Journal of Physical Chemistry & Biophysics

Sabin, J Phys Chem Biophys 2015, 5:2
DOI: 10.4172/2161-0398.1000e125

Editorial Open Access

Stopping Power of Biological Systems

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Recent advances in heavy ion radiology have made the understanding and prediction of the interaction of fast ions with biological systems increasingly important. In particular, the ability to tailor swift ion radiation to preferentially damage specific sites and specific molecules, for example, DNA or RNA would be particularly useful. Can this be done?

Heavy ion radiation has an advantage over photon radiation in oncological applications in that energy is deposited in the target much more locally in the ion case, minimizing damage to surrounding, non-cancerous tissue. As can be seen in the schematic Figure 1, the energy deposited is much more localized in the case of fast particles as opposed to photons. For ion projectiles the position of the peak in the dose/depth curve, known as the Bragg Peak, can thus be chosen to be at particular depth by choice of the initial projectile kinetic energy. Thus, for radiation treatment of a tumor, surrounding tissue is much less damaged when protons rather than X-rays or gamma rays are used. As this is the case, it is reasonable to query if it is possible to tailor swift ion radiation to preferentially damage specific sites and types of molecules such as DNA or RNA.

Energy deposition by a fast heavy ion colliding with a molecule comes primarily from the conversion of the ion's kinetic energy into target electronic energy, which can result in target molecule excitation, ionization, fragmentation, any other process that results from electronic excitation.

Energy deposition is characterized by the stopping cross section, $S(v)$, of the target [1]. This quantity is the density weighted stopping power, $dE(v)/dx$, of the target material, and depends on the projectile velocity:

$$S(v) = -\frac{1}{n}\frac{dE(v)}{dx} = \frac{4\pi e^4 Z_1^2 Z_2}{m_e v^2} L(v) \quad (1)$$

The quantity $L(v)$ is referred to as the stopping number, which is comprised of several components, of which the first two are largest:

$$L_0 = L_{00} + L_{01} = \ln\frac{2mv^2}{I_0} - \frac{C(v)}{Z_2} \quad (2)$$

The important quantity for this study is the mean excitation energy, I_0, which measures the ability of a molecule to absorb energy in a collision with an ion:

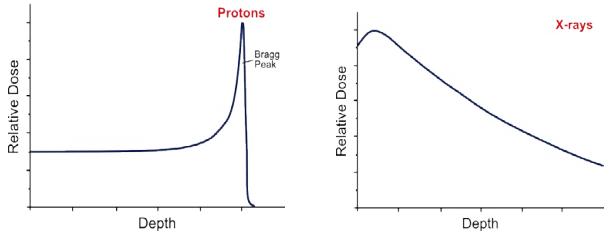

Figure 1: Relative dose (the amount of enefgy deposited) vs. depth (from the sample surface)
curves for photon (X-rays) and heavy ion (protons) projectiles in ordinary matter.

$$\ln I_0 = \frac{\int \frac{df}{dE} \ln E \, dE}{\int \frac{df}{dE} dE} \quad (3)$$

It should be noted that I_0, is a property of the dipole oscillator strength distribution (DOSD) of the target only - there is no dependence on properties of the projectile.

As the peak in the stopping, or the relative dose delivered by an ion beam occurs at a particular energy, the depth of the peak below the target surface can be accurately chosen by choosing the ion kinetic energy, that is, its velocity. Thus the correct incident energy can be chosen so that the greatest energy is delivered at a specific depth, such as to a tumor.

The next question deals with whether or not it is possible to select a particular substance for energy deposition. That is, if there is a target composed of several substances, can an ion beam be designed to target a specific one of them? From the equations above, the energy deposition by an ion beam into target substances is determined by the mean excitation energies of the molecules that make up the target. Thus, the fast ion radiation will interact most strongly with radiation having a Bragg peak at a particular energy. As the molecules associated with radiotherapy are biomolecules, the mean excitation energies of these substances are most important. In Table 1, the mean excitation energies of several biomolecules [2] are presented. As is evident, all the mean excitation energies of the biomolecules lie close to 70 eV. When converted to Hartree atomic units and the natural log is taken as in equation 2, there is very little difference in the resulting values of the stopping. In addition, the mean excitation energy of water is calculated to be 73.56 eV, again, in the same range as that of the biomolecules. Solvation will not change the mean excitation energy either: The mean excitation energy of glycine is calculated [3] as 71.10 eV, but when solvated with 511 water molecules, the calculated mean excitation energy [4] changes only to 69.79 eV. It is apparent, then, that nucleobases, and other biological materials, including water all have mean excitation energy of around 70 eV. Hydrogen bonding only seems to lower mean excitation energies by about 0.5%, and Solvation seems to lower mean excitation energies, at least for small molecules, only by about 2%. It is thus apparent that solvation, base pairing (hydrogen bonding), or nucleoside formation have little apparent effect on the energy absorption characteristics of biological materials.

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Received: March 05, 2015; **Accepted:** March 18, 2015; **Published:** March 20, 2015

Citation: Sabin JR (2015) Stopping Power of Biological Systems. J Phys Chem Biophys 5: e125. doi: 10.4172/2161-0398.1000e125

amino acids	I_0 (eV)
glycine	71.1
alanine	67.4
nucleobases	
cytosine	69.6
uracil	73.1
thymine	70.0
adenine	69.1
guanine	71.6
nucleoside	
cytidine	69.96
uridine	71.41
methyl uridine	70.12
adenosine	69.68
guanosine	70.89

Table 1: Mean Excitation Energies of Some Biomolecules.

So, if one asks the question: "Can one tailor swift ion radiation to preferentially damage specific sites and types of DNA or RNA?", then the conclusion must be probably not, as they all have the same mean excitation energies. However, it is possible to irradiate a particular site due to the dependence of the location of the Bragg peak on incident ion energy.

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