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Evaluation on Geant4 Hadronic Models for Pion Minus, Pion Plus and Neutron Particles as Major Antiproton Annihilation Products

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ABSTRACT

Geant4 is an open source simulation toolkit based on C++, which its advantages progressively lead to applications in research domains especially modeling the biological effects of ionizing radiation at the sub-cellular scale. However, it was shown that Geant4 does not give a reasonable result in the prediction of antiproton dose especially in Bragg peak. One of the reasons could be lack of reliable physic model to predict the final states of annihilation products like pions. Since most of the antiproton deposited dose is resulted from high-LET nuclear fragments following pion interaction in surrounding nucleons and we tried to reproduce depth dose curves of most probable energy range of pions and neutron particle using Geant4. We consider this work one of the steps to understand the origin of the error and finally verification of Geant4 for antiproton tracking. Geant4 toolkit version 9.4.6.p01 and Fluka version 2006.3 were used to reproduce the depth dose curves of 220 MeV pions (both negative and positive) and 70 MeV neutrons. The geometry applied in the simulations consist a 20 × 20 × 20 cm^3 water tank, similar to that used in CERN for antiproton relative dose measurements. Different physic lists including Quark-Gluon String Precompound (QGSP)_Binary Cascade (BIC)_HP, the recommended setting for hadron therapy, were used. In the case of pions, Geant4 resulted in at least 5% dose discrepancy between different physic lists at depth close to the entrance point. Even up to 15% discrepancy was found in some cases like QBBC compared to QGSP_BIC_HP. A significant difference was observed in dose profiles of different Geant4 physic list at small depths for a beam of pions. In the case of neutrons, large dose discrepancy was observed when LHEP or LHEP_EMV lists were applied. The magnitude of this dose discrepancy could be even 50% greater than the dose calculated by LHEP (or LHEP_EMV) at larger depths. We found that effect different Geant4 physic list in reproducing depth dose profile of the beam of pions was not negligible. Because the discrepancies were pronounced in smaller depth and also regarding the contribution of pions in deposited dose of a beam of antiproton, further investigation on choosing most suitable and accurate physic list for this purpose should be done. Furthermore, this study showed careful attention must be paid to choose the appropriate Geant4 physic list for neutron tracking depending to the applications criteria. We failed to find any agreement between results from Geant4 and Fluka to reproduce depth dose profile of pion with the energy range used in this study.

Key words: *Radioation, Ionizing, Antiproton, Mesons, Neutrons, GEANT4, depth dose*

INTRODUCTION

Gray and Kalogeropoulos first suggested radiation therapy with antiprotons in 1984 based on Monte Carlo calculation of a significant enhancement of physical dose in the Bragg peak.[1] Following that in 2002 a group called Antiproton Cell Expriment in Antiproton Decelerator (AD-4/ACE) has been working on the dosimetric and radiobiological properties of beam of antiprotons to estimate the suitability of antiprotons for radiotherapy using the AD at CERN.[2] The stopping power of high-energetic antiprotons in tissue is similar to that of protons. Most energy is lost per unit distance as it comes to rest, but when the antiprotons stops, each one will annihilate on the nuclei and 1.9 GeV energy is released mostly in the form of pions. Because of both the mixed particle spectrum and the pulsed form of the antiproton beam, absolute dose measurement and radiobiological study of this potential new radiotherapy modality is complicated.[3] Currently, only one laboratory in the world has the capability to produce anti-protons at energies and flux high enough to be of interest in radiation therapy research: The CERN proton synchrotron/AD. For this reasons, attempts were focused to use a suitable Monte Carlo simulation toolkit to predict and to calculate radiation

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effect in cellular and sub-cellular level to investigate the radiobiological effects of antiproton.

