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### ***De novo* transcriptome assembly and the identification of gene-associated single-nucleotide polymorphism in ginseng roots**

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We performed *de novo* transcriptome sequencing for *Panax ginseng* and *Panax quinquefolius* accessions using the 454 GS FLX Titanium System and discovered annotation-based genome-wide single-nucleotide polymorphism (SNPs) using next-generation ginseng transcriptome data without reference genome sequence. The comprehensive transcriptome characterization with the mature roots of four *ginseng* accessions generated 297,170 reads for 'Cheonryang' cultivar, 305,673 reads for 'Yunpoong' cultivar, 311,861 reads for the G03080 breeding line, and 308,313 reads for *P. quinquefolius*. In transcriptome assembly, the lengths of the sample read were 156.42 Mb for 'Cheonryang', 161.95 Mb for 'Yunpoong', 165.07 Mb for G03080 breeding line, and 166.48 Mb for *P. quinquefolius*. A total of 97 primer pairs were designed with the homozygous SNP presented in all four accessions. SNP genotyping using high-resolution melting (HRM) analysis was performed to validate the putative SNP markers of 97 primer pairs. Out of the 73 primer pairs, 73 primer pairs amplified the target sequence and 34 primer pairs showed polymorphic melting curves in samples from 11 *P. ginseng* cultivars and one *P. quinquefolius* accession. Among the 34 polymorphic HRM-SNP primers, four primers were useful to distinguish ginseng cultivars. In the present study, we demonstrated that *de novo* transcriptome assembly and mapping analyses are useful in providing four HRM-SNP primer pairs that reliably show a high degree of polymorphism among ginseng cultivars.

#### **Biography**

Ick Hyun Jo has completed his PhD from Chungbuk National University and Post-doctoral studies from National Institute of Horticultural and Herbal Science (NIHHS) in South Korea. He is the Public Agricultural Research Worker at Rural Development Administration (RDA). He has published more than 32 papers in reputed journals and serving as an Editorial Board Member for Medical Crop Science Journal.

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