

# Elevated mitochondrial genome variation after 50 generations of radiation exposure in a wild rodent

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## Abstract

Currently, the effects of chronic, continuous low dose environmental irradiation on the mitochondrial genome of resident small mammals are unknown. Using the bank vole (*Myodes glareolus*) as a model system, we tested the hypothesis that approximately 50 generations of exposure to the Chernobyl environment has significantly altered genetic diversity of the mitochondrial genome. Using deep sequencing, we compared mitochondrial genomes from 131 individuals from reference sites with radioactive contamination comparable to that present in northern Ukraine before the 26 April 1986 meltdown, to populations where substantial fallout was deposited following the nuclear accident. Population genetic variables revealed significant differences among populations from contaminated and uncontaminated localities. Therefore, we rejected the null hypothesis of no significant genetic effect from 50 generations of exposure to the environment created by the Chernobyl meltdown. Samples from contaminated localities exhibited significantly higher numbers of haplotypes and polymorphic loci, elevated genetic diversity, and a significantly higher average number of substitutions per site across mitochondrial gene regions. Observed genetic variation was dominated by synonymous mutations, which may indicate a history of purify selection against non-synonymous or insertion/deletion mutations. These significant differences were not attributable to sample size artifacts. The observed increase in mitochondrial genomic diversity in voles from radioactive sites is consistent with the possibility that chronic, continuous irradiation resulting from the Chernobyl disaster has produced an accelerated mutation rate in this species over the last 25 years. Our results, being the first to demonstrate this phenomenon in a wild mammalian species, are important for understanding genetic consequences of exposure to low-dose radiation sources.

## KEYWORDS

bank vole, Chernobyl, chronic exposure, environmental radiation, mitochondrial genome

## 1 | INTRODUCTION

It is well documented that high doses of acute radiation cause mutations with frequent negative genetic and health consequences

(Hallahan, Spriggs, Beckett, Kufe, & Weichselbaum, 1989; Hong et al., 1995; Little, Nagasawa, Pfenning, & Vetrovs, 1997; Morgan, Day, Kaplan, McGhee, & Limoli, 1996; Müller et al., 1996; Tucker, Cofield, Matsumoto, Ramsey, & Freeman, 2005; Ward, 1995). What is not

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