**Fiscal Year:** FY 2018  
**Task Last Updated:** FY 06/27/2018

**PI Name:** Hada, Megumi Ph.D.  
**Project Title:** Computational Model Prediction and Biological Validation using Simplified Mixed Field Exposures for the Development of a GCR Reference Field  
**Division Name:** Human Research  
**Program/Discipline:**  
- **Program/Discipline--Element/Subdiscipline:** HUMAN RESEARCH--Radiation health

**Joint Agency Name:**  
**TechPort:** No

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**Space Biology Cross-Element Discipline:** None  
**Space Biology Special Category:** None  
**PI Email:** mehada@pvamu.edu  
**Fax:** FY  
**PI Organization Type:** UNIVERSITY  
**Phone:** 936-261-3155  
**Organization Name:** Prairie View A&M University  
**PI Address 1:** College of Arts and Sciences, PO BOX 519, MS-2230, New Science Bldg  
**PI Address 2:**  
**PI Web Page:**  
**City:** Prairie View  
**State:** TX  
**Zip Code:** 77446  
**Congressional District:** 10  
**Comments:**

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**Contact Monitor:** Simonsen, Lisa  
**Contact Phone:**  
**Contact Email:** lisa.c.simonsen@nasa.gov  
**Flight Program:**  
**Flight Assignment:** NOTE: End date changed to 3/31/2020 per NSSC information (Ed., 8/8/18)  

**Key Personnel Changes/Previous PI:**

**COI Name (Institution):**  
- Patel, Zarana Ph.D. (Wyle Laboratories, Inc.)  
- Plante, Ianik Ph.D. (Wyle Laboratories, Inc.)  
- Ponomarev, Artem Ph.D. (Wyle Laboratories, Inc.)  
- Shavers, Mark Ph.D. (Wyle Laboratories, Inc.)  
- Slaba, Tony Ph.D. (NASA Langley Research Center)  

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**Performance Goal Text:**

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This work addresses the need to develop and utilize mixed field irradiation protocols that approximately represent the...
Rationale for HRP Directed Research:
This work addresses the need to develop and utilize mixed field irradiation protocols that approximately represent the shielded tissue environment in space and that can be combined with single-beam studies to validate and further improve cancer risk models. Extensive studies have been carried out on the induction of chromosomal aberrations by low- and high-LET (linear energy transfer) radiation in human lymphocytes, fibroblasts, and epithelial cells exposed in vitro. The results, which are consistent with computational modeling predictions, establish chromosome aberration models as an LET-sensitive tool for predicting damage from single ion exposures. However, there is a lack of data on chromosome aberrations induced by low dose rate chronic exposure and mixed field beams such as those expected in space. These proposed studies will define a simplified mixed field and make model predictions of the effects of dose rate, mixed fields, and shielding on expected biological damage. Chromosome aberration studies at NASA Space Radiation Laboratory (NSRL) will provide the biological validation needed to extend the computational models over a broader range of experimental conditions ((more complicated mixed fields leading up to the galactic cosmic radiation (GCR) simulator)), helping to reduce uncertainties in radiation quality effects and dose-rate dependence in cancer risk models (Cancer-3 and -4). These models can then be used to answer some of the open questions regarding requirements for a full GCR reference field, including particle type and number, energy, dose rate, and delivery order.

Research Impact/Earth Benefits:
This strategy of single and mixed field exposures and varying dose rates along with a well-defined biological assay and established computational models will provide a unique opportunity to develop an intermediate mixed field that can closely approximate the GCR reference field. This represents a critical step towards using the GCR simulator at NSRL to reduce uncertainties in radiation quality effects and dose-rate dependence in cancer risk models.

