

Genome-wide candidate gene analysis for identification of the cold tolerance responsible genes in Cucumber

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[Introduction]

Cucumber is one of major crops in Korea, however genetic backgrounds of major cucumber species are very similar to each others and most inbred lines are vulnerable under various abiotic stresses. So development of abiotic stress tolerant inbred lines of cucumber and molecular marker assisted breeding technologies are necessary. In this research chilling stress tolerance was main target trait and many polymorphic sites in CDS and intron regions of chilling tolerance related genes were analyzed for marker development.

[Materials and Methods]

Genome sequences of three chilling susceptible inbred lines and two chilling tolerant inbred lines were analyzed by Illumina Miseq. Reference genome sequences were downloaded from NCBI GenBank and annotation data was collected from cucumber genome database. Sequence alignment was done using MEGA7 program. Developed markers were validated by PCR and agarose gel electrophoresis.

[Results and Discussions]

In this research, totally 26,579 polymorphic sites were identified in nuclear genome sequences of cold-tolerant lines when compared with cold-sensitive lines. Chromosome three shows most diverse polymorphism between cold-tolerant lines and cold-sensitive lines. Least polymorphic sites were found on chromosome four. 1182 polymorphic sites were mapped in CDS regions, 548 polymorphic sites were found in 3' and 5' UTR regions, 4,829 polymorphic sites were in intron sites, and in intergenic regions there were 20,020 polymorphic sites. Two polymorphic sites were mapped on mitochondrial genome sequences of cold-tolerant and cold-sensitive lines and both of them were in intron regions. 16 candidate genes which were thought to be related to chilling tolerance were selected and 12 of candidate genes have polymorphic sites in CDS regions or intron regions between cold-tolerant and cold-sensitive cucumber inbred lines. Totally 18 dCAPS markers were developed based on polymorphic sites of 12 candidate genes. This research will be useful for understanding of cucumber chilling tolerance mechanisms and applying to molecular breeding of cucumber inbred lines.

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