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Radiation resistance of novel SARS-CoV-2: A Monte Carlo investigation on characterization and determination of gamma-ray attenuation properties

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Abstract

In late December 2019, the new viral pneumonia outbreak was first detected in Wuhan, the largest metropolitan area in China's Hubei province. The 2019–20 coronavirus pandemic is an ongoing pandemic, caused by the severe acute respiratory syndrome-2 (SARS-CoV-2), was named as Coronavirus disease 2019 (COVID-19) by World Health Organization (WHO). It is well known that radiation can cause mutations in bacteria and viruses. Therefore, characterization of the radiation resistance and interaction properties of viruses provides the opportunity in terms of risk assessment and future aspects. In this study, 3 types of viruses (SARS-CoV-CAS Number 587886-51-9, Influenza-CAS Number 141368-69-6 and SARS-CoV-2 GlycoProtein 6VSB.) were modeled with the Monte Carlo simulation method (MCNPX version 2.6.0). The vital radiation attenuation properties such as linear attenuation coefficients, energy absorption buildup factors (EABF), exposure buildup factors (EBF), relative dose distributions (RDD) were examined using advanced simulation methods. Moreover, the spike protein of SARS-CoV-2 is modelled from the structures in the Protein Data Bank. As a result of the study, we could say that the most radiation resistance was observed in SARS-CoV when compared with Influenza and Covid-19. It could be one of the reasons for SARS-CoV's resistance to mutation from its outbreak time. On the other hand, Covid-19 is more resistant to radiation than Influenza. Therefore it could be expected that Covid-19 would have the similar behaviors against ionizing radiation as Influenza has.

Keywords: SARS-CoV-2, radiation, radiation attenuation, Monte Carlo simulation

1. Introduction

In the last twenty years, several viral outbreaks such as “Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) (2002-2003), H1N1 influenza (2009) and the Middle East Respiratory Syndrome Coronavirus (MERS-CoV) (2012) have been identified in the world [1]. In late December 2019, the new viral pneumonia outbreak was first detected in Wuhan, the largest metropolitan area in China's Hubei province [2]. The 2019–20 coronavirus pandemic is an ongoing pandemic, caused by the severe acute respiratory syndrome-2 (SARS-CoV-2), was named as Coronavirus disease 2019 (COVID-19) by World Health Organization (WHO) [1]. The high mortality is high in older adults 65 years, is unique characteristic of SARS-CoV-2 pandemic [3]. Among these deaths, one of this is quite remarkable because of a newborn death in England. This

death is unofficially associated with SARS-CoV-2. People with potential exposure to SARS-CoV-2 were interviewed with a standardised symptom history like cough, fever, kidney failure, pneumonia and severe acute respiratory syndrome both in older adults and people with any age [4]. This approach has been not particularly useful because some infected people have clinically milder or no symptoms that can be linked transmission of the virus on to others. Recently, it has been shown that infection pediatrics with mild symptoms had positive test results for fecal transmission [5]. Many scientists believed that those patients whose not in the “detected pool of infected cases”, created new “epidemic hotspots” including different materials (plastic, cardboard, metal) during traveling or working [6]. As the results of Cov pandemic, most of countries around the world are stepping up efforts to tackle with COVID-19 based on standard recommendations including covering mouth & nose when coughing and sneezing, regular hand washing [5]. The literature review showed that term of ionizing radiation is a considerable tool for virus inactivation aims. The term of radiation is the emission or transmission of energy in the form of waves or particles. It is divided into ionizing and non- ionizing radiation based on its energy and causing of biological effect. The main two characteristics of ionising radiation are high energy levels and high penetration through biological and non-biological materials. Drastic increase in the utilization of ionizing radiation in the field of medicine and industry has been noted over the past years [7,8]. Therefore, ionising radiation is used in food applications, clinical sterilization, and vaccine preparation. Ionising radiation possessed an ability to inactivate viruses and used for vaccine development as it damages the nucleic acids rather than proteins [9]. However, chemical and physical methods can be used for viruses’ inactivation, but ionizing radiation has the advantages of penetration throughout the material. On the other hand, the radiation dose can be measured precisely [10,11]. Furthermore, exposure to ionizing radiation has multiple effects on viability and

further proliferation of the irradiated cell and damage might occur if the exposure dose exceeded the threshold of each specific tissue. Therefore, fractionation is used to deliver the total radiation dose over fractions to allow intracellular repair [12,13] and the live attenuated microorganisms can be used as vaccine materials [13]. Withal, radiation sensitivity is determined by decimal reduction value (D_{10}) and the shape of the inactivation curve. It is difficult to predict radiation sensitivity but most of the viruses are relatively radiation resistant in a D_{10} range from 1-10 kGray for gamma photons (Co^{60}) [14]. High energy electron and gamma photons are usually used, and in some cases, x ray and ultraviolet rays are used. However, due to the production of Bremsstrahlung radiation, proteins damage can occur during the process of virus's inactivation using gamma rays [9, 15]. It's worth to mention that Gamma radiation is an effective way to inactivate influenza. An exposure of 0.65 kiloGrays (kGy) leads to complete inactivation of the virus, and disruption of protein and haemagglutinating activity occurred at exposure to higher than 200KGy [16,17]. Additionally, the effect on the proteins can be reduced with the use of electron, but electron irradiation is less penetrating than gamma rays [15]. In contrast to high energy electron (>1 MeV), the low energy electron irradiation (LEEI, <500 keV), does not generate x ray radiation and thus, does not require complex shielding [18]. LEEI works efficiently in inactivation of different viruses such as (influenza A (H3N8) and porcine reproductive and respiratory syndrome virus (PRRSV) [18]. On the other hand, ultraviolet radiation demonstrated an efficient role in inactivation of the enveloped MHV coronavirus [19], the enteric human adenovirus (HAdV) reported to be the most UV-resistant virus [20]. Evaluation of the virus, radiation, temperatures are crucial factors [21]. The radiation dose used for viral inactivation should be calculated based on the virus concentration, the size, and the temperature of irradiation [22]. Therefore, it is important to assess the use of radiated inactivation and attenuation in virology. On the other hand, direct prediction of virus mutation