Geant4 is an open source simulation toolkit based on C++, which provides remarkable flexibility and extensibility. Its advantages progressively lead to the development of novel Geant4 applications in research domains especially modeling the biological effects of ionizing radiation at the sub-cellular scale. In this regard Geant4-DNA project, initiated in 2001 by Nieminen at the European Space Agency for the development of Geant4 toolkit to estimate the biological effects of ionizing radiation.[4] The other major advantage of Geant4 is its openness to physics and different available physic so called physic lists, which can be used based on the issue of interest. The concept of a physic list arises from the fact that Geant4 cannot offer a single modeling algorithm to cover the entire energy domain from zero to the TeV scale, for all known processes and particles. Instead, a combination of ideas and approaches is typically used to perform a simulation task. Beside unlimited combination of physic list, which can be used by its user, there are different standard physic lists, under development, which can cover most routine cases of energy transport consequents.[5]

Unfortunately, it was shown that attempts to verify standard physic list of Geant4 to transport a beam of antiproton does not give a reasonable result especially in prediction of dose in Bragg peak.[6] Regarding to the only available measurments data from CERN, Geant4 is able to locate the Bragg Peak in the right place. But the dose level in plateau and peak region is undegone over or under estimations depending to the physic llist applied This discrepancy between results achieved through simulation and measurements could be because of lack of reliable cross section data,[7] nonreliable model to predict the final states of annihilated particles or a combination of these effects.

Most of the antiproton deposited dose is resulted from high-LET nuclear fragments following pion interaction in surrounding nucleons. Paganetti *et al*. reported that most of the annihilation energy from rest of an anti-proton/proton in water to be transferred into kinetic energies of negative pions (32%), positive pions (18%) and neutron (5%).[8] Even further, the contribution from charged pions increased as the antiproton energy increased.[8] The average energies of these products are as follows: $+\pi$ (205 MeV), $-\pi$ (221 MeV) and neutron (68 MeV).[8] One or more of these pions, especially negative pions, may strike the nucleus of the atom, in which the anti-proton annihilates at leading to an intra-nuclear cascade. Secondary nuclear fragments may result from the intra-nuclear cascade, and these fragments deposit significant energy locally per anti-proton (up to 30 MeV).[9]

This study tried to reproduce depth dose curves of beam of pions and neutrons Particles with the kinetic energy range probable in antiproton annihilation using Geant4. We investigate the effect of changing Geant4 standard physic list on depth dose profiles of these particles and compare the results with those from Fluka. The reason to choose Fluka was because of its verification for antiproton in Bassler study.[10] Through the result of this study, we will be able to conclude whether or not Geant4 standard physic lists are reliable to transport pion as the most important antiproton annihilation products or not.

METHODS

In this study, Geant4 toolkit version 9.4.6.p01 and Fluka version 2006.3 as the verified Monte Carlo code for antiproton simulation were used.[10] The geometry applied in our simulations including beams of 220 MeV pions and 70 MeV neutrons. The geometry setup was a $20 \times 20 \times 20$ cm^3 water tank, similar to those used in antiproton relative dose measurements in CERN.[10] To reduce the dose fluctuation, optimizing numbers of primary particles (events) were required in some physic lists. Hence, to compensate the effect of different primary events on our results, all calculated doses were normalized to the number of primary particles used for the corresponding physic list. Since most of the antiproton dose will deposit in the close point to the annihilation vertex, the length of scoring region along Z axis was selected to be 10 cm long from the point of entrance at the phantom surface. The scoring mesh was a $4 \times 4 \times 10$ cm^3 box placed at the entrance to the water phantom in the center of the beam and consists of 100 bins and every bin has the dimension of $4 \times 4 \times 1$ mm^3. The lateral dimension of scoring mesh (perpendicular to the beam axis) was 4 cm to match our result to those were used in dose measurements study in CERN.[10] Delta-ray production and particle transport cuts were set to 1 mm in water. The Physic lists used in this study were LHEP_EMV, LHEP, QGSP_BERT, QGSP_BERT_EMV, FTFP_BERT_EMV, QGSP_BIC_HP, QBBC, and CHIPS. Geisha cross section data are used to calculate the inelastic interactions steps length in all the applied physic lists. The abovementioned hadronic and electromagnetic models are described on the web,[11] and the Physics Reference Manual[12] is also available.

