

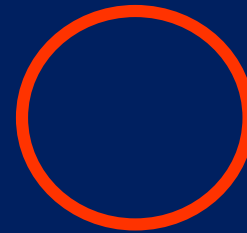
SREL' s Low Dose Irradiation Facility (LoDIF)



Unique in the World For Aquatic Organisms

LoDIF

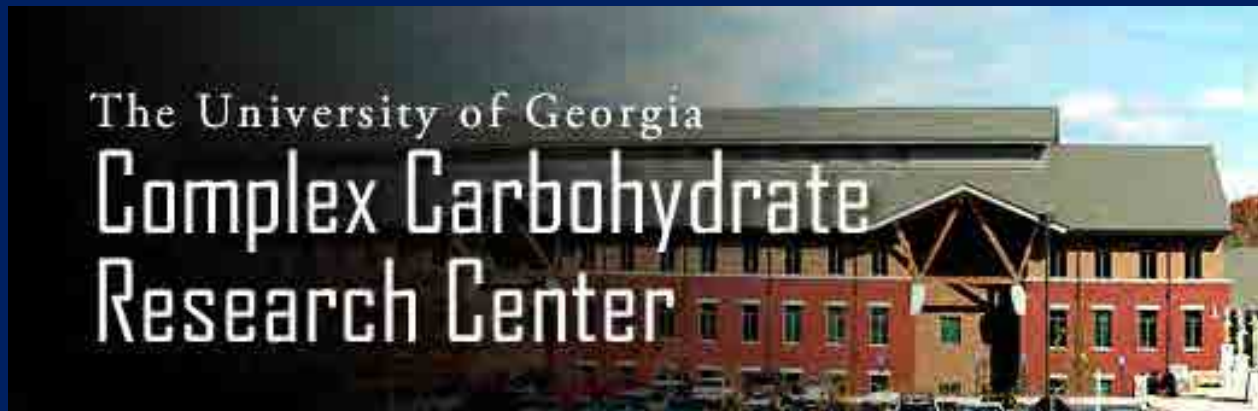
- **40** mesocosms
 - **8** pads of **5** mesocosms
 - Each pad has
 - **2** controls
 - **1** - $\sim 2\text{mGy/day}$
 - **1** - $\sim 20\text{mGy/day}$
 - **1** - $\sim 200\text{mGy/day}$
 - **3-4** buckets/mesocosm
- * **Doses can be modified**



◎ **Proteomics,
Glycomics, and
Epigenetics of
Radiation Exposure
in Medaka**



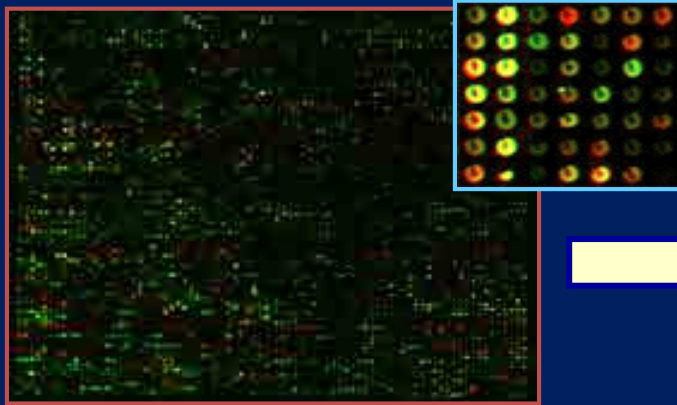
Collaborating with UGA faculty from the:



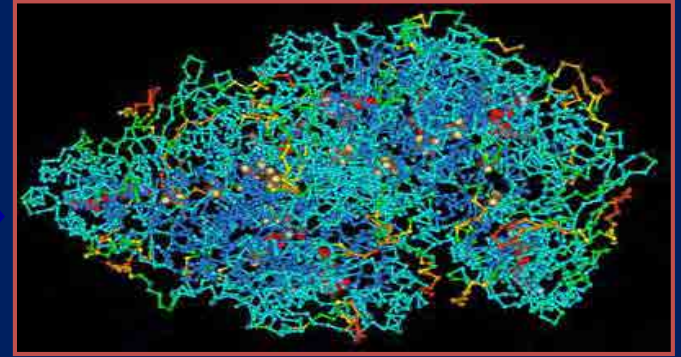
Low Dose Radiation Surveillance and Monitoring Research and Development



