

**Modern Achievements in Population, Evolutionary, and Ecological Genetics :
International Symposium, Vladivostok – Vostok Marine Biological Station,
September 9–14, 2007 : Program & Abstracts. – Vladivostok, 2007. –45 p. – Engl.
ISBN 5-7442-1442-9**

HELD BY:

*Vladivostok Public Foundation for Development of Genetics,
Far Eastern Branch of Russian Academy of Sciences,
A.V. Zhirmunsky Institute of Marine Biology FEB RAS,
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Administration of Nakhodka City*

SPONSORS:

*Far Eastern Branch of Russian Academy of Sciences,
Russian Foundation for Basic Research
Nakhodka City Territorial Ecological Foundation*

Editors Yuri Ph. Kartavtsev & Alexey P. Kryukov

**Современные достижения в популяционной, эволюционной и
экологической генетике : Международный симпозиум, Владивосток –
Морская биологическая станция “Восток”, 9–14 сентября 2007 : программа и
тезисы докладов. – Владивосток, 2007. –45 с. – Англ.**

ОРГАНИЗАТОРЫ:

*Владивостокский общественный фонд развития генетики,
Дальневосточное отделение РАН,
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ФИНАНСОВАЯ ПОДДЕРЖКА:

*Дальневосточное отделение РАН,
Российский фонд фундаментальных исследований
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Ответственные редакторы Ю.Ф. Картавец, А.П. Крюков

ISBN 5-7442-1442-9

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POPULATION GENETIC STRUCTURE OF A RELICT PLANT, *ARISTOLOCHIA MANSHURIENSIS* (ARISTOLOCHIACEAE)

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Aristolochia manshuriensis is a rare plant, endemic of Manchurian floristic region. It is the woody liana with flowers specialized for outcrossing. The plant represented in Russia by few small relict populations in the southwest part of the Primorskiy krai along Nezhinka, Ananievka and Malaya Borisovka rivers. *A. manshuriensis* is a valuable medicine plant; however, its natural populations are badly exhausted and needed in protection and urgent conservation measures. The plant is listed in the Red Data Book of Russia as endangered species. Yet gene pool and genetic structure of the populations have not studied by now that obstructs an evaluation of their condition and a design of the conserve program. In a current research we attempted to estimate variation and differentiation within and among the populations by using allozyme markers.

Samples were collected in 13 localities (sub-populations) of three natural *A. manshuriensis* populations during 2002-2004. Using starch gel electrophoresis we investigated variation of five polymorphic loci, which were determined earlier (*Acp-2*, *Gpt*, *Gpi-2*, *Pgm*, *Fe-2*).

Allozyme analysis have shown no difference in allele set between all localities studied. However, statistical differences in allele frequencies among populations and localities were significant both at some loci and overall estimate. The Wright's F-statistics analyses revealed an excess of heterozygotes in the populations and in the localities, while approximately 2.73% heterozygote deficiency were found for the whole species. That may indicate a subdivision of the population into separate small groups. This differentiation corresponds to spatial fragmentation of the *A. manshuriensis* natural populations and exiting of a "patch structure" within the populations and may be explained by the species specific life history and evolution of these populations during the past glaciation in Pleistocene.

Interestingly, in a most exhausted population of Nezhinka river basin the highest polymorphism level and the most subdivision level were revealed, while these parameters were the smallest in the safe Malaya Borisovka River population. It is known, that population differentiation is connected with gene flow level. This parameter, estimated via Nm, comprised 2.7 for all populations and have varied in each population. Within two populations that undergone by the most strict anthropogenic pressure, Nezhinka and Ananievka rivers gene flow was 1.82 and 4.08, respectively. It is conspicuous that gene flow between sub-populations are low enough for preventing the destructive consequences of a genetic drift within small locality patches. In the Malaya Borisovka River population the highest gene flow was revealed (6.10). Noteworthy, that in this population the path structure are weekly expressed. It may be supposed, that the existence of intensive gene flow between localities within Malaya Borisovka River population allows to maintain their equilibrium and temporal stability.

Thus the data supposed that genetic drift is contributing the main input to formation of population genetic structure of the *A. manshuriensis*. The genetic drift is connected with reduce of population reproductive and genetically effective sizes, which are increasing by anthropogenic influence. On the one hand it is known that a system of sub-populations, which is connected by a gene flow, is stable for long time. On the other hand, loss any of sub-populations will dramatically influence on conservation *A. manshuriensis* populations as the whole species.