicted according to the QTL-allele matrices.