The GEANT4 physic list QGSP BIC HP including the G4 Binary Light Ion (LI) Reaction, so called BICLI, is the currently recommended configuration of hadronic physics settings for hadron therapy and was used as standard configuration.[13] In this list, electromagnetic interactions were described with a set of models included in the 'electromagnetic standard package option 3'. They account for energy loss, straggling and multiple Coulomb scattering of charged particles. In this configuration, hadronic nucleon–nucleus interactions are described by the BIC model. Finally, every depth dose profile was normalized to the maximum quantity (dose) and compared with those from other physic lists and Fluka results.

RESULTS

The comparison of depth dose profile of 220 MeV beam of pions ($+\pi$ and $-\pi$) and 70 MeV beam of neutrons simulated using Geant4 version 9.4.6.p01 and Fluka version 2006.3 were shown in Figures 1 and 2, respectively. The effect of varying Geant4 physic list on depth dose profile was investigated and compared to those from Fluka, which was considered as the verified Monte Carlo code for antiproton tracking.

In the case of pions, Geant4 resulted in at least 5% dose discrepancy between different physic lists at depth close to the entrance point. Since most of the local deposited dose by an antiproton beam is due to high-LET nuclear fragments following pion interaction in surrounding nucleons, this discrepancy can led to an error for antiproton dose calculation. Even up to 15% discrepancy was found in some cases such as QBBC compared to QGSP_BIC_HP, which is considered as the recommended physic list for hadron therapy.[11] Furthermore as it was shown in Figures 1a and 1b, there are noticeable differences between QGS_BERT_EMV with FTF_BERT_EMV models in calculated dose of pions particles. Despite of using the same cross section data, low energy inelastic model and the same electromagnetic option different results were achieved with these two physic lists for beam of pion.

In the case of neutrons, the magnitude of this dose discrepancy could be even 50% greater than dose calculated by LHEP (or LHEP_EMV) at larger depths. Although neutron does not have a considerable contribution to the overall dose of an antiproton beam (5%),[8] but the result of this study showed that enough cares should be taken to choose an appropriate physic list depend to the user application

DISCUSSION

This study could not find any agreements between Geant4 and Fluka to reproduce depth dose profiles of pion minus and pion plus beams. The most noticeable difference in a comparison of results was that the same pion inelastic cross section data (Geisha) have been using in all investigated physic lists. The same level of the dose discrepancy was found in calculating charged pion fluxes when comparing Geant4 results with HZETRN.[14] Furthermore, Brooks *et al*. concluded that there is a large amount of variation in pion yields in a Tantalum Rod target at low energies from different Geant4 hadronic models compared to MARS[15] which agreed with our results. Collot compared pion yield and characteristic spectra between FLUKA and MARS with some measurements.[16] They claim good agreement between data and code simulation results, which proved verification of Fluka for pion tracking as it was considered in our study.

As it was shown in Figures 1 and 2, the amount of relative difference is larger at the smaller depths. It means that the error in pion dose calculation could lead to dose discrepancies at the close distances to the annihilation point (i.e. Bragg peak). As stated above, pions are responsible for producing high-LET nuclear fragments, which are the most important source of the deposited dose at the close distance to the antiproton annihilation vertex.[1] As a result, any small discrepancies in the dose calculation of pions will result in larger difference in antiproton dose.