DNA molecule



DNA micro array



protein



organisms



ecosystem

Protocol

An Effective Protocol for Proteome Analysis of Medaka (*Oryzias latipes*) after Acute Exposure to Ionizing Radiation

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Received: 11 June 2019; Accepted: 20 July 2019; Published: 30 July 2019

Abstract: All terrestrial organisms are subject to evolutionary pressures associated with natural sources of ionizing radiation (IR). The legacy of human-induced IR associated with energy, weapons production, medicine, and research has changed the distribution and magnitude of these evolutionary pressures. To date, no study has systematically examined the effects of environmentally relevant doses of radiation exposure across an organismal proteome. This void in knowledge has been due, in part, to technological deficiencies that have hampered quantitative environmentally relevant IR dose and sensitive detection of proteomic responses. Here, we describe a protocol that addresses both needs, enabling quantitative IR delivery with a reliable method to yield proteomic comparisons of control and irradiated Medaka fish. Experiments were conducted at the Savannah River Ecology Laboratory (SREL, in Aiken, SC) where fish were subsequently dissected into three tissue sets (scavenged, organs and intestines) and frozen until analysis. Tissue proteins were extracted, resolved by Sodium Dodecyl Sulfate-Polyacrylamide Gel Electrophoresis (SDS-PAGE), and each sample lane was divided into six equal portions. Following in-gel tryptic digestion, peptides released from each gel portion were identified and quantified by Liquid Chromatography-Mass Spectrometry (LC-MS/MS) to obtain the most complete, comparative study to date of proteomic responses to environmentally relevant doses of IR. This method provides a simple approach for future ongoing epidemiologic studies of chronic exposure from environmentally relevant levels of IR and should also serve well in physiological, developmental, and toxicological studies.

Keywords: in-gel digestion; ionizing radiation; medaka; *Oryzias latipes*; proteome

1. Introduction

Ionizing radiation (IR), from other than natural sources, has become an aspect of daily life over the course of the last century. While sites such as Fukushima and Chernobyl are well known and well documented sources of exposure to radiation, there remain over 1000 locations within the United States alone that are contaminated with radiation and have yet to be sufficiently studied to fully understand the risk to human health and to the environment. Testing and manufacturing related to nuclear proliferation (for both energy and weapons) and rapid increases in the use of nuclear medicine [1], are becoming increasingly identified as sources of radioactive contamination. Such contamination can have long lasting effects on public health and the environment, particularly in aquatic systems.

Article

Proteogenomic Analysis of *Burkholderia* Species Strains 25 and 46 Isolated from Uraniferous Soils Reveals Multiple Mechanisms to Cope with Uranium Stress

