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ABSTRACTS

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GENETIC DIVERSITY AMONG WILD AND CULTIVATED *PANAX GINSENG* MEYER BASED ON CHLOROPLAST DNA DATA

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Panax ginseng Meyer is a medically important plant species and is widely used in cultivation in the northeastern Asia. The genetic diversity of wild and cultivated ginseng was estimated using sequence variation of chloroplast DNA regions such as *ycf1a*, *trnH-psbA* and *matK-rps16*. These cpDNA regions are traditionally used for DNA barcoding of plants. In this study we analyzed ginseng from natural populations of the Primorye Territory. A total of 5135 bp of aligned chloroplast sequence were obtained, comprising 668, 483 and 3984 bp for *ycf1a*, *trnH-psbA* and *matK-rps16*, respectively. These sequences were compared with accessions of wild and cultivated *P. ginseng* from China and Korea downloaded from GenBank. The sequences of these cpDNA regions of *P. vietnamensis* Ha et Grushv. were used as an outgroup. The analysis revealed seven haplotypes in *P. ginseng* that were separated from outgroup by fifty-seven mutational steps. High frequency of occurrence has been in haplotypes H1 (44 %) and H4 (34 %). Haplotype H1 was represented primarily wild ginseng from the Primorye Territory, and all representatives from China, and two from Korea. Haplotype H4 was revealed in two plants from the Primorye Territory (Dalnegorsk population) and nine accessions from Korea. The rest of haplotypes belonged to ginseng populations from the Primorye Territory (H2, H3, H5, H6) and one sample of wild ginseng from south of Korea Peninsula (H7). All haplotypes of *P. ginseng* from the Primorye Territory were at a distance of one mutational step from H1 and formed a star-like network. Such structure may indicate on recent divergence of these populations. As for ginseng from Korea three haplotypes were identified: two for cultivated accessions and one for wild plant. It was interesting that all sequences of ginseng from China, belonging to four different landraces, had one haplotypes and this consistent with conclusion that Chinese landraces were not domesticated independently.

In general, it was found that wild ginseng from the Primorye Territory has greater haplotypic diversity in compare with wild and cultivated ones from China and Korea by four cpDNA regions studied. Thus, it can be assumed that domestication significantly reduces genetic diversity.