MEETING IN ST. PETERSBURG

Abstracts
Papers by Young Scientists

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«MODERN PROBLEMS OF GENETICS, RADIOBIOLOGY,
RADIOECOLOGY, AND EVOLUTION»

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A REAPPRAISAL OF BASIC MECHANISMS OF RADIATION»

St. Petersburg, 2–6 June 2015

ABSTRACTS
PAPERS BY YOUNG SCIENTISTS

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NARROW-HEADED VOLE EXPERIMENT DOES NOT CONFIRM A FAMILY SPECIFICITY OF THE ^{90}SR METABOLISM HYPOTHESIS

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Northern mole vole is subterranean rodent, colonies of this animals consist of families. 84% of a variability of ^{90}Sr accumulation for northern mole voles, caught in East-Ural radioactive trace (EURT), referred to a factor "a family" (Starichenko, 2011). The author associates this fact with a heterogeneity of ^{90}Sr contamination or family specificity of the ^{90}Sr metabolism. It is important to explore ^{90}Sr metabolism differences for EURT-rodents population for a comprehension the adaptation to the radiation. This activity is our pilot research of this area. The object of the research is narrow-headed vole. Colonies of voles consist of initial couple of animals and its progeny. Animals had been caught by live-traps in the EURT-area dimensions 80*100 sq. m. We took mandibles for radiometry analysis (Malinovsky et al., 2012). We defined allelic composition of four microsatellite loci: MSMoe02, Mar49, Mar80, MSMM2 (Ruda et al., 2009). Genotypes of voles were analyzed using program Structure v. 2.3.4 (Pritchard et al., 2000). This method identifies genetically distinct clusters on the basis of individual genotypes at multiple loci. We marked out three groups of animals. 32 of 38 individuals were included in one of these groups with support more than 75%. Most of animals, included in one cluster, were caught in traps, located in close from each other. These aggregations of voles we consider as a colony. One individual was put to the cluster №2, but this animal was caught in a territory of the colony, populated by animals from cluster №1. We considered this individual as a migrant. Specific activity of accumulated in vole's mandibles ^{90}Sr for colony № 1 is (N=7, mean=493, min-max=433-534), for colony №2 is (N=7, mean=392, min-max=341-426,), for the migrant it is 529 Bq/g. Colony №1 and №2 animals differ in specific activity of ^{90}Sr and in genotypes. The migrant has genotype as colony №2 animals, but specific activity of ^{90}Sr as colony №1 animals. A mosaic structure of contamination is more simple explanation of this fact, then metabolism of ^{90}Sr differences of different families. This study was supported by Russian Foundation for Basic Research (project 14-04-01484_a)