amounts are significant to understand the evolution of the viruses and to struggle with them [23]. It is well known that radiation can cause mutations in bacteria and viruses. Therefore, characterization of the radiation resistance and interaction properties of viruses provides the opportunity in terms of risk assessment and future aspects. However, the literature review showed that no study was performed to investigate the radiation interaction mechanisms of these three types of viruses (SARS-CoV-CAS Number 587886-51-9, Influenza-CAS Number 141368-69-6 and SARS-CoV-2 GlycoProtein 6VSB.), which occurred in an extraordinary way and creates serious concerns. This has strongly encouraged us to perform this extensive investigation. Taking all this current information and the extraordinary situation in the world into consideration, in this study, spike of 3 types of viruses (SARS-CoV-CAS Number 587886-51-9, Influenza-CAS Number 141368-69-6 and SARS-CoV-2 GlycoProtein 6VSB.) were modeled with the Monte Carlo simulation method. The vital radiation attenuation properties such as linear attenuation coefficients, energy absorption buildup factors (EABF), exposure buildup factors (EBF), relative dose distributions (RDD) were examined using advanced simulation methods. Moreover, the spike protein of SARS-CoV-2 is modelled from the structures in the Protein Data Bank [24]. As it can be seen from the **Fig.1**, spike protein part is the most external part of viruses. Therefore, it is highly expected to observe the first interactions in spike protein during the interaction between incoming radiation and virus structure. This study aimed to compare gamma ray attenuation properties of GlycoProtein structure of aforementioned virus types. It is well-known that radiation investigations such as dosimetry and radiation detection in micro-scale are difficult or physically impossible. Therefore, advanced simulation techniques and mathematical methods are highly required. Therefore, GlycoProtein structure of viruses structure has been modeled in MCNPX (version 2.6.0) Monte Carlo code [25]. We shall discuss simulation details and calculation steps in

next sections. The hypothesis of this study is to observe a straight connection between radiation attenuation features and elemental properties of viruses structure. In addition, this study aimed to create a new relationship hypothesis between mutation resistance of viruses and radiation attenuation properties for future investigations. In addition, the obtained outcomes from this theoretical study can provide a general idea on radiation attenuation properties of investigated viruses. Moreover, the outcome can also be useful for further investigations on radiation-virus interactions, efforts to improve the harmful effects of viruses.

2. Materials and Methods

2.1. Viruses

Coronaviruses have five structural proteins in their structures: the Spike (S), Membrane (M), Envelope (E) glycoproteins, Hemagglutinin Esterase (HE) and Nucleocapsid (N) protein (See Figure 1). All viruses have envelope proteins and N protein in their structure but HE is found only in some beta coronaviruses such as SARS-CoV-2 virus. The spike protein of SARS-CoV-2 is modelled from the structures in the Protein Data Bank [24]. The cartoon depiction of the protein is given in **Fig. 2** from different viewpoints. (PDB ID: 6VSB) [26]. Mass weight percentage of SARS-CoV-2 is calculated with Materials Studio program and given in **Table 1**. These weight percentage of atoms are approximately similar for big size proteins. For example for Influenza spike protein weight percentage of C atom is 51.53 %, H atom 9.39 %, O atom 22.11 %, N atom 16.10, S atom 0.88 %. Since viruses are composed of complex proteins, lipid layer and nucleic acids, their buoyant densities are obtained by a combination of sucrose and cesium chloride density gradient equilibrium centrifugation techniques and proteins have approximately 1.3 g/ml (with Sedimentation coefficients between 1-10) (**Fig. 2**), nucleic acids have 1.7 g/ml and overall

viruses have 1.35-1.4 g/ml bouyant densities (See **Fig.3**) [27]. In this study spike protein structure and its atom weight percentages and 1.3 g/ml bouyant density are used in gamma radiation Monte Carlo simulations.

2.2. Monte Carlo simulations

In this study, version 2.6.0 of MCNPX [25] (Monte Carlo N-Particle eXtended) general-purpose Monte Carlo code was utilized for extensive investigation of mass attenuation coefficients of three different types of viruses namely SARS-CoV-CAS Number 587886-51-9, Influenza-CAS Number 141368-69-6 and SARS-CoV-2 GlycoProtein 6VSB considering their GlycoProtein part. A virus structure has been modeled considering essential parts. The GlycoProtein part cell environment of viruses has been filled with *MI* definition, which has been defined in the part of material definition in MCNPX input file. Next, *MI* has been defined considering the elemental mass fractions of SARS-CoV-CAS Number 587886-51-9, Influenza-CAS Number 141368-69-6 and SARS-CoV-2 GlycoProtein 6VSB, respectively. The Lambert-Beer law was employed for determination of mass attenuation coefficients (see **Fig 4b**). On the other hand, the mass attenuation coefficients were defined for each photon energies at the range of 0.015-15 MeV. This process (cell definition and mass attenuation coefficients calculations) has been repeated for each virus structures. The appearance of modeled simulation setup can be seen in **Figure 4a**. It is worth to be mention that visualization of modeling simulation setup was performed in Visual Editor of MCNPX (VE X_22S).

