Using single-cell DNA sequencing as a dosimetric tool – An exploratory study

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Mutation signature of radiation









Our proposal





Our single-cell sequencing experiment



- B-lymphoblastoid cells6 MV Photons
 - Control
 - 0.5 Gy
 - 1.5 Gy
 - 3.0 Gy





24 hrs incubation for the cells to undergo one cell cycle (one repair cycle) ³Sequencing



Single-Cell Whole Genome Sequencing

~500 cells per sample





Mutation analysis of each individual cell sequenced.

Large deletions and structural variations in the genome are measured

Preliminary result



Single-cell sequencing experiment result

Radiation dose (Gy)

Our single-cell irradiation simulation



Monte Carlo single-cell geometric nuclear DNA model

- Model built in TOPAS-nBIO simulation toolkit
- More than 100 cells were individual irradiated with doses:
 - 0.5 Gy
 - 1.5 Gy
 - \circ 3.0 Gy
- Cluster of DNA damages (damages within 40bp from each other) that has at least one double strand break (DSB) is counted

Poster by James Manalad (P2-17)







Double strand break cluster

Montgomery et al. 2001



Single-cell irradiation simulation results

Survival curve of our cells



Simulation results adjusted for cell death



Summary

- We believe we will be able to discern radiation induced tumours according to the radiation quality based on the mutational patterns involved.
- We performed single-cell sequencing of irradiated cells and found a dose dependent increase in the number mutations across the genome.
- We also performed single-cell irradiation simulations and found agreement between simulation and experiment.
- Experiment needs to be repeated and the preliminary findings must be validated.

Potential applications of this work

- Learn about carcinogenesis and mutation signature of neutrons.
- Discern radiation type involved in biological data.
- Develop new bio-dosimetry techniques
- Develop predictive risk models.

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