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Integrating RNA-Seq and QTL Results to Identify Candidate Genes for Flooding Tolerance in Soybean

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[Introduction]
Flooding stress causes a significant yield loss in soybean worldwide. Information on the candidate genes for flooding tolerance is useful to develop tolerant cultivars. The objective of this study was to identify potential candidate genes for flooding tolerance by integrating the results of QTL analysis and RNA sequencing.

[Materials and Methods]
The seedlings of parents and recombinant inbred lines (RILs) developed from a flood-tolerant 'Paldalkong' and susceptible 'NTS1116' were grown in a well-watered condition up to the V1－V2 stage and flood-stressed by inundating ~10 cm water for 14 days. The total RNA was extracted from the leaf tissues of parents and RILs collected at 14 days after flooding. cDNA was synthesized through reverse transcription reaction. Differentially expressed genes within the QTL regions were searched and primers were developed for gene expression analysis in the parental cultivars and RILs.

[Results and Discussion]
Out of the 31 genes selected as potential candidate gene, 19 genes showed good amplification in capillary electrophoresis and further analyzed through reverse transcription quantitative polymerase chain reaction (qRT-PCR), out of which two genes showed differential expression among tolerant and susceptible lines. The expression of *Glyma.12g030900* and *Glyma.10g050300* in leaf and root tissues, respectively, were higher in several tolerant lines than in the susceptible lines under flooding stress. The chlorophyll index of the tolerant lines was also consistently higher than the susceptible ones over two years, supporting the qRT-PCR results. The results provide useful information on flooding tolerance studies, and the genes could be applicable in the marker-assisted selection to develop flooding stress tolerant soybean cultivars.

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