

COMPUTATIONAL MODEL PREDICTION AND BIOLOGICAL VALIDATION USING SIMPLIFIED MIXED FIELD EXPOSURES FOR THE DEVELOPMENT OF A GCR REFERENCE FIELD

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ABSTRACT

The yield of chromosomal aberrations has been shown to increase in the lymphocytes of astronauts after long-duration missions of several months in space. Chromosome exchanges, especially translocations, are positively correlated with many cancers and are therefore a potential biomarker of cancer risk associated with radiation exposure. Although extensive studies have been carried out on the induction of chromosomal aberrations by low- and high-LET radiation in human lymphocytes, fibroblasts, and epithelial cells exposed *in vitro*, 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.

Chromosome aberration studies at 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 rays (GCR) simulator), helping to reduce uncertainties in radiation quality effects and dose-rate dependence in cancer risk models. 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.

In this study, we designed a simplified mixed field beam with a combination of proton, helium, oxygen, and iron ions with shielding or proton, helium, oxygen, and titanium without shielding. Human fibroblasts cells were irradiated with these mixed field beam as well as each single beam with acute and chronic dose rate, and chromosome aberrations (CA) were measured with 3-color fluorescent *in situ* hybridization (FISH) chromosome painting methods. Frequency and type of CA induced with acute dose rate and chronic dose rates with single and mixed field beam will be discussed.

A computational chromosome and radiation-induced DNA damage model, BDSTRACKS (Biological Damage by Stochastic Tracks), was updated to simulate various types of CA induced by acute exposures of the mixed field beams used for the experiments. The chromosomes were simulated by a polymer random walk algorithm with restrictions to their respective domains in the nucleus [1]. The stochastic dose to the nucleus was calculated with the code RITRACKS [2]. Irradiation of a target volume by a mixed field of ions was implemented within RITRACKS, and the fields of ions can be delivered over specific periods of time, allowing the simulation of dose-rate effects. Similarly, particles of various types and energies extracted from a pre-calculated spectra of galactic cosmic rays (GCR) can be used in RITRACKS. The number and spatial location of DSBs (DNA double-strand breaks) were calculated in BDSTRACKS using the simulated chromosomes and local (voxel) dose. Assuming that DSBs led to chromosome breaks, and simulating the rejoining of damaged chromosomes occurring during repair, BDSTRACKS produces the yield of various types of chromosome aberrations as a function of time (only final yields are presented). A comparison between experimental and simulation results will be shown.

REFERENCES

- [1] Ponomarev A.L. et al (2014) Rad Res 181, 284-292.
- [2] Plante I. et al (2013) Phys. Med. Biol. 58, 6393-6405.