2.3. Radiation attenuation properties

In this study, Lambert-Beer's law was used with the help of the following equation to calculate the mass attenuation coefficients (μ_p) of spine protein structure of investigated viruses [28].

$$I = I_0 e^{-\mu_\rho t} \quad (1)$$

In the formula, ρ denotes the density, t denotes the material thickness and μ_ρ denotes the mass attenuation coefficient. Units are g/cm^3 , cm and cm^2/g , respectively. Considering the mixture of elements, the mass attenuation coefficient is calculated by the equation [29] (2).

$$\frac{\mu}{\rho} = \mu_\rho = \frac{N_A}{M} \sigma_{tot} = \sum_i w_i (\mu/\rho)_i \quad (2)$$

where, w_i is a weight fraction of i^{th} element in the virus structure. With the help of the calculation of the mass attenuation coefficient, which is the key parameter to calculate the attenuation parameters, calculations of MFP values were also calculated (Equation 3). The Mean Free Path (MFP) can be described for both charged particles and photons. It represents the path that a gamma photon takes without interacting with the material and is expressed in terms of linear attenuation coefficient [30].

$$\text{MFP} = 1/\mu \quad (3)$$

The term of build-up factor can be defined as the ratio of the amount of radiation at a given location to the amount of radiation coming from this location without interference. The agglomeration factor is defined as the function of the depth of interaction, ie the mean free path. The mean free path (MFP) varies with linear distance, the unit mean free path depends on the absorption coefficient of the material medium and corresponds to a linear value. Exposure buildup factors (EBF), Energy absorption buildup factors (EABF) are the determining quantities in radiation attenuation and radiation measurement studies. In the interaction of gamma radiation with the target material, two radiation components are formed inside or beyond the attenuator; collided and un-collided photons. Compton partial attenuation coefficient $(\mu_\rho)_{\text{Compton}}$ and total attenuation coefficient $(\mu_\rho)_{\text{Total}}$ values were obtained for three types of viruses in the energy range of 0.015–

15.0 MeV to calculate the EBF and EABF buildup factors. Then the equivalent atomic number (Z_{eq}) values of the glass samples were calculated by matching the $(\mu_{\rho})_{Compton}/(\mu_{\rho})_{Total}$ ratio of the particular energy to the corresponding ratios of the elements of the same energy. When the $(\mu_{\rho})_{Compton}/(\mu_{\rho})_{Total}$ ratio is between two consecutive rates, its interpolation is calculated by the following equation:

$$Z_{eq} = \frac{Z_1(\log R_2 - \log R) + Z_2(\log R - \log R_1)}{\log R_2 - \log R_1} \quad (4)$$

where Z_1 and Z_2 are the atomic numbers of the elements corresponding to the ratios of R_1 and R_2 , respectively. R indicates the proportion of glasses studied in a particular energy.

The EBF and EABF values of Hematite doped glasses were estimated for gamma energies up to 15 MeV and for penetration depth up to 40 mfp by using G-P method [31]:

$$C = \frac{C_1(\log Z_2 - \log Z_{eq}) + C_2(\log Z_{eq} - \log Z_1)}{\log Z_2 - \log Z_1} \quad (5)$$

$$B(E, X) = 1 + \left(\frac{b-1}{K-1}\right)(K^x - 1) \quad \text{for } K \neq 1 \quad (6)$$

$$B(E, X) = 1 + (b-1)x \quad \text{for } K = 1 \quad (7)$$

where,

$$K(E, x) = cx^a + d \frac{\tanh\left(\frac{x}{X_K} - 2\right) - \tanh(-2)}{1 - \tanh(-2)} \quad \text{for } x \leq 40 \text{ mfp} \quad (8)$$

Moreover, the G-P fitting parameters (a, b, c, d and X_K) were utilized. These equations contain x as the distance between the source and detector. At 1 mfp, the EBF is coded by b . $K(E, X)$ factor has a meaning of dose multiplication.

Finally, Relative Dose Distribution (RDD) values were determined for investigated viruses. The term of RDD at distance X is calculated using the formula below [32]:

$$RDD = \frac{\exp(-\mu x)(EBF)}{x^2} \quad (9)$$

3. Results and discussions

For the three different types of viruses SARS-CoV-CAS Number 587886-51-9, Influenza-CAS Number 141368-69-6 and SARS-CoV-2 GlycoProtein 6VSB), chemical structures along with densities and weight fractions of GlycoProteins are reported in **Table 1**. Linear attenuation coefficients (LAC) values are computed at the energy range between 0.015 to 15 MeV by using MCNPX code. The results are shown in **Fig.5**. From the figure, it can be seen that LAC values are correlated to the applied energy as well as the chemical composition of the GlycoProteins. While the applied energy increases up to 15 MeV, the LAC values shows a declining rate. Among the investigated viruses, linear attenuation coefficients values of (CAS Number 587886-51-9) were higher than Influenza and Covid-19. To evaluate attenuation characteristic and quality, linear absorption coefficient (LAC) values as a function of photon energy were determined (See **Fig.6**). The results showed that attenuation properties of each type of GlycoProtein structure were higher in low energy region. However, similar behaviors with LAC trend was observed in absorption characteristic of investigated viruses. The term of mean free path (MFP) is important parameter to determine the average distance of radiation in material environment. The MFP values for the studied viruses are reported in the **Fig. 7**. The values of the energy absorption buildup factor (EABF) and the exposure buildup factor (EBF) prove useful when choosing a replacement composite material instead of an element for a specific energy region. As such EABF and EBF are key to define the absorption of the material. In this study, EBF-EABF values are calculated by using G-P fitting approach, which a common method used by various researcher. The penetration depth for the calculation is at 1-5-10-20-40 MFP respectively. The **Fig.8** and **Fig.9** list the EBF-EABF values in the energy levels up to 15 MeV for Sars-Cov, Influenza and Sars-Cov-2. From

the figure, it can be seen that different energies yield various incidents. Photoelectric effect, Compton scattering, and pair production are the three interactions taking place between energy and matter. Photoelectric effect happens as electrons are released by matter while subjected to electromagnetic radiation. Photoelectric effects occurs at low energy regions yielding increasing rate of EBF and EABF with an inverse relations to $E^{3.5}$. EBF-EABF values decline with the increasing energy after reaching its maximum at 0.1 MeV. Compton scattering is the result of a photon of high energy occuring in the the intermediate energy region, it yields higher EBF-EABF values owing to multiple scattering processes. Pair production is a simple translation of the radiant energy into matter. By this way the gamma-ray is converted into matter in the shape of a pair of electrons (negatron and positron) charged negatively and positively. Pair production occurs just for high-energy gamma-rays yielding lower EAB-EABF. Sars-Cov is the smallest possible EBF-EABF element among the studied sample with a maximum value of Z_{eq} . Fig.s 7 and 8 shows that since the higher energy penetrations move through the substance, higher EBF-EABF values can be seen in the energy from 0.015 Mev to 15 MeV and up to 40 mfp. It is known that chemical composition has significant effects on the EBF and EABF. As it can be seen in the Fig.7-8, Sars-Cov, Sars-Cov-2 possess the smallest EBF-EABF values at the low energies. EABF and EBF values were found to increase with declining Z_{eq} of all of the investigated samples. This inverse relation between Z_{eq} and EBF-EABF is recorded in the **Table 2, 3 and 4**. Having the minimum Z_{eq} Influenza possess the largest EBF-EABF, while Sars-Cov yields the maksimum Z_{eq} and smallest EBF-EABF. A high value of Z_{eq} for a material means it's a strong absorber of radiation. Energy matter interaction can be divided into three areas for Z_{eq} values as well. In the high and intermediate energies, Z_{eq} 's dependence on energy declines and maksimum Z_{eq} is found in intermediate energy regions owing to the dominating Compton scattering process. Vis-à-vis

