

6205 Genetic Structure of Amur Tiger (*Panthera tigris altaica*) Population: How Are Segregated Sikhote-Alin and Southwest Primorye Groups?

Pavel Sorokin¹, Vyatcheslav Rozhnov², Victor Lukarevskiy³, Sergey Naidenko², Jose Hernandez-Blanco², ¹A. N. Severtsov Institute of Ecology and Evolution, Russian Academy of Sciences, Moscow, Russian Federation; ²A. N. Severtsov Institute of Ecology and Evolution, Moscow, Russian Federation; ³Sayano-Shushensky Nature Reserve, Krasnoyarsk, Russian Federation. Contact: sorokin-p@yandex.ru

We developed the procedure of noninvasive individual identification of the Amur tigers by molecular genetic methods. Using this technique, relationships in groups of tigers in the Russian Far East was defined. We identified 63 different animals as a result of genotyping 240 feces, 7 hair and 10 blood samples collected within southern Sikhote-Alin (Ussurisky Reserve), northern Sikhote-Alin (Khabarovskiy Krai) and Southwest Primorye. Analysis of nuclear DNA at 9 microsatellite loci has demonstrated genetic similarity of animals from the Ussurisky Reserve and Khabarovskiy Krai, and their difference in comparison to the animals in Southwest Primorye. Genetic differentiation between the Sikhote-Alin and Southwest Primorye populations was not very high ($RST = 0.22$; $P < 0.05$). Four individuals genetically associated with the Sikhote-Alin samples were geographically located within the Southwest Primorye population, with over 90% of their genotypes assigned to Sikhote-Alin. There were no animals that were genetically assigned to the Southwest Primorye that were sampled in Sikhote-Alin. Thus gene flow is conducted between these two populations mainly in one direction, from a large group to a small one. Genetic diversity of the population from Southwest Primorye is higher than that of the Sikhote-Alin population. According to our data the average observed heterozygosity for the Sikhote-Alin population is $H_o=0.57\pm0.02$, for the tigers from Southwest Primorye $H_o=0.61\pm0.04$. The average number of alleles per locus is 3.33 ± 1.00 and 3.56 ± 0.73 respectively. The research was supported by the Russian Geographic Society and the grant of the President of the Russia Federation № MK-4313.2014.4.