Task Progress:
1) A new simulation program named RITCARD (Radiation induced tracks, chromosome aberrations, repair, and damage) was created. This code is based on NASARTI (NASA Radiation Track Image) and is simulating chromosome damage by random walk, radiation-induced chromosome breaks, repair, and aberrations. The code is largely using C++ objects named classes, and mostly follows coding standards.
2) The random walk algorithm for simulating chromosome aberrations was isolated from NASARTI and is now a stand-alone program.
3) The RITRACKS 3D OpenGL interface was adapted to display the chromosomal fragments and aberrations.
4) A graphic user interface (GUI) was created to display chromosome aberration results, the repair kinetics, the fragment size distribution, and a schema of the fragment sequences.
5) A GUI was created to select some input parameters for the random walk algorithm.
6) The Windows interface of RITRACKS was modified to execute RITCARD in parallel.
7) Script were made to execute RITCARD on the Langley cluster.
8) The post-simulation program was updated and improved to collect results from RITCARD, adding a component to calculate error bars.
9) A wrapper script was written to execute multiple simulations consecutively on the Langley cluster.
10) Investigating the discrepancies in restitution kinetics curves between the codes NASARTI and RITCARD have been measured.
11) New simulation program RITCARD:
   - Mixed beam with shielding (4 beams combination): H (344 MeV) + He (344 MeV/n) + O (350 MeV/n) + Ti (300 MeV/n); 10.62 + 3.17 + 1.08 + 0.74, 21.24 + 6.33 + 2.16 + 1.47, 42.48 + 12.66 + 4.32 + 2.94 with acute and chronic dose rate.
   - Mixed beam with shielding (2 beams combination): H (344 MeV) + Fe (950 MeV/n); 18.03 + 5.64 with acute and chronic dose rate.
   - Mixed beam without shielding: H (250 MeV), He (250 MeV/n), O (350 MeV/n), and Ti (300 MeV/n); 0, 0.5, 1, 5, 10, 20, and 40 cGy with acute and chronic dose rate.
   - Mixed beam with shielding (2 beams combination): H (344 MeV) + Fe (950 MeV/n); 18.03 + 5.64 with acute and chronic dose rate.
   - Beams, energy and dose used are followed. Single beam with shielding: H (344 MeV), He (344 MeV/n), O (450 MeV/n), and Fe (950 MeV/n); 0, 0.5, 1, 5, 10, 20, and 40 cGy with acute and chronic dose rate.
   - Single beam without shielding: H (250 MeV), He (250 MeV/n), O (350 MeV/n), and Ti (300 MeV/n); 0, 0.5, 1, 5, 10, 20, and 40 cGy with acute and chronic dose rate.

Chromosome samples were collected in the first mitosis after exposure (total 213 samples). Analysis of chromosome aberrations (CA) with 3-color fluorescent in situ hybridization (FISH) chromosome painting methods has been progressing and currently about 40% of samples analysis has completed.

Preliminary results show: 1) Shielding fully blocked the 56Fe beam. The 344.1 MeV proton beam punched through the shield with roughly 250 MeV remaining. Although shielding blocked 100% of the primary 56Fe beam, chromosome aberrations were observed behind the shielding from the secondary exposure.
2) Chronic exposure induced less chromosome aberrations than acute exposure with proton beam without shielding, but more chromosome aberrations than acute exposure in with shielding. Chronic exposure induced more chromosome aberrations than acute exposure in Ti-ions but no difference in acute and chronic exposure in Fe-ions with shielding.
3) Proton and Fe ion mixed exposure with shielding induced more damage than additive of two single exposures.

New simulation program RITCARD:
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revealed that some errors are present in the NASARTI restitution algorithm. The errors are being corrected, and new calculations are performed to evaluate the impact of these new changes. 11) Calculations of chromosome aberrations were simulated with the code RITCARD for various ion types and conditions.

a. Single beams: 1H+, 4He2+, 12C6+, 16O8+, 20Ne10+, 28Si14+, 48Ti22+, and 56Fe26+, with energies varying from 10 to 1,000 MeV/u; b. For shielded beams, calculations of chromosome aberrations were made using simplified and detailed particle spectra.

Updates to RITRACKS: Several changes were made in the code RITRACKS (Relativistic Ion Tracks) to simulate mixed beams and galactic cosmic rays (GCR). More specifically, the code is currently able to simulate stochastic track by multiple beams of particles of various ion types, energies, and dose/fluence specified by the user.

Another sub-program was included in RITRACKS to simulate beams representative of the GCR environment. By using known GCR fluence spectra, the code generates sample of ions at various energies impacting a given surface during a specific time frame (e.g., the tracks impacting a 10 microm nucleus during a 3-years mission).

Dose-rate was added later in RITRACKS. Specifically, the time intervals (begin and end) of a given ion type are added in the input parameters. The time intervals can be separated and/or overlapping. All these parameters are entered in various graphic user interfaces (GUI).

Using the parameters, the tracks are simulated as usual. In the visualization interface, it is now possible to select the individual tracks to display. The time-dependent differential and cumulative voxel dose map is calculated. The differential voxel dose map will be used for future dose-rate effect studies.

A new GUI was added to display the time of creation of each particle in the beam.

For additional validations, changes in the code to generate statistics for individual tracks are in progress.

Beams calculations: Calculations of the input parameters were made for the beams after shielding for the ion types used in the experiments of this project. The calculation part was implemented in the new cluster for parallel calculations, as a part of the simulation code BDSTracks.

Bibliography Type: Description: (Last Updated: 06/28/2018)

Abstracts for Journals and Proceedings

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