Internal dosimetry of salivary glands in PSMA-targeted PET/CT: a Monte Carlo based study

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Background: Prostate-Specific Membrane Antigen (PSMA) targeted radiopharmaceuticals are used for diagnosis and therapy of prostate cancer (PS). Salivary glands (SGs) exhibit high PSMA uptake, and represent the dose-limiting organ in PSMA-targeted therapies. SGs dosimetry studies are usually carried out with simplified approaches such as organ-level MIRD formalism, where SGs are often treated as a unique organ. Aim of this work was to perform a 3D patient-specific dosimetry separately for right and left parotids and submandibular SGs in ^{18}F-PSMA-1007 PET/CTs, by means of direct Monte Carlo (MC) simulation, and to compare it with simplified approaches.

Material and Methods: PET/CTs of patients with biochemical PS recurrence, acquired at 3 time points after ^{18}F-PSMA-1007 administration, were used as input for Geant4-based GATE MC simulations to evaluate 3D dose rate maps. After segmentation of SGs volumes of interest (VOIs), their average absorbed doses (*AADs*) were calculated via trapezoid + physical decay tail integration. PET activity spill-outs with respect to morphologic SGs were taken into account by using VOIs segmented on functional imaging via threshold method (25% of the max. PET activity). In addition, the dosimetry was carried out using: A) spherical model of OLINDA/EXM 2.1, B) ellipsoidal model by Amato et al. [1], C) MIRD formalism with OLINDA and D) OpenDose S-factors. In all methods some degree of patient-specificity was introduced by adjusting volume, mass and activities of the SGs.

Preliminary results: Depending on the patient, *AAD* in the right and left counterpart of the same SG can differ up to 50%. A and B systematically underestimate SGs *AADs* with respect to MC by 10-15%; C and D can underestimate even more, depending on the specific patient.

[1] Amato et al. *AAPP Phys Math Nat Sci*, Vol 92 No 1 (2014), pp. A1-1 - A1-8