

Rapuz

INTERNATIONAL SYMPOSIUM

MAPEEG-2007

*PROGRAM &
ABSTRACTS*

MODERN ACHIEVEMENTS IN POPULATION, EVOLUTIONARY AND ECOLOGICAL GENETICS

Convener: Dr. Yuri Kartavtsev

VLADIVOSTOK & VOSTOK MBS

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,
Institute of Biology and Soil Science FEB RAS,
Far Eastern State University,
Administration of Primorsky Krai,
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,
Институт биологии моря им. А.В. Жирмунского ДВО РАН,
Биолого-почвенный институт ДВО РАН,
Дальневосточный государственный университет,
Администрация Приморского края,
Администрация г. Находка*

ФИНАНСОВАЯ ПОДДЕРЖКА:

*Дальневосточное отделение РАН,
Российский фонд фундаментальных исследований
Территориальный экологический фонд г. Находка*

Ответственные редакторы Ю.Ф. Картавец, А.П. Крюков

ISBN 5-7442-1442-9

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VARIATION IN ISLAND POPULATIONS OF FAR EASTERN VOLES, *MICROTUS FORTIS* BUCHNER, 1889 (RODENTIA, CRICETIDAE): MORPHOLOGICAL, KARYOLOGICAL, ALLOZYME AND MOLECULAR GENETIC ANALYSES

I.N. Sheremetyeva, I.V. Kartavtseva, G.N. Chelomina

Institute of Biology and Soil Science FEB RAS, Vladivostok, 690022 Russia,

e-mail: sheremet76@yandex.ru

The Far Eastern vole *Microtus fortis* Buchner, 1889 is the most widespread species on islands in Peter the Great Bay. Its existence has been registered for all islands except Stenin, Verkhovsky and Askold. Populations of this species are able to survive even on very small islands due to intrinsic mechanisms of population density regulation. Therefore, island population sizes do not reach critically high levels (Katin, 1989). The islands of Peter the Great Bay have a mainland origin and were connected to the continent up to the last transgression of the sea. The time of their isolation is dated at 7–10 or 8–12 thousand years ago (Velizhanin, 1976). Hence, the formation of the fauna of these islands descended into the last Holocene cold snap period. Thus, the above mentioned islands may represent a convenient model for studying the features of microevolutionary processes in small isolated populations of rodents.

In the study in 10 isolated *M. fortis* populations from islands of the Peter the Great Bay: Russky, Putyatina, Popova, Klikova, Reineke, Bolshoy Pelis, Rikorda, Matveeva, Skrebtsova, and Lissiy.

Three morphological types of individuals were specified (Sheremetyeva, 2003). The first types includes individuals from the populations of the Lissiy and Rikorda Islands, the second, from Russky and Putyatina Islands and the third from mainland. These types differed statistically significantly in upper tooth row length, condylobasal length and interorbital distance. The population of the Matveev Island deviated statistically significantly in tail length, diastema length, zygomatic breadth and foot length.

The kariological analysis in island populations revealed similar data to that shown previously for voles from the mainland of the Russian Far East: $2n=52$ $NF=64$ (Sheremetyeva et al., 2006).

Using electrophoretic analysis of ten enzyme systems and three proteins of non-enzyme nature for examination of the continental and island populations of the Far Eastern vole, we have identified 25 interpretable loci in them. In the animals examined, all the loci but one proved to be monomorphic (Sheremetyeva et al, 2006). For instance, in the population of the Reineke Island, in addition to the major allele ESTplasma-3-a, we have recorded another allele of this locus, ESTplasma-3-b, in one out of two animals examined. In the Far Eastern vole population from Matveeva Island, allele ESTplasma-3-b was found in all 14 animals scored.

Random amplified polymorphic DNA markers were used to estimate the level and pattern of genetic diversity in *M. fortis* populations from mainland and islands of the Russian Far East (Sheremetyeva, Chelomina, 2003; Chelomina, Sheremetyeva, 2007). No markers were found as for individual populations, as for mainland or island voles in whole, however they appeared to be different in both their allele frequencies and microevolution mode based on correlation pleiad analysis. Besides, the island populations demonstrated a higher level of genetic differentiation among themselves, and each mainland population represented more species genetic diversity, than any population of islands. Nevertheless, exact test did not support belonging of both united mainland and united island populations to the same genetic unit ($p=0.0025$). RAPD data reliably differentiated voles of Matveeva Island, strongly differentiated also on morphological traits, as the most distant among all local populations examined that did not exclude the island speciation event. In the tree derived from the DNA sequences, *M. fortis* forms a distinct clade with low intraspecific differentiation. However, the population from one of Matveeva Island tends to fix a rare haplotype.