

# Validation of Monte Carlo Simulations to Assess DNA Damage from <sup>225</sup>Ac for Radiopharmaceutical Therapy

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# Outline

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  - Biological effect, DNA strand breaks
- Methods
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  - Monte Carlo simulations in Geant4 and TOPAS-nBio
  - Comparison of DNA double strand breaks
- Results
- Conclusion and future work



### Decay chain of <sup>225</sup>Ac





Actinuim-225 in a vial

- Max range of 2 MeV  $\beta^2$  = 10 mm
- Max range of 1.4 MeV  $\beta^-$  = 6.3 mm
- Max range of  $\alpha$ -particles from decay chain = ~95  $\mu$ m

# Radiobiology: Biological effect

- Energy deposition in volumes corresponding to single cells or cell organelles
- Particles release energy differently along their tracks (LET): sparse ionizations (β<sup>-</sup>), dense ionizations (α)
- Biological effect of radiation depends upon the LET
- DNA is the critical target for radiation-induced cell death

Particle types	Energy (MeV)	LET (keV/µm)
electron	0.1 1.0	0.42 0.25
250 kV x-rays	0.25	2.0
proton	10 250	4.7 6.5-14
alpha	5	50-200



# **RBE** as a function of LET



- Ratio between the dose from a standard radiation and the test radiation to produce the same biological effect
- One track of x-rays (100 kV) is unlikely to cause a DSB
- Efficient radiation is the one with LET approximately 100 keV/µm, as the distance between two consecutive ionization events is equal to the diameter of the DNA
- Further increases in LET beyond 100 keV/µm results in a decrease in RBE

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# Cell culture experiment with <sup>225</sup>Ac

#### Cell line before irradiation





Nucleus staining shows ~rounded nucleus with an average diameter of 10  $\mu m$ 



- Mouse breast cancer cell line (E-0771)
- Cells seeding density: (1.5-3) × 10<sup>3</sup> cells/well
- Cells were irradiated with varying levels of <sup>225</sup>Ac for 24 h: 2.4, 5.3, 11.8, 18.9, 41.5, 83.0, 175.1, and 345.2 nCi/well
- Excess activities were removed after 24 h using the phosphatebuffered saline (PBS)
- Stage of cells in a cell cycle were not controlled
- DNA DSBs estimated using γ-H2AX immunofluorescent staining



# **TOPAS-nBio Monte Carlo Simulation**

- TOPAS-nBio is an extension of TOPAS Monte Carlo toolkit, supports radiobiology simulation
- Direct, indirect and complex DNA damage can be scored
- Full nucleus DNA model is available in TOPAS-nBio (Zhu et al, 2020)



(a) Nucleosome with 200 base pairs (bp)

(b) Chromatin fiber with 15.15 kbp

(c) Nucleus with 6.08 Gbp and 46 chromosomes

Voxels of same color represent chromosome Total voxels in nucleus = 14,328 filled with chromatin fibers

#### Scoring of DNA strand breaks

- Strand break was scored when accumulated energy deposition exceeded 17.5 eV
- If at least 2 stand breaks occurred within 10 base pair distance, then it was recorded was as DSB, otherwise recorded as SSB



### Monte Carlo Simulation of Cell Culture



Cell well dimension:

- Height 10.8 mm
- Well diameter 7.15 mm
- Solution height 5 mm
- Wall thickness 0.5 mm



### Simulation workflow for DNA damage estimation



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TOPAS-nBio Simulation

# **Results: Experimental measurement**

- Measurement results are in #foci/nuclei
- We averaged out the hot or bright spots from the images to get DSBs
- Image analysis were performed in ImageJ software



Bright spot represents focus of  $\gamma$ -H2AX formation (DNA DSBs location in cell nucleus)



### Results: Experimental measurement – preliminary



- We observed a linear doseresponse curve at low activity of <sup>225</sup>Ac
- Saturation/plateau occurred at higher doses
- This indicates that effects of indirect damage at higher doses (activity) become less significant compared to the direct damage



# **Results: Experimental vs Simulation**



Limitations of this work:

- Small sample size
- Cells were randomly defined, does this truly reflect the experimental situation?
- Generic nuclear model was used
- Effects of cross talk of radiation between different wells is not included
- > DNA repair simulations



# Conclusion and future works

- Experimental measurement of DSB agrees with Monte Carlo simulation
- This work did not incorporate the cross-talk between the particles in cell well, future work should include this information
- DNA repair simulations should be the next step, because repair can happen immediately after irradiation
- Monte Carlo simulation with TOPAS-nBio platform seems a great tool for radiation biology simulations





# Thank you





Indiana University Health







# Cross-talk: Ongoing work

1 mm



Figure: Illustration of cross-talk

Cross talk from  $\alpha$  is ZERO

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- Cross talk from  $\beta$  is non-zero, as the wall thickness of cell well is << than the max. range of  $\beta$  particles
- $\gamma$  can easily escape from the wells

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#### Nucleus voxel filling mechanism



Voxel is filling using a fractal pattern based on a 3D Hilbert space-filling.

