

PB-003

Identification of Quantitative Trait Loci for Flooding Tolerance at Seedling Stage of Soybean (*Glycine max* L. Merr.)

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[Introduction]

Flooding stress causes a significant yield reduction in soybean worldwide. The onset of rainy season during the early growth of soybean in Korea and many parts of Asia potentially renders the soybean plants to flooding stress in uplands as well as in low lands, including converted rice fields. The objective of this study was to identify quantitative trait loci (QTL) for flooding tolerance at the seedling stage of soybean.

[Materials and Methods]

A recombinant inbred line (RIL) population was derived from a cross between a flood-tolerant ‘Danbaekkong’ and flood-susceptible ‘NTS1116’ cultivars. The plants were flood-stressed at the V1-V2 stage by collecting ~10 cm water level for 14 days. Leaf chlorophyll content and shoot dry weight, two of the most affected traits due to the stress, were measured for phenotyping the population over two years (2017 and 2018). IciMapping V4.1 was used to construct a linkage map using 180K Axiom® SoyaSNP markers and QTL Cartographer V2.5 was used for QTL analysis.

[Results and Discussion]

Twenty-four QTL having 3.35 ~ 18.57 logarithm of odds scores and explaining 7.2 ~ 36.4% phenotypic variations (PVE) were identified on 11 chromosomes. Several candidate genes related to chlorophyll content/photosynthesis, plant growth, and stress response have also been found in the QTL regions. One QTL on chromosomes 6 and 15 each and three QTL on chromosome 7 contributing up to 30.7% PVE were identified at least in two environments, indicating their consistent detection across different environments. These consistent QTL could potentially be applied in the soybean breeding programs through marker-assisted selection technology. The results provide useful information for unraveling the genetic basis of flooding tolerance and developing tolerant cultivars of soybean.

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