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ALLOZYME VARIATION OF THE MEDICINAL PLANT *ELEUTHEROCOCCUS* *SESSILIFLORUS* (ARALIACEAE)

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Eleutherococcus sessiliflorus (Rupr. et Maxim) S.Y. Hu, a low-branched shrub, is distributed only in northeast Asia such as Korean Peninsula, northeast China and Far East of Russia. In Russia the species is represented by small fragmented populations in the southwest part of the Primorsky Krai, south part of Khabarovsk Region and southeast part of the Amur Region (Strogii, 1934) only. *E. sessiliflorus* is a valuable medicine plant applied in traditional medicine of Korea and China (Zhuravlev, Kolyada, 1996). Allozyme polymorphism of *E. sessiliflorus* populations was analyzed only in Korea by now (Huh, Huh, 2005). In the present study we estimated genetic variation of the Russian populations of *E. sessiliflorus* using the isozyme analysis. The data obtained were compared with those reported for other representatives of Araliaceae.

Samples were collected from 5 natural *E. sessiliflorus* populations located near Novogeorgievka (24 plants), Fadeevka (21), Konstantinovka (11), Pokrovka (6), and Krasnii Yar (10) villages (Primorsky Krai, Russia). Electrophoretic analysis of 13 *E. sessiliflorus* enzymes revealed 28 different electrophoretic variants, presumably encoded by 17 loci. Nine loci (*Acp-2*, *Acp-3*, *Fe-2*, *Fe-3*, *Gpi-4*, *Idh-2*, *Ndh-2*, *Lap*, *6-Pgd-2*) were polymorphic. Allozyme variation level in *E. sessiliflorus* was rather high ($P_{95} = 43.5$, $A = 1.55$; $H_o = 0.211$; $H_e = 0.168$) as compared with the mean values for plants with regional geographic range ($P_{95} = 36.4$, $A = 1.55$, $H_e = 0.118$) (Hamrick, Godt, 1989), as well with the values reported for most of the representatives of the family Araliaceae examined so far. Obtained values are comparable with those for the two Korean populations of *E. sessiliflorus* ($P_{95} = 47.8$ (47.8); $A = 1.52$ (1.57); $H_o = 0.129$ (0.114); $H_e = 0.168$ (0.142)). An excess of heterozygosity was observed in all populations studied. Mode of reproduction of *E. sessiliflorus* that display both sexual and vegetative regeneration may contribute to maintaining genetic diversity. We suggest that unique, highly adapted multilocus genotypes generated via sexual reproduction would be subsequently conserved through clonal regeneration. The highest level of the genetic variation was revealed in the population near Novogeorgievka village, whereas the lowest one was found in the Pokrovka population. This fact may be explained by the most anthropogenic pressure on this territory which resulted in reducing of effective population size.

Thus, the research showed a high level of genetic diversity in Russian *E. sessiliflorus* populations. It may be due cross-pollination contributes the main input to the genetic variation at present, whereas vegetative reproduction conserves marginal populations of the species.