
Complete chloroplast genomes and 45S nrDNAs of *P. stipuleanatus* and *P. trifolius*, and develop chloroplast CDS gene-derived SNP markers for authentication of seven *Panax* species

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[Introduction]

The genus *Panax* (family Araliaceae) that comprises approximately 14 species of slow-growing perennial plants with fleshy roots. *Panax* species are recorded to have exhibited a wide variety of beneficial pharmacological effects and has become a popular and worldwide known health supplement and medicine. However, their evolutionary, taxonomical relationship, and origin remain largely unresolved.

[Materials and Methods]

We completed chloroplast genomes and 45S nuclear ribosome DNA (nrDNA) sequences from the two *Panax* species: *Panax stipuleanatus* and *Panax trifolius* by *de novo* assembly using low-coverage whole-genome shotgun next-generation sequencing (dnaLCW). Chloroplast sequence comparative analysis was conducted to elucidate the genetic diversity, and develop markers for authentication of seven *Panax* species. To authenticate between seven *Panax* species as inter-species polymorphism using chloroplast CDS sequences, dCAPS primers were designed based on SNP polymorphic sites after eliminating intra-species polymorphic sites, and chloroplast gene transfer regions.

[Results and Discussions]

Complete chloroplast genomes of *P. stipuleanatus* and *P. trifolius* were 156,064 bp and 156,157 bp, respectively and consisted of common 79 protein-coding, 30 tRNA and 4 rRNA genes without structural variation compared to that of other reported *Panax* species. Complete 45S nrDNA units were 7,336 bp and 5,991 bp including 5.8 kb long 45S cistron region and partial intergenic spacer region. Phylogenetic analysis was conducted for nineteen Araliaceae species revealed that the nineteen species could be divided into two monophyletic lineages consisting of the *Aralia-Panax* group and the other group comprising the seven remaining genera. Large numbers of SNP were identified in seven *Panax* chloroplast genomes including 1128 SNPs in CDS regions and 1783 SNPs in whole chloroplast genomes. Twelve large fragments of chloroplast were characterized in mitochondrial genome. We developed 18 chloroplast CDS SNP-derived markers to authenticate the seven *Panax* species with at least two unique specific markers for each species. These markers were successful to discriminate one species from others, and can apply for species identification and EMA inspection.

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