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Yann Thibaut, Carmen Villagrasa, Sébastien Incerti, Yann Perrot

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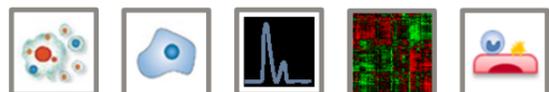


MODELING THE RADIATION-INDUCED DNA DAMAGE TOPOLOGY AT THE CELL POPULATION LEVEL

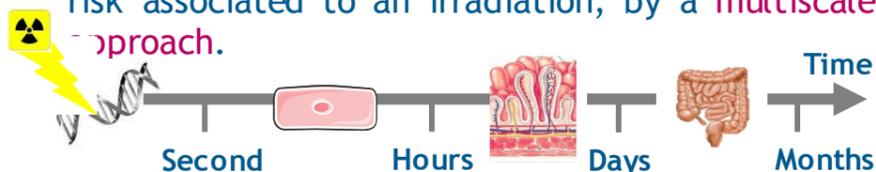
Y. THIBAUT¹, C. VILLAGRASA¹, S. INCERTI², and Y. PERROT¹
¹ IRSN/PSE-SANTE/SDOS/LDRI, ² CNRS/IN2P3/CENBG

ROSIRIS PROGRAM

- Goal: Define a **multiparametric EBR**.



- Why: To **optimize the risk estimation** in radiation therapies.
- How: Developing a simulation tool to predict the risk associated to an irradiation, by a **multiscale approach**.



INTRODUCTION

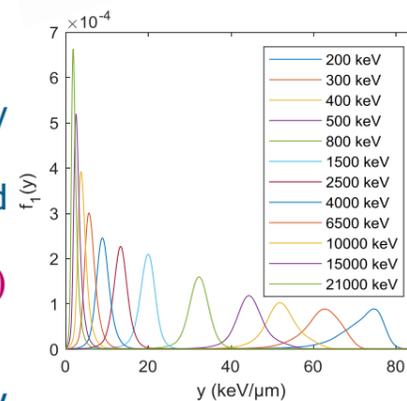
A nanodosimetric simulation chain, based on **Geant4-DNA** toolkit (geant4-dna.org), has already been developed at IRSN, to **model the DNA damage topology** induced by different radiation qualities at the cell nucleus scale. The next step consists in extending this modeling at the cell population level. To this, the stochastic distribution of the **energy imparted for each nucleus** of the population must be considered (*Gruel, Plos One, 2016*).



MATERIALS and METHODS

- Building a **microdosimetric database of monoenergetic spectra** over a large energy range (1 keV to 20 MeV) for different particles (e⁻, p⁺, α) in endothelial nucleus.
- Interpolating between the database spectra to obtain any non-simulated monoenergetic spectra ($f_1(y)$).
- Combining the spectra, according to a given beam quality, to obtain the $f_1(z)$ **spectrum of the cell population**.
- Distributing the events cell by cell in the population.

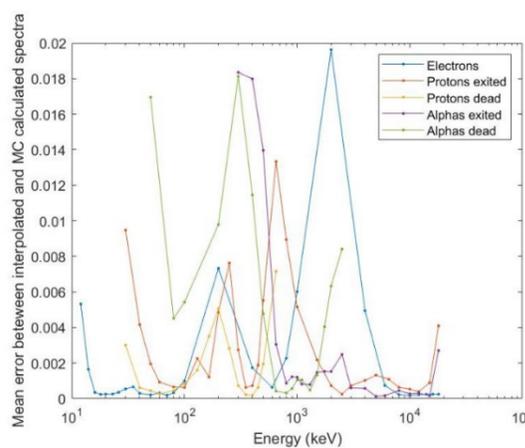
To benchmark our method, we compare the event distribution obtained for a 14.5 MeV neutrons irradiation with the one obtained by Monte-Carlo simulation.



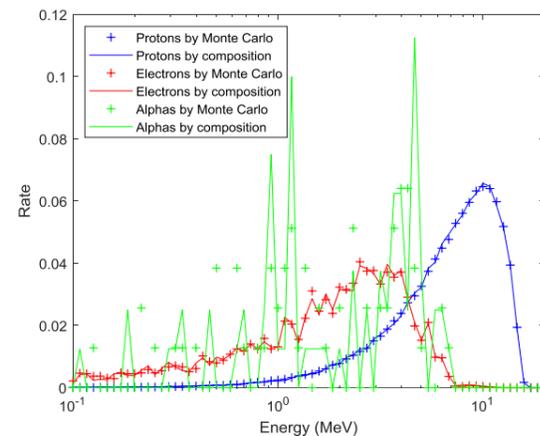
Protons that pass through the nucleus (exited): database spectra

RESULTS

It can be observed that the mean error for the calculation by interpolation of the microdosimetric spectra database **does not exceed 2%** on the entire energy range. The energy distribution of the events obtained corresponds to that calculated by Monte Carlo method.



Mean error evaluation of interpolated spectra



Energy comparison of events distributed by interpolation or calculated by Monte Carlo method

DISCUSSION

The results of the benchmark of the event distribution method in the cell population are satisfactory. Indeed, **the events distribution agrees with the results obtained by Monte Carlo modeling**. The next step is to link each of these events to a damage topology using nanodosimetric calculations. To validate this step, we will compare our results to **experimental measurements**.

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