

ABSTRACT

Flooding and chilling stresses are among the most important abiotic factors affecting the yield and seed quality of soybean in Japan. In the present investigation, the genetic and molecular bases of flooding and chilling tolerance were studied. The seed yield and the root length response to flooding stress were evaluated in an F₉ RIL population developed from the cross between susceptible cultivar Tachinagaha and moderately tolerant Iyodaizu. A QTL for FTI (*flood1*) was found close to SSR marker Sat_267 in MLG A1 and accounted for 17% of the total phenotypic variation observed. Similarly, a consistent QTL for root length (*flood2*) was found in MLG H. The existence of *flood2* is being confirmed through the development of NILs from the RIL population. With respect to the chilling stress tolerance, the molecular identity of the QTL responsible for the seed coat discoloration found in seeds of soybean genotypes having the *I* allele for seed quality improvement and the *T* allele for chilling tolerance, was determined in an F₂ population developed from the cross of two breeding lines with contrasting seed coat discoloration. This gene corresponds to a variant of *GmIRCHS* and constitutes the genomic region involved in the post-transcriptional gene silencing of chalcone synthase genes that regulate the seed coat color. The combination of the *GmIRCHS* allele from the tolerant line and the *T* allele enables the combination of chilling tolerance and good seed quality. Furthermore, the genomic position of maturity gene *E5*, which was reported to be associated with chilling tolerance, was mapped in an F₂ population derived from a cross between cultivar Harosoy and Clark-*e2E5*. These results provide insights into the physiological aspects involved in the response of

soybean to abiotic stresses and may be important references for the improvement of soybean's response to flooding and chilling stresses.