Effect of spatially correlated ions predicted by LEM IV*

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In previous work, the full simulation of cell survival curves has been implemented in the Local Effect Model LEM IV [1]. With this implementation, biological effects resulting from intertrack effects can be modeled, allowing the accurate simulation of cell survival probabilities up to arbitrarily high doses. This approach is particularly suitable also to analyse in detail the effect of spatially correlated ions, as they were used e.g. in the "Molecular Beam" experiment [2]. The results showed an increased biological effectiveness with decreasing separation distance in the submicrometer range.

As described in [3], LEM IV predicts the effect E_1 of an ionizing particle based on the linear-quadratic-linear (LQ-L) photon dose response curve and the spatial distribution of double strand breaks (DSBs) in the cell nucleus. According to the number of DSB induced in 2Mbp chromatin domains, they are classified as isolated DSB (iDSB), if exactly 1 DSB is induced, or clustered DSB (cDSB), if 2 or more DSB are induced. The photon equivalent dose is defined by the photon dose generating the same ratio cDSB to the total number of damages, iDSB+cDSB, for a given pattern of particle traversals. The biological effect E_1 is then determined by rescaling the corresponding photon equivalent effect according to the total number of affected domains in both cases.

In contrast to the LQ-L model, the recently developed GLOBLE model [4] evaluates the biological effect of photon radiation by directly assigning mean numbers of lethal events to every iDSB and cDSB, respectively. In this work, photon dose response curves as predicted by the GLOBLE have been also used in LEM IV as an alternative to the standard LQ-L representation.

For simplicity, instead of deuterons, protons with the same linear energy transfer (LET) are simulated. The mean numbers of iDSBs and cDSBs for different track distances are compared in Figure 1. It is obvious that the numbers of iDSBs and cDSBs are influenced at track distances up to 0.5 µm, although the track radius is less then 0.1 µm. In the experiment, the zero separation distance was mimicked by using helium ions with twice the LET of single deuterons. Therefore, we also present the corresponding calculation for He ions in Table 1. They show a slightly increased number of iDSBs and cDSBs, even though the energy deposition is the same as for two protons.

The initial slope α of an ion dose response curve is calculated by

$$\alpha = [1 - \exp(-E_1)]\, d^{-1}\,,$$

where d is the dose of one ion traversal through the cell nucleus (doubled for spatially correlated ions). Table 1 shows the ratio of the initial slope of correlated (α_{dd}) and uncorrelated (α_d) particle radiation.

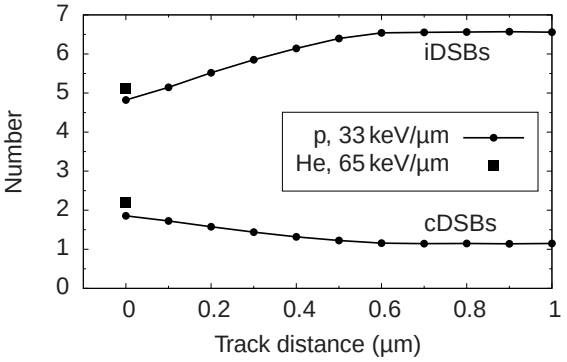

Figure 1: Modeled mean numbers of iDSBs and cDSBs for spatially correlated protons and single helium ions.

Table 1: Experimental and modeled ratio of α_{dd} and α_d. The given model errors are based on Monte Carlo fluctuations.

(mean) track distance (µm)	α_{dd}/α_d Experiment	α_{dd}/α_d LEM IV LQ-L	LEM IV GLOBLE
0.255	1.21(22)	1.005(2)	1.123(4)
0.156	1.33(22)	1.024(2)	1.211(4)
0.091	1.33(22)	1.033(2)	1.256(4)
0	—	1.046(2)	1.319(4)
He	2.09(27)	1.188(2)	1.532(5)

The model findings clearly demonstrate an increased biological effect of correlated ions even at larger track distances, where no physical overlap between the tracks occurs. Furthermore, LEM IV with GLOBLE based photon dose response curve shows a better agreement with the experimental data than LEM IV with the LQ-L based photon dose response curve.

References

[1] U. Scholz et al., GSI Scientific Report, 2011.

[2] A. M. Kellerer et al., Radiat. Res., 83(**3**) (1980), 511-528.

[3] T. Friedrich et al., Int. J. Radiat. Biol., 88(**1-2**) (2011), 103-7.

[4] T. Friedrich et al., Rad. Res., 178(**5**) (2012), 385-94.

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