We found that the impact of changing different Geant4 physic list in reproducing depth dose profile of the beam of pions is not negligible. The most noticeable difference in a comparison of results was that the same pion inelastic cross

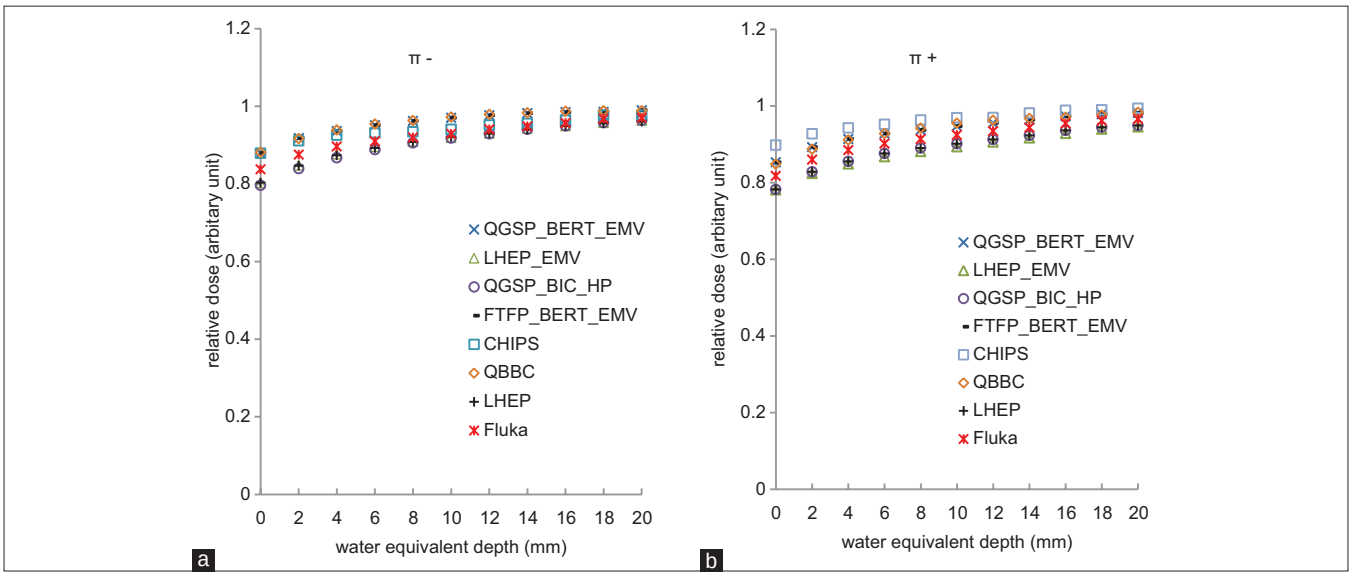

Figure 1: (a) Normalized depth dose profiles of 220 MeV beam of $\pi-$ (a) and $\pi+$ (b)

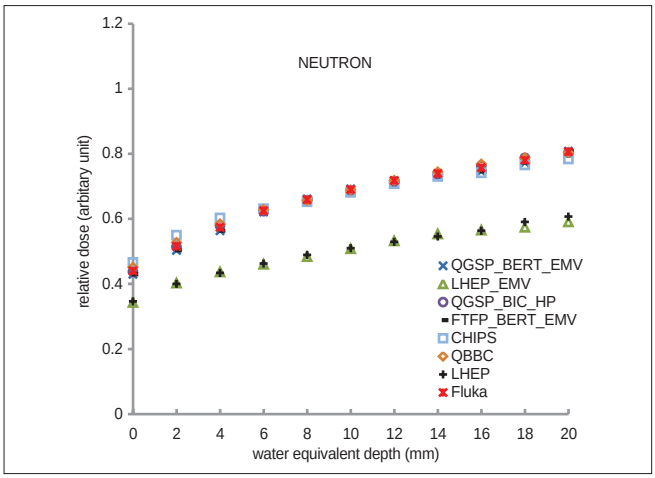

Figure 2: Normalized depth dose profile of 70 MeV beam of neutron

section data (Gheisha) have been using in all investigated physic lists. Because the discrepancies were pronounced in smaller depth and also regarding the contribution of pions in deposited dose of a beam of antiproton, further investigation on choosing most suitable and accurate physic list for this purpose should be done. Furthermore, this study showed careful attention must be paid to choose the appropriate Geant4 physics list for neutron tracking depending to the applications criteria. We failed to find any agreement between results from Geant4 and Fluka to reproduce depth dose profile of pion with the energy range used in this study.

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