

Possible example of locus heterogeneity in soybean

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Aim: Genome-wide association studies (GWAS) have now become the standard and favored approach for identifying quantitative trait loci. However, GWAS typically detect only synthetic associations – those most strongly correlated with the phenotype – rather than causal mutations. One of the possible issues is locus heterogeneity, a situation when a locus may contain several genes, mutations in which affect the same trait. Previously, we identified the qDTF-7 locus, associated with soybean flowering, and *GmTOE1* (*TARGET OF EAT 1*) as the most likely candidate gene for this locus. In this study, we revisited the qDTF-7 locus and found that its effect on flowering time could be explained by two closely located genes, *GmTOE1* and *GmRVE8* (*REVEILLE 8*).

Material and methods: The material was a collection of 129 soybean accessions, which were studied for flowering and maturity time during 2021–2022 in the conditions of the Novosibirsk and Orel regions. We also used the genotypes and phenotypes of soybean accessions from the SoyOmics database.

Results: The late-flowering allele *GmRVE8*⁸⁶ arose on the genetic background of the early-flowering allele *GmTOE1*^C and apparently partially restores the effect of *GmTOE1*^C on flowering time. Also, *GmRVE8* shows epistatic interaction with the main repressor of soybean flowering – the *E1* gene and *GmRVE8* is probably its negative regulator.

Conclusions: Thus, our work provides a theoretical basis for studying flowering time in soybean and may serve as another example of a heterogeneous locus in quantitative plant genetics.

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