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A genome-wide analysis of mutation induction in the mouse germ-line

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The ability to predict the genetic consequences for humans of exposure to ionizing radiation and chemical mutagens has been one of the most important goals of human genetics in the past fifty years. However, despite numerous efforts, little is known about the genetic effects of radiation exposure in humans and the only definitive evidence for germ-line mutation induction *in vivo* in mammals comes from mouse studies. Recent advances in genetic technologies have provided new microarray-based and next generation sequencing-based tools for the genome-wide analysis of genetic variation, which have the potential for characterizing germ-line mutation in humans and mice. Using microarray-based comparative genomic hybridization and high depth (>22X) whole genome HiSeq sequencing we have recently carried out a matched case control experiment to investigate the effects of ionizing radiation on germ-line mutation in mice. We found that the frequency of *de novo* Copy Number Variants (CNVs) and insertion/deletion events indels was significantly elevated in offspring of exposed fathers. We also showed that the spectrum of induced *de novo* SNVs is strikingly different; with clustered mutations being significantly over-represented in the offspring of irradiated males. Our study highlights the specific classes of radiation-induced DNA lesions that evade repair and result in germ-line mutation and paves the way for similarly comprehensive characterizations of other germ-line mutagens.

Biography

Yuri E Dubrova has completed his PhD from NI Vavilov Institute of General Genetics, Moscow. He is a Professor of Genetics at the Department of Genetics, University of Leicester. He has published more than 90 papers in reputed journals and has been serving as an Editorial Board Member of Mutation Research.

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