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A prerequisite for applying high-LET radiation like protons or carbon ions to patients is the precise knowledge of absorbed dose, specifically the depth dose distribution. The legal restraints imposed by the authorities requires the Bragg peak position to be reproduced within 0.5 mm and the calculated absorbed dose distribution to agree within 5% (on average) with the measurements. These conditions are usually met by our treatment planning code TRiP98 [1, 3] and its builtin beam model [4]. This code uses semiempirical fragmentation cross sections and external energy loss tables to compute numerically the depth dose distributions. The question now arises whether microscopic Monte Carlo (MC) codes based on single interactions of ions and  $\delta$ -electrons could reproduce depth dose distributions with similar accuracy. The answer is not obvious since ab-initio simulations would need very accurate primary interaction cross sections.

To address this question an established heavy ion track structure MC code [5] was reworked (TRAX, [6]). In particular, the restriction to track segment conditions has been removed so that ion depth dose profiles can easily be calculated. In addition, other therapy-relevant quantities like ionization yields in dosimetric setups and possibly even W-values could be simulated on a very basic level.

Total and differential elastic scattering cross sections for electrons were fitted to experimental data, as well as the excitation cross sections. Total electron ionization cross sections are calculated according to the relativistic model of Kim [7] with empirical corrections to match low-energy experimental data.

Ion cross sections are contructed semi-empirically as well. The relativistic Kim model was modified for ions to obtain the total ionization cross section, whereas the energy differential  $\delta$ -electron cross section was evaluated with Rudd's formulae [8]. The angular distribution of  $\delta$ -electrons was taken from the Binary Encounter Approximation. However, since depth dose distributions are one-dimensional projections and because the path of  $\delta$ electrons in water is short compared with the ion penetration depth, the accuracy of the angular distribution plays only a minor role. In contrast to track segment calculations where excitations by ions are usually neglected, these processes have to be included here to obtain reasonable agreement with the established energy loss tables. Since there are no experimental or theoretical data available an empirical approach was chosen by resorting to the electron excitation cross sections with the same velocity.

At first only exploratory calculations were performed, so nuclear fragmentation processes have not been considered, they will certainly be included in future simulations.

A first criterion is the correctness of the energy loss curve compared with the conventional approach. Figure 1 shows the ion energy loss obtained by integrating the  $\delta$ -electron spectra and adding the binding energy as well as the en-

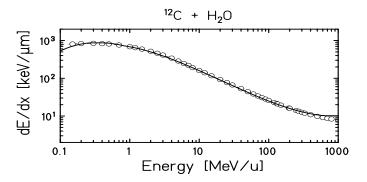


Figure 1: Energy loss for  ${}^{12}C$  in  $H_2O$ . Symbols: from TRiP98, solid line: from TRAX

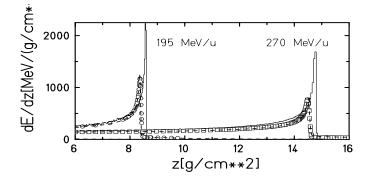


Figure 2: Depth dose profiles of  ${}^{12}C$  in H<sub>2</sub>O. Symbols: experimental data, dashed lines: TRiP98, solid lines: TRAX

ergy loss from excitation. The agreement with the table used in our planning code is surprisingly good, with local deviations up to 4% in the therapy-relevant energy range from 1 MeV/u to 300 MeV/u. For very high and very low energies deviations are larger.

Figure 2 compares the present MC results with depth dose calculations from treatment planning as well as experimental data. Bragg peak positions are overestimated by 1.5 to 2.5 mm, this corresponds to a systematic underestimation of the energy loss. Since nuclear fragmentation has not yet been included, the dose values around the Bragg peak are largely overestimated. To bring the MC results in sync with TRiP98 and experiments the ionization and excitation cross sections have to be ameliorated and nuclear fragmentation has to be accounted for.

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