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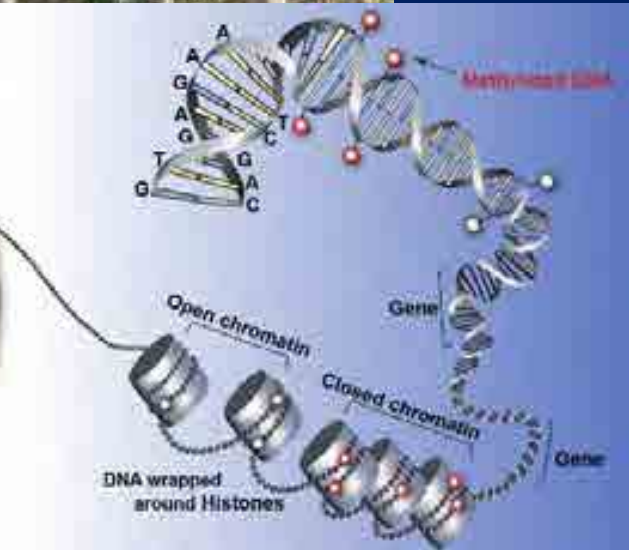
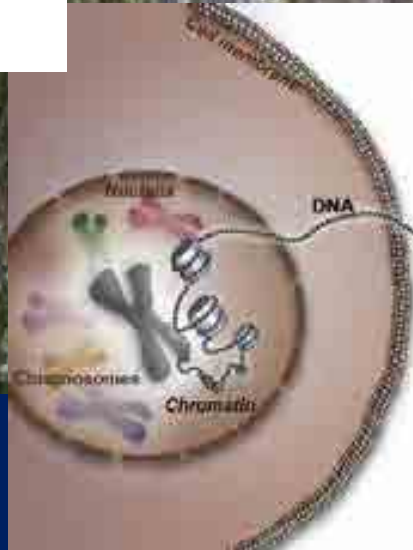
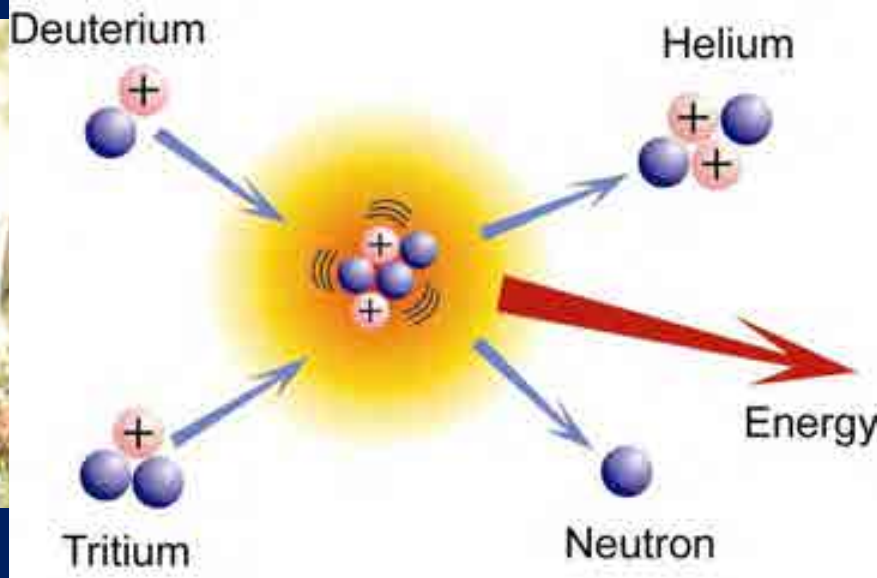
Received: 3 November 2019; Accepted: 31 December 2019; Published: 12 December 2019



Abstract: Two *Burkholderia* spp. (strains SR5-25 and SR5-46) were isolated from high concentrations of uranium (U) from the U.S. Department of Energy (DOE)-managed Savannah River Site (SRS). SR5 contains soil gradients that remain co-contaminated by heavy metals from previous nuclear weapons production activities. Uranium (U) is one of the dominant contaminants within the SRS impacted soils, which can be microbially transformed into less toxic forms. We established microcosms containing strains SR5-25 and SR5-46 spiked with U and evaluated the microbially-mediated depletion with concomitant genomic and proteomic analysis. Both strains showed a rapid depletion of U; draft genome sequences revealed SR5-25 genome to be of approximately 6,152,324 bp with a G + C content of 66.5, containing a total 7604 coding sequences with 77 total RNA genes. Similarly, strain SR5-46 contained a genome size of 6,397,429 bp with a G + C content of 67.1, 7995 coding sequences, with 73 total RNA genes, respectively. An in-depth, genome-wide comparison between strains 25, 46 and a previously isolated strain from our research (*Burkholderia* sp. strain SR5-W-3-2016) revealed a common pool of 3126 genes; many were found to be homologous to previously characterized metal resistance genes (e.g., for cadmium, cobalt, and zinc), as well as for transport, stress/detoxification, cytochromes, and drug resistance functions. Furthermore, proteomic analysis of strains with or without U stress, revealed the increased expression of 34 proteins from strain SR5-25 and 32 proteins from strain SR5-46, similar to the genomic analysis, many of these proteins have particularly been shown to function in stress response, DNA repair, protein biosynthesis and metabolism. Overall, this comparative proteogenomics study confirms the importance of metabolic and stress response functions likely mediating the ecological competitiveness to the isolated strains for colonization and survival in the heavy metals contaminated SR5 soil habitat.

Keywords: proteomics; proteogenomics; uranium; *Burkholderia*

Other Relevant Externally Funded Research





SAVANNAH RIVER ECOLOGY LABORATORY



THANK YOU