changing energies, the variation of EBF and EABF values for the Sars-Cov, Influenza and Sars-Cov-2 samples are reported in **Figs. 8** and **9**. Thanks to the K absorption edge of Sulfur an abrupt peak is located in this region in the low region between 0.015–0.1 MeV and decrease swiftly after 0.1 MeV. Here, EBF-EABF values get to the minimum levels for all investigated viruses. In the 0.015–0.1 MeV, EBF and EABF incrementally rise and sharply decline after 0.1 MeV. EBF-EABF values show an increasing trend yet again for high penetration depths (15–40 Mfp). From **Figs. 8** and **9**, the EBF and EABF values are lowered by growing the percentage of sulfur in the virus samples and hence the total EABF and EBF values were obtained by the Sars-Cov. The smaller EBF-EABF implies improved properties of radiation shielding. So, we may assume that Sars-Cov has greater value than Sars-Cov-2 in terms of the radiation shielding. Sars-Cov, with the maximum sample of Zeq virus among the investigated virus samples, arrived at the smallest EABF-EBF as the SARS-Cov-2, with minimum sample of Zeq, reaches the largest EBF-EABF. A technique for the quantitative evaluation of the relative dose distribution (RDD) is a measurement of the distance x to the EBF values. Variations of the RDD were found as a feature of distance (x) for various samples of viruses. **Figure 10** indicates the variation in the relative dose distribution of Sars-Cov, Influenza, and Sars-Cov-2 viruses at penetration depths of 10, 20, 30 and 40 mfp for specific event energies up to 15 MeV and for various distances up to 1 cm. As seen in these statistics, the RDD values increase to maturity based on the samples' penetration depth and chemical composition. Of both tests, the RDD values grow quickly as the photon energy rises to 0.1 MeV. Increases in photon energy often contribute to decrease of the RDD values. Moreover, **Figure 11** shows that, RDD behaviors of investigated viruses did not change in different penetration depths (10 mfp, 20 mfp, 30 mfp, 40 mfp). However, slight differences in the lower penetration depths were relatively increased in higher penetration depths.

4. Conclusion and future aspects

Although many studies have been carried out about the radiation and biological interaction mechanism in the historical process, some issues still remain mysterious. One of these issues is radiation and virus interactions. Different types of studies have been performed in terms of inactivation of viruses using ionizing and non ionizing radiations. On the other hand, many applications are under investigation. It is well-known that radiation investigations such as dosimetry and radiation detection in micro-scale are difficult or physically impossible. Therefore, advanced simulation techniques and mathematical methods are highly required. The importance of investigated virus types and this difficult situation in the world strongly encouraged us to do this extensive theoretical study and to examine the radiation resistance properties of these viruses. Of course, outcomes of this investigation should be considered as a first step. Therefore, experimental and clinical investigations will be planned, immediately. On the other hand, obtained results would be useful to compare the mutation possibilities of Covid-19 with SARS-CoV and Influenza in terms of ionizing radiation resistance. As a result of the study, we could say that the most resistant was observed in SARS-CoV when compared with Influenza and Covid-19. It could be one of the reasons for SARS-CoV's resistance to mutation from its outbreak time. On the other hand, Covid-19 is more resistant to radiation than Influenza. Therefore it could be expected that Covid-19 would have the mutating ability as Influenza has. Furthermore, it is not predictable if Covid-19 will resist to sunlight's UV radiation. Because a large number of people are expecting that its spread will decline when the weather gets warm up due to sunlight. To clarify this problem, some experiments should be carried out in the lab conditions. The obtained outcomes from this theoretical study has provided a general idea on radiation attenuation properties of investigated viruses. The hypothesis of recent investigation was to observe a direct behavior relationship

between spike protein and incoming radiation. The obtained result was approved our hypothesis and slight differences were observed. Of course, this hypothesis should be approved by experimental and clinical investigation in near future.

5. Declaration of Interests

All authors declare no competing interest

6. Acknowledgment

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References

- [1] Dey, S. K., Rahman, M. M., Siddiqi, U. R., & Howlader, A. (2020). Analyzing the Epidemiological Outbreak of COVID-19: A Visual Exploratory Data Analysis (EDA) *Approach. Journal of Medical Virology*.
- [2] Ibrahim, I. M., Abdelmalek, D. H., Elshahat, M. E., & Elfiky, A. A. (2020). COVID-19 Spike-host cell receptor GRP78 binding site prediction. *Journal of Infection*.
- [3] Andersen, K. G., Rambaut, A., Lipkin, W. I., Holmes, E. C., & Garry, R. F. (2020). The proximal origin of SARS-CoV-2. *Nature Medicine*, 1-3.
- [4] Ghinai, I., McPherson, T. D., Hunter, J. C., Kirking, H. L., Christiansen, D., Joshi, K., & Fricchione, M. J. (2020). First known person-to-person transmission of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in the USA. *The Lancet*, 1-8.
- [5] Xu, Y., Li, X., Zhu, B., Liang, H., Fang, C., Gong, Y., & Zhang, H. (2020). Characteristics of pediatric SARS-CoV-2 infection and potential evidence for persistent fecal viral shedding. *Nature Medicine*, 1-4.

