

Hadronic Radiation of Biological Molecules

John R Sabin*

Department of Physics- Quantum Theory Project, University of Florida, USA

*Corresponding author: John R Sabin, Department of Physics, Quantum Theory Project, University of Florida, USA, Tel: +456-557-4379; E-mail: sabin@qtp.ufl.edu

Received Date: January 05, 2017; Accepted Date: January 06, 2017; Published Date: January 20, 2017

Copyright: © 2017 Sabin JR. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Citation: Sabin JR. Hadronic Radiation of Biological Molecules. Br J Res 2017, 4: e01.

Editorial

As hadronic radiation therapy becomes an ever more important treatment method for various forms of carcinogenesis, it becomes ever more important to understand the interaction of fast, heavy, ions, such as protons or alpha particles, with biologically significant molecules. In general, this implies understanding of the transfer of the kinetic energy of the incoming ion to electronic energy of the target molecule, which can subsequently lead to fragmentation, and thus loss of function, of the carcinogen target.

The use of hadronic radiation projectiles instead of X-rays has a large advantage in modern times, as the energy deposited by hadronic projectiles is much more localized than that from X-rays, as shown in the **Figure 1** [1]. Thus, energy from the radiation can be much more accurately focused on the carcinogenic area.

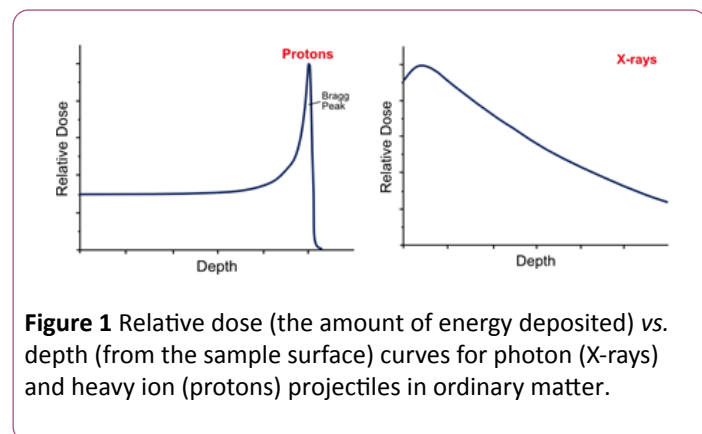


Figure 1 Relative dose (the amount of energy deposited) vs. depth (from the sample surface) curves for photon (X-rays) and heavy ion (protons) projectiles in ordinary matter.

The crucial quantity is the ability of the target to absorb energy from the projectile, or energy loss of the projectile per unit length traveled in the target at velocity v , $-dE(v)/dx$ the stopping power of the target.

Division of the stopping power by the target particle density, N , gives the target density independent stopping cross section $S(v)$:

$$-dE(v)/dx = NS(v) \quad (1)$$

Here

$$S(v) = \frac{4\pi e^4 Z_1^2 Z_2}{mv^2} \ln \frac{2mv^2}{I_0} \quad (2)$$

Where I_0 is the mean excitation energy of the target, which measures the ability of a target molecule to absorb energy from a projectile ion, and is determined from the target oscillator strength distribution:

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

Here Z_1 is the projectile charge, Z_2 is the target electron number and m is the electron mass. One must note that I_0 is a property of the oscillator strength (f) distribution of the target molecule only, and does not depend on the properties of the projectile.

Thus, in order to predict/understand the energy deposition properties of hadronic projectiles in a target, such as in hadronic radiation therapy, the composition of the target and the mean excitation energies of the components must be known. The former is not difficult to obtain, but the latter is, as biological molecules such as DNA are large and complex, and thus difficult to either make measurements or calculations on. An alternative possibility is presented by the Bragg Rule [2] which states that the stopping cross section of a compound system is the weighted sum of the constituent stopping cross sections. The Bragg rule can be generalized to molecular fragments of a complex system,

$$S(v)_{\text{aggregate}} = \sum_i \omega_i S_i(v) \quad (4)$$

Converted to an expression for mean excitation energies, thus [2]:

$$\ln I_0^{\text{aggregate}} = \frac{1}{N_e} \sum_{i=\text{fragments}} \omega_i \ln I_0^i \quad (5)$$

where ω_i is the total number of electrons in each fragment and N_e is the total number of electrons in the aggregate.

As an example, consider the mean excitation energies of some amino acids [3,4]. All amino acids have the general formula $R-CH(NH_2)COOH$, or $R-A$. Using the fragment mean excitation energies and weights given in **Table 1**, the mean

excitation energy and weight of the common fragment, A, are found to be $I_0^A=78.8$ eV with $\omega=38$.

Table 1 Fragment mean excitation energies and weights.

Fragment	I_0^{frag} (eV)	ω
-CH ₂ -	60.6	6
-CH ₃	47.1	8
-COOH	65.8	22
-C ₆ H ₅ (-Phe)	77.8	40
-NH ₂	58.7	22/3
-OH	104.4	6
-C ₆ H ₁₁ (-Ch)	54.3	46

As different amino acids are reflected in the different compositions of -R, eq. 5 can be modified to read

$$\ln I_0 = \frac{1}{\omega_R + 38} [38 \ln I_0^A + \omega_R \ln I_0^R] \quad (6)$$

In **Table 2**, the mean excitation energies of various amino acids are presented, calculated from eq.6 [3,4].

Table 2 Mean excitation energies, I_0 of some common amino acids.

Amino Acid	-R	I_0 (eV)
Phenylalanine	-CH ₂ -Phe	74
Tyrosine	-CH ₂ -Phe-OH	66.8
Lysine	-(CH ₂) ₄ -NH ₂	65.3

Glycine	-H	74
Alanine	0	72
Serine	-CH ₂ -OH	74
Glutamic Acid	-(CH ₂) ₂ -COOH	67.4
Aspartic Acid	-CH ₂ -COOH	69.4
Threonine	-CHOHCH ₃	70.9
Leucine	-CH ₂ -CH(CH ₃) ₂	63.4
Asparagine	-CH ₂ -CO-NH ₂	74.4
Isoleucine	-CHCH ₃ -CH ₂ -CH ₃	63.4

Thus, using this scheme, the energy absorption properties of various biologically relevant molecules can be determined and used in such practices as hadronic radiotherapy.

References

1. Sabin JR (2015) Stopping Power of Biological Systems. J Phys Chem Biophys 5: e125.
2. Bragg WH, Kleeman R (1905) On the Alpha Particles of Radium, and Their Loss of Range in Passing Through Various Atoms and Molecules. Philos Mag 10: 318.
3. Brunn-Ghalbia S, Sauer SPA, Oddershede J, Sabin JR (2010) Mean Excitation Energies and Energy Deposition Characteristics of Bio-organic Molecules. J Phys Chem B 114: 633.
4. Sauer SPA, Oddershede J, Sabin JR (2011) Mean Excitation Energies for Biomolecules: Glycine to DNA. Adv Quantum Chem 62: 215.