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TILDA-V: A full-differential code for proton tracking in biological matter

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Synopsis Monte Carlo track structure codes are commonly used for predicting the radio-induced biological damages at the cellular scale. However most of them are based on semi-empirical cross sections as well as the use of water as surrogate of the biological matter. The aim of this work is to present our *home-made* Monte Carlo code, called TILDA-V, based on a quantum-mechanical cross section data base able to model all the proton- and secondary electron-induced collisions in both water and DNA.

Understanding the radiation-induced effects at the cellular level is of prime importance for predicting the future of irradiated biological organisms. Thus, whether it is in radiobiology to identify the DNA critical lesions or in medicine to adapt the radio-therapeutic protocols, an accurate knowledge of the numerous interactions induced by charged particles in living matter is required. To do that, Monte-Carlo track-structure codes represent the most suitable and powerful tools, in particular for modeling the full slowing-down of the ionizing particles in biological matter. However, it is worth mentioning that such numerical codes are reliable only if the input database used for modeling the charged particle induced interactions is precise and complete. In this context, the literature reports several numerical codes for proton and electron transport in water, the latter being commonly used as surrogate of the living medium.

The current work aims at going beyond this artifice with the development of an *event-by-event* Monte Carlo code - called ***TILDA-V*** - based on a complete set of multiple-differential and total cross sections for describing all the inelastic and elastic processes occurring throughout the slowing-down of protons in water and DNA [1]. ***TILDA-V*** (an acronym for **T**ransport d'**I**ons **L**ourds **D**ans **A**qua & **V**ivo) refers to an extension of the *TILDA* code previously developed by Champion *et al.* [2]. It is currently based on a complete set of quantum-mechanical cross sections for all the electron- and proton/hydrogen-induced interactions in water as well as in biological targets including the DNA nucleobases as well as the sugar-phosphate backbone [3-5].

Finally, a realistic description of the biological medium has been considered by modeling a typical nucleotide equivalent unit of hydrated DNA, namely, a nucleobase-pair plus a sugar phosphate group both surrounded by a hydration shell composed by 18 water molecules. Intra-comparisons between water and hydrated DNA in terms of proton range and stopping power will be presented in this work.

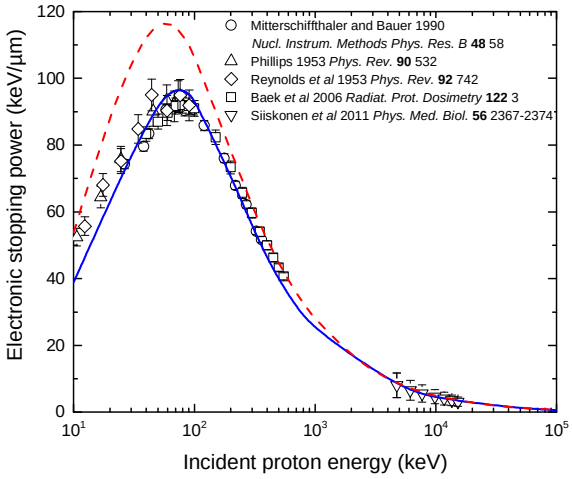

Figure 1. Electronic stopping power (induced by H^+/H^0) in water and hydrated DNA (blue and red line, respectively). Experimental data for water are reported for comparison.

References

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