



Contribution ID: 20

Type: not specified

A Monte Carlo study of target fragmentation in Protontherapy

Thursday 5 September 2019 10:30 (30 minutes)

In protontherapy, secondary particles can be produced through primary beam interactions with the patient's body. Fragments created in inelastic interactions of the beam with the target nuclei have low kinetic energy, high atomic number and high LET as compared to primary protons.

These secondary particles produce an altered dose distribution, due to their different ranges. The residual range of such fragments is of the order of 10-100 μm so they are in general confined within a single cell [1]. They have high LET, locally leading to an increase of RBE for the same delivered dose. The energy dependence of the nuclear interaction cross section makes target fragmentation relevant mostly in the entrance region [2] for normal healthy tissues.

The inclusion of target fragmentation processes can be important for the accurate calculation of the dose in the treatment. Nowadays, target fragmentation is not implemented in commercial TPSs.

Furthermore, the production yield of fragments at therapeutic energy is still poorly measured.

In the MoVe IT (Modeling and Verification for Ion beam Treatment planning) project, the effect of target fragmentation will be included in the TPS. The TRiP98 code[3] is able to properly account for the mixed radiation field for the description of biological effects of target fragmentation. In order to implement the transport of fragments in the TPS, a database for fragments fluence will be created.

In this work, Monte Carlo simulations were employed to evaluate the impact of target fragmentation in protontherapy. MC codes are able to take full account of the mixed radiation fields and provide detailed predictions of particles originating in the nuclear interactions [4].

To include the impact of fragmentation in the TPS and estimate the biological effect of fragments, the fluence of target fragments at different depths has been calculated with FLUKA MC code [5].

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