- [6] Van Doremalen, N., Bushmaker, T., Morris, D. H., Holbrook, M. G., Gamble, A., Williamson, B. N., & Lloyd-Smith, J. O. (2020). Aerosol and Surface Stability of SARS-CoV-2 as Compared with SARS-CoV-1. *New England Journal of Medicine*
- [7] Barker CA, Postow MA. Combinations of radiation therapy and immunotherapy for melanoma: a review of clinical outcomes. *Int J Radiat Oncol Biol Phys* 2014;88:986–997.
- [8] McDonald JC. Industrial radiation processing: working behind the scenes. *Radiat Prot Dosimetry* 2004;109:173–174.
- [9] Lowy, R. J., Vavrina, G. A., & LaBarre, D. D. (2001). Comparison of gamma and neutron radiation inactivation of influenza A virus. *Antiviral research*, 52(3), 261-273.
- [10] Block, S. S. (Ed.). (2001). *Disinfection, sterilization, and preservation*. Lippincott Williams & Wilkins.
- [11] Grassly NC. Immunogenicity and effectiveness of routine immunization with 1 or 2 doses of inactivated poliovirus vaccine: systematic review and meta-analysis. *J Infect Dis* 2014;210 Suppl 1:S439–S446.
- [12] Fulda, S., A.M. Gorman, O. Hori, A. Samali. 2010. Cellular stress responses: cell survival and cell death. *International Journal of Cell Biology*, 2010: 214074.
- [13] Syaifudin, M., Nurhayati, S., Darlina, D., LusiYanti, Y., & Kisnanto, T. (2019). Irradiation of intraerythrocytic Plasmodium berghei with a fractionated dose of gamma rays does not effectively reduce the infectivity in mice Mus musculus. *Aceh Journal of Animal Science*, 4(1), 18-26.
- [14] Lowy, R. J. (2005). Ionizing radiation inactivation of medically relevant viruses. *Radiation Inactivation of Bioterrorism Agents*, 365, 175.
- [15] Gaidamakova, E.K.; Myles, I.A.; McDaniel, D.P.; Fowler, C.J.; Valdez, P.A.; Naik, S.; Maheshwari, R.K. Preserving immunogenicity of lethally irradiated viral and bacterial vaccine epitopes using a radio-protective Mn(2+)-peptide complex from Deinococcus. *Cell Host Microbe* 2012, 12, 117–124
- [16] International Atomic Energy Agency. The Manual on Radiation Sterilization of Medical and Biological Material: The technical reports series. Vienna: 1973. pp. 62–63.
- [17] Astill, J., Alkie, T., Yitbarek, A., Taha-Abdelaziz, K., Bavananthasivam, J., Nagy, É., ... & Sharif, S. (2018). Examination of the effects of virus inactivation methods on the induction of antibody-and cell-mediated immune responses against whole inactivated H9N2 avian influenza virus vaccines in chickens. *Vaccine*, 36(27), 3908-3916.
- [18] Fertey, J., Bayer, L., Grunwald, T., Pohl, A., Beckmann, J., Gotzmann, G., ... & Thoma, M. (2016). Pathogens inactivated by low-energy-electron irradiation maintain antigenic properties and induce protective immune responses. *Viruses*, 8(11), 319.

- [19] Walker, C. M., & Ko, G. (2007). Effect of ultraviolet germicidal irradiation on viral aerosols. *Environmental science & technology*, 41(15), 5460-5465.
- [20] Pimenta, A. I., Guerreiro, D., Madureira, J., Margaça, F. M., & Verde, S. C. (2016). Tracking Human Adenovirus Inactivation by Gamma Radiation under Different Environmental Conditions. *Appl. Environ. Microbiol.*, 82(17), 5166-5173.
- [21] House, C., House, J. A., & Yedloutschnig, R. J. (1990). Inactivation of viral agents in bovine serum by gamma irradiation. *Canadian journal of microbiology*, 36(10), 737-740.
- [22] Salehi, B., Motamedi-Sedeh, F., Madadgar, O., Khalili, I., Ghalyan Chi Langroudi, A., Unger, H., & Wijewardana, V. (2018). Analysis of antigen conservation and inactivation of gamma-irradiated avian influenza virus subtype H9N2. *Acta microbiologica et immunologica Hungarica*, 65(2), 163-171.
- [23] Rafael Sanjuán, Miguel R. Nebot, Nicola Chirico, Louis M. Mansky, Robert Belshaw. *Journal of Virology* Sep 2010, 84 (19) 9733-9748; DOI: 10.1128/JVI.00694-10
- [24] H.M. Berman, J. Westbrook, Z. Feng, G. Gilliland, T.N. Bhat, H. Weissig, I.N. Shindyalov, P.E. Bourne. (2000) The Protein Data Bank *Nucleic Acids Research*, 28: 235-242.
- [25] RSICC Computer Code Collection, MCNPX User's Manual Version 2.4.0. Monte Carlo N-Particle Transport Code System for Multiple and High Energy Applications, (2002).
- [26] Wrapp, D.; Wang, N.; Corbett, K. S.; Goldsmith, J. A.; Hsieh, C.-L.; Abiona, O.; Graham, B. S.; McLellan, J. S., Cryo-EM structure of the 2019-nCoV spike in the prefusion conformation. *Science* 2020, 367 (6483), 1260.
- [27] Mazzone, Horace M. *CRC Handbook of Viruses: Mass-Molecular Weight Values and Related Properties*. Boca Raton, FL: CRC Press, 1998.
- [28] H.O. Tekin, Mesut Karahan, Turker Tekin Erguzel, Tugba Manici, Muhsin Konuk. Radiation Shielding Parameters of Some Antioxidants using Monte Carlo Simulation. *Journal of Biological Physics*, 44(4), 579-590. <https://doi.org/10.1007/s10867-018-9507-6>
- [29] M. A. M. Uosif, A.M.A. Mostafa, Shams A.M. Issa, H.O. Tekin, Z.A. Alrowaili, O. Kilicoglu. Structural, mechanical and radiation shielding properties of newly developed tungstenlithium borate glasses: An experimental study. *Journal of Non-Crystalline Solids*. *Journal of Non-Crystalline Solids* 532 (2020) 119882. <https://doi.org/10.1016/j.jnoncrysol.2019.119882>
- [30] Yasser B. Saddeek, Shams A.M. Issa, Thamer Shalih Al-Harbi, H.O. Tekin, O. Kilicoglu, T.T. Erguzel, Kamal A. Aly, Mahmoud Ahmad. Improvement of radiation shielding properties of some tellurovanadate based glasses. *Physica Scripta*. Accepted Manuscript Online: 4 November 2019. <https://doi.org/10.1088/1402-4896/ab541d>

- [31] H.O. Tekin, E. Kavaz, Athanasia Papachristodoulou, M.Kamislioglu, O.Agar, E.E.Altunsoy Guclu, O.Kilicoglu, M.I. Sayyed. Characterization of $\text{SiO}_2\text{--PbO--CdO--Ga}_2\text{O}_3$ glasses for comprehensive nuclear shielding performance: Alpha, proton, gamma, neutron Radiation. *Ceramics International* 45 (2019) 19206 - 19222. <https://doi.org/10.1016/j.ceramint.2019.06.168>
- [32] Shams A.M. Issa, G. Susoy, Atif Mossad Ali, H.O. Tekin, Y.B. Saddeek, Ali Al-Hajry, Hamed Algarni, P.S. Anjana, O. Agar. The effective role of La_2O_3 contribution on zinc borate glasses: radiation shielding and mechanical properties. *Applied Physics A*. (2019) 125:867. <https://doi.org/10.1007/s00339-019-3169-5>

Figure 1: Coronavirus structure with structural proteins. N: Nucleocapsid protein; S: Spike protein, M: Membrane protein, HE: Hemagglutinin-Esterase and E: Envelope protein

Figure 2. The Structure of Human Coronavirus GlycoProtein (6VSB) (a) side view (b) top view (c) bottom view

Figure 3. Virus/Cell Organelle densities and S values

Figure 4. (a) Axial view of modeled virus structure in MCNPX code (b) Radiation transmission setup for calculation of attenuation coefficients

Fig. 5 Linear attenuation coefficient (LAC) values as a function of photon energy of Sars (CAS Number 587886-51-9), Influenza (CAS Number 141368-69-6) and Covid-19 GlycoProtein 6VSB.

Fig. 6 linear absorption coefficient (LAC) values as a function of photon energy of Sars (CAS Number 587886-51-9), Influenza (CAS Number 141368-69-6) and Covid-19 GlycoProtein 6VSB.

Fig. 7 Mean free path (MFP) values as a function of photon energy of Sars (CAS Number 587886-51-9), Influenza (CAS Number 141368-69-6) and Covid-19 GlycoProtein 6VSB.

Fig. 8 Exposure buildup factor (EBF) values as a function of photon energy of Sars (CAS Number 587886-51-9), Influenza (CAS Number 141368-69-6) and Covid-19 GlycoProtein 6VSB.

Fig. 9 Energy absorption buildup factor (EABF) values as a function of photon energy of Sars (CAS Number 587886-51-9), Influenza (CAS Number 141368-69-6) and Covid-19 GlycoProtein 6VSB.

Fig. 10 Relative dose distribution (RDD) values as a function of photon energy at different penetration depth (mfp) and distances (cm) of Sars (CAS Number 587886-51-9), Influenza (CAS Number 141368-69-6) and Covid-19 GlycoProtein 6VSB.

Fig. 11 Relative dose distribution values as a function of photon energy at different penetration depth (mfp) and distance (cm) of Covid-19 GlycoProtein 6VSB.

Table 1 . Elemental mass percentages (%) of investigated virüs types

Atom Type	Influenza	Sars	Covid-19
Carbon (C)	60.9129	49.8293	52.38
Hydrogen (H)	7.8242	7.5397	9.51
Nitrogen (N)	13.0474	18.4896	15.59
Oxygen (O)	18.2155	22.1258	21.55
Sulfur (S)	0	2.0156	0.97

Table 2 (EBF and EABF) G–P fitting coefficients (b, c, a, X_k and d) of Sars (CAS Number 587886-51-9).

E (MeV)	Z_{eq}	EBF					EABF				
		b	c	a	X_k	d	b	c	a	X_k	d
0.015	7.04	1.2302	0.4730	0.1718	14.2803	-0.0863	1.2322	0.4822	0.1646	14.5034	-0.0796
0.020	7.10	1.5239	0.5778	0.1332	14.9645	-0.0652	1.5389	0.5703	0.1370	14.8564	-0.0680
0.030	7.16	2.5275	0.8216	0.0584	15.8188	-0.0408	2.6231	0.8123	0.0626	15.3063	-0.0389
0.040	7.19	3.7854	1.2219	-0.0402	13.5543	0.0127	3.8329	1.2163	-0.0386	13.6874	0.0110
0.050	7.20	4.8315	1.5688	-0.1009	13.7841	0.0424	4.7397	1.5626	-0.0997	13.8431	0.0416
0.060	7.22	5.2973	1.8484	-0.1412	13.6965	0.0643	5.0247	1.8382	-0.1397	13.7464	0.0629
0.080	7.29	5.2377	2.1644	-0.1796	13.4288	0.0817	4.9220	2.1313	-0.1752	13.3521	0.0779
0.100	7.18	5.0707	2.2596	-0.1858	14.2864	0.0804	4.6547	2.2162	-0.1805	14.3323	0.0770
0.150	7.14	3.9557	2.3941	-0.2019	14.6266	0.0896	3.7754	2.2713	-0.1861	14.4085	0.0753
0.200	6.86	3.4416	2.4461	-0.2113	13.5512	0.0913	3.3398	2.2173	-0.1812	14.7961	0.0760
0.300	6.93	2.9739	2.1595	-0.1820	14.0826	0.0767	2.8382	2.0607	-0.1685	14.2583	0.0670
0.400	5.00	2.8620	2.6300	-0.2450	12.5800	0.1109	2.5330	2.0270	-0.1670	14.3400	0.0653
0.500	7.86	2.4832	1.7376	-0.1303	14.1909	0.0504	2.4768	1.7511	-0.1328	14.2592	0.0530
0.600	5.93	2.5433	1.8708	-0.1540	13.6057	0.0636	2.3964	1.6666	-0.1196	14.9641	0.0460
0.800	7.93	2.1886	1.5351	-0.1036	14.2265	0.0431	2.2132	1.5206	-0.1003	14.3684	0.0398
1.000	8.00	2.0980	1.4180	-0.0840	14.3500	0.0333	2.1040	1.4270	-0.0860	14.2000	0.0347
1.500	4.94	2.0791	1.3392	-0.0851	13.7372	0.0486	1.9349	1.2856	-0.0622	14.3083	0.0280
2.000	6.10	1.8939	1.1904	-0.0436	13.9859	0.0203	1.8422	1.1679	-0.0373	14.4708	0.0146
3.000	6.13	1.7474	1.0584	-0.0140	12.2459	0.0058	1.7141	1.0509	-0.0113	14.2474	0.0029
4.000	6.10	1.6507	0.9863	0.0040	24.6045	-0.0076	1.6263	0.9890	0.0034	12.9755	-0.0025
5.000	6.08	1.7412	0.9391	0.0171	14.4253	-0.0111	1.5642	0.9457	0.0146	14.9250	-0.0074
6.000	6.06	1.5245	0.9075	0.0263	14.2360	-0.0151	1.5174	0.9023	0.0292	12.6626	-0.0184
8.000	6.07	1.4387	0.8695	0.0376	16.6652	-0.0336	1.4300	0.8828	0.0335	12.1046	-0.0164
10.000	6.07	1.3721	0.8563	0.0416	12.4869	-0.0209	1.3770	0.8598	0.0399	14.3207	-0.0221
15.000	6.07	1.2756	0.8410	0.0425	15.2524	-0.0299	1.2822	0.8381	0.0472	15.8404	-0.0326

Table 3 (EBF and EABF) G–P fitting coefficients (b, c, a, X_k and d) of Influenza (CAS Number 141368-69-6).

E (MeV)	Z_{eq}	EBF					EABF				
		b	c	a	X_k	d	b	c	a	X_k	d
0.015	6.33	1.3329	0.5167	0.1547	14.2960	-0.0767	1.3415	0.5117	0.1565	14.4724	-0.0779
0.020	6.34	1.7562	0.6792	0.0974	16.0023	-0.0481	1.7767	0.6808	0.0970	15.8959	-0.0471
0.030	6.35	3.1842	1.0388	0.0024	13.8812	-0.0091	3.3530	1.0392	0.0020	13.8479	-0.0083
0.040	6.36	4.7654	1.5697	-0.1004	13.7859	0.0428	4.6603	1.5608	-0.0984	13.9872	0.0410
0.050	6.34	6.1036	1.9389	-0.1494	14.1629	0.0646	5.3411	1.9085	-0.1448	14.2921	0.0613
0.060	6.36	6.5665	2.2143	-0.1814	14.2086	0.0816	5.3181	2.1478	-0.1728	14.3235	0.0752
0.080	6.34	6.2863	2.5445	-0.2151	14.0306	0.0960	4.8803	2.3936	-0.1975	14.3144	0.0829
0.100	6.33	5.6521	2.6451	-0.2223	14.3965	0.0969	4.4292	2.4434	-0.1999	14.7405	0.0812
0.150	6.36	4.2276	2.7118	-0.2322	14.1288	0.1021	3.6074	2.4193	-0.1990	14.7547	0.0784
0.200	6.86	3.4430	2.4473	-0.2114	13.5582	0.0914	3.3390	2.2180	-0.1813	14.7959	0.0760
0.300	4.00	3.4480	3.4420	-0.3040	14.2000	0.1422	2.7220	2.1830	-0.1750	15.8800	0.0592
0.400	5.00	2.8620	2.6300	-0.2450	12.5800	0.1109	2.5330	2.0270	-0.1670	14.3400	0.0653
0.500	5.93	2.6585	2.0350	-0.1744	14.0904	0.0811	2.4543	1.8049	-0.1387	15.9498	0.0617
0.600	5.93	2.5433	1.8715	-0.1541	13.6059	0.0637	2.3963	1.6668	-0.1197	14.9635	0.0460
0.800	7.00	2.2410	1.5800	-0.1120	14.0300	0.0484	2.2020	1.5440	-0.1050	14.2000	0.0434
1.000	8.00	2.0980	1.4180	-0.0840	14.3500	0.0333	2.1040	1.4270	-0.0860	14.2000	0.0347
1.500	6.35	1.9950	1.2957	-0.0649	14.1070	0.0300	1.9373	1.2757	-0.0600	14.3235	0.0264
2.000	5.73	1.9126	1.1974	-0.0455	14.1052	0.0224	1.8404	1.1711	-0.0383	14.4276	0.0156
3.000	5.73	1.7603	1.0608	-0.0150	12.1702	0.0072	1.7150	1.0510	-0.0115	14.1170	0.0034
4.000	5.74	1.6605	0.9841	0.0045	23.5781	-0.0072	1.6270	0.9890	0.0032	13.3379	-0.0024
5.000	5.72	1.7162	0.9374	0.0173	14.6163	-0.0106	1.5658	0.9447	0.0148	14.6185	-0.0076
6.000	5.73	1.5291	0.9070	0.0260	14.5040	-0.0147	1.5205	0.9008	0.0292	12.5608	-0.0175
8.000	5.74	1.4417	0.8692	0.0373	16.3783	-0.0315	1.4350	0.8773	0.0354	11.8793	-0.0175
10.000	5.75	1.3754	0.8545	0.0418	12.6041	-0.0201	1.3806	0.8583	0.0400	14.3647	-0.0218
15.000	5.74	1.2784	0.8384	0.0434	14.9658	-0.0283	1.2859	0.8370	0.0470	15.4645	-0.0310

Table 4 (EBF and EABF) G–P fitting coefficients (b, c, a, X_k and d) of Covid-19 GlycoProtein 6VSB.

E (MeV)	Z_{eq}	EBF					EABF				
		b	c	a	X_k	d	b	c	a	X_k	d
0.015	6.67	1.2820	0.4952	0.1631	14.2826	-0.0814	1.2872	0.4979	0.1598	14.5226	-0.0782
0.020	6.70	1.6373	0.6272	0.1156	15.4434	-0.0565	1.6553	0.6235	0.1176	15.3406	-0.0577
0.030	6.74	2.8390	0.9182	0.0334	15.0022	-0.0279	2.9601	0.9189	0.0327	15.1977	-0.0261
0.040	6.77	4.2358	1.3821	-0.0698	13.6530	0.0275	4.2237	1.3744	-0.0678	13.8664	0.0255
0.050	6.79	5.3757	1.7345	-0.1245	13.9490	0.0539	5.0354	1.7181	-0.1217	14.0650	0.0517
0.060	6.80	5.8337	2.0220	-0.1624	13.8420	0.0745	5.1974	1.9891	-0.1577	13.9396	0.0708
0.080	6.80	5.6857	2.3606	-0.2003	13.5170	0.0912	4.9033	2.2751	-0.1894	13.6926	0.0826
0.100	6.82	5.3263	2.4000	-0.1993	14.3917	0.0863	4.5992	2.3000	-0.1875	14.5494	0.0781
0.150	6.78	4.0538	2.5372	-0.2165	14.1161	0.0968	3.7029	2.3381	-0.1923	14.5221	0.0771
0.200	6.83	3.4524	2.4549	-0.2120	13.6046	0.0918	3.3340	2.2225	-0.1817	14.7951	0.0760
0.300	4.00	3.4480	3.4420	-0.3040	14.2000	0.1422	2.7220	2.1830	-0.1750	15.8800	0.0592
0.400	5.00	2.8620	2.6300	-0.2450	12.5800	0.1109	2.5330	2.0270	-0.1670	14.3400	0.0653
0.500	5.91	2.6587	2.0398	-0.1750	14.0706	0.0815	2.4539	1.8057	-0.1388	15.9298	0.0617
0.600	5.91	2.5433	1.8755	-0.1547	13.6071	0.0642	2.3958	1.6675	-0.1198	14.9602	0.0461
0.800	7.00	2.2410	1.5800	-0.1120	14.0300	0.0484	2.2020	1.5440	-0.1050	14.2000	0.0434
1.000	8.00	2.0980	1.4180	-0.0840	14.3500	0.0333	2.1040	1.4270	-0.0860	14.2000	0.0347
1.500	6.23	2.0006	1.3011	-0.0663	13.9605	0.0311	1.9386	1.2755	-0.0600	14.3117	0.0265
2.000	5.63	1.9178	1.1993	-0.0461	14.1461	0.0231	1.8395	1.1725	-0.0387	14.3913	0.0160
3.000	5.77	1.7592	1.0604	-0.0149	12.1458	0.0070	1.7150	1.0509	-0.0114	14.1689	0.0033
4.000	5.76	1.6599	0.9842	0.0044	23.7502	-0.0072	1.6269	0.9891	0.0032	13.2947	-0.0023
5.000	5.77	1.7233	0.9377	0.0172	14.5959	-0.0107	1.5655	0.9451	0.0146	14.6942	-0.0075
6.000	5.74	1.5288	0.9070	0.0260	14.4940	-0.0147	1.5204	0.9007	0.0293	12.5462	-0.0176
8.000	5.77	1.4415	0.8691	0.0374	16.4481	-0.0318	1.4345	0.8779	0.0352	11.9022	-0.0174
10.000	5.76	1.3752	0.8546	0.0418	12.5868	-0.0202	1.3804	0.8583	0.0400	14.3617	-0.0218
15.000	5.75	1.2783	0.8385	0.0434	14.9796	-0.0284	1.2857	0.8371	0.0470	15.4846	-0.0311

Figures

Figure 1

Coronavirus structure with structural proteins. N: Nucleocapsid protein; S: Spike protein, M: Membrane protein, HE: Hemagglutinin-Esterase and E: Envelope protein

Figure 2

The Structure of Human Coronavirus GlycoProtein (6VSB) (a) side view (b) top view (c) bottom view

Figure 3

Virus/Cell Organelle densities and S values

Figure 4

(a) Axial view of modeled virus structure in MCNPX code (b) Radiation transmission setup for calculation of attenuation coefficients

Figure 5

Linear attenuation coefficient (LAC) values as a function of photon energy of Sars (CAS Number 587886-51-9), Influenza (CAS Number 141368-69-6) and Covid-19 GlycoProtein 6VSB.

Figure 6

linear absorption coefficient (LAC) values as a function of photon energy of Sars (CAS Number 587886-51-9), Influenza (CAS Number 141368-69-6) and Covid-19 GlycoProtein 6VSB.

Figure 7

Mean free path (MFP) values as a function of photon energy of Sars (CAS Number 587886-51-9), Influenza (CAS Number 141368-69-6) and Covid-19 GlycoProtein 6VSB.

Figure 8

Exposure buildup factor (EBF) values as a function of photon energy of Sars (CAS Number 587886-51-9), Influenza (CAS Number 141368-69-6) and Covid-19 GlycoProtein 6VSB.

Figure 9

Energy absorption buildup factor (EABF) values as a function of photon energy of Sars (CAS Number 587886-51-9), Influenza (CAS Number 141368-69-6) and Covid-19 GlycoProtein 6VSB.

Figure 10

Relative dose distribution (RDD) values as a function of photon energy at different penetration depth (mfp) and distances (cm) of Sars (CAS Number 587886-51-9), Influenza (CAS Number 141368-69-6) and Covid-19 GlycoProtein 6VSB.

Figure 11

Relative dose distribution values as a function of photon energy at different penetration depth (mfp) and distance (cm) of Covid-19 GlycoProtein 6VSB.