

World Congress on

Plant Genomics and Plant Science

October 15-16, 2018 London, UK

Integrated approach of QTL mapping and gibberellin oxidase gene diversity unraveled the genetic architecture of vine growth habit in wild soybean (*Glycine soja*)

Javaid Akhter Bhat, Ruikai Wang, Li Liu, Jiejie Kong, Zhiyong Xu and Tuanjie Zhao
Nanjing Agricultural University, China

Vine Growth Habit (VGH) is considered an important domesticated-related trait in wild and cultivated soybean and is a beneficial phenotype in many wild plants. However, very little is known about the genetic basis of this trait. Hence, in the present study we used combined strategy of linkage mapping and population genome diversity analyses to unravel the genetics of VGH in soybean. In this regard, two Recombinant Inbred Line (RIL) populations viz., NJRINP (PI342618B × NN 86-4) and NJRI4P (PI342618B × NN 493-1), and their respective high-density SNP linkage maps were used to map Quantitative Trait Loci (QTL) for VGH. Here, we identified seven and five QTLs at flowering stage (R1) and maturity stage (R8), respectively, and among them *qVGH-18-1*, *qVGH-18-2*, *qVGH-19-3*, *qVGH-19-4* were identified as major loci ($R^2 > 10\%$ and detection time ≥ 2). However, *qVGH-18-2* was considered as a main QTL for VGH being consistently identified in both RIL populations as well as all growth stages and cropping years. Out of all the annotated genes within *qVGH-18-2*, *Glyma18g06870* was identified as the candidate gene and named as *VGH1*, which was a gibberellin oxidase (*GA2ox*) belongs to 2-oxoglutarate-dependent dioxygenase (2-ODD). It was noteworthy that one member of 2-ODD were also found in *qVGH-18-1* and *qVGH-19-4*, named as *VGH2* and *VGH3*, respectively. In addition, the *qVGH-19-3* possesses one gene as *Glyma19g37890* which is well known as soybean growth habit gene (*Dt1*). Moreover, from sequence polymorphism analysis of 50 2-ODDs, *VGH1* and three other *GA2ox* genes were found significantly divergent between vine and erect soybean with FST value larger than 0.25. Hence, 2-ODD was assumed to play a major role in governing inheritance of VGH in soybean. Therefore, elucidating the genetic mechanism of 2-ODD/*GAox* is very useful for exploring VGH and other stem traits, as well as genetic improvement of plant type in soybean.

javid.akhter69@gmail.com

Notes: