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Development and application of paralogous specific dCAPS markers on *Panax ginseng* C. A. Meyer for genetic map construction

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[Introduction]

Panax ginseng C. A. Meyer, a herb of the Araliaceae, is a valuable medicinal plant in Korea. Although genetic map in crops provides valuable information for breeding, researches on this plant are insufficient still. Because ginseng has the complicated genome structure as allotetraploid. Hence, developing markers and constructing genetic map on this plant also had difficulty.

[Materials and Methods]

Panax giseng C. A. Meyer F2 96 plants, the progeny of Panax giseng C. A. Meyer "Chunpoong" and "Yunpoong", were served from RDA and used as mapping population for genetic map construction. SNPs(Single Nucleotide Polymorphisms) in paralogous scaffolds were obtained and dCAPS markers(Derived Cleaved Amplified Polymorphic Sequences) targeting the SNPs were developed for genotyping to calculate recombination frequency and construct genetic map. With this markers designed in the light of ginseng's paralogous regions, only one target sequence is amplified except another paralogous sequence. At the same time, "Chunpoong" and "Yunpoong" are differentiated by length difference. Using developed markers, mapping population is genotyped and segregation ratio of them is calculated.

[Results and Discussions]

Panax giseng C. A. Meyer F2 96 plants were genotyped with 17 dCAPS markers. These markers are applied to *Panax* ginseng C. A. Meyer faster and more accurately than already developed DNA markers in previous researches. Already developed markers, newly developed dCAPS markers and GBS genotyping data as a part of Ginseng Genome Project are used for genetic map construction and, by extension, for ginseng breeding as useful resources.

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