recent. Thus, a growing need exists to validate software performance in different tasks in different diseases. **Objectives:** To evaluate the performance of artificial intelligence software to determine metabolic tumor burden in the primary staging of rectal cancer. **Materials and Methods:** A cross-sectional retrospective analysis was conducted on 51 histology-proven rectal cancer patients (35% females; mean age = 61 years) who underwent a staging 18F-FDG PET/CT. Whole-body metabolic tumor burden parameters (wbMTV and wbTLG) were quantified semi-automatically and through AI algorithm (Syngovia VB60; Siemens Healthineers Medical Solutions). The AI software's ability to correctly identify and classify the primary lesion, regional lymph nodes, and distant metastases was evaluated. In addition, the intraclass correlation coefficient (ICC) was applied to evaluate concordance between the AI-based software and the semiautomatic software in determining wbMTV and wbTLG. Values above 0.7 were considered to indicate substantial agreement. Resultados: The AI and semiautomatic tumor burden metrics correlated strongly for both wbMTV (ICC = 1.00; 95% CI = 0.94 - 0.99; P < 0.0000) and wbTLG (ICC = 1.00; 95% CI = 0.80 – 0.90; P < 0.0000). Additionally, the AI software's ability to correctly identify lesions compared to the documented staging was better for the identification of distant metastasis (78,57% of patients), mildly adequate to identify regional lymph nodes (50,00%) and had poor performance for identification of the primary lesion (5,76%). On the other hand, the time spent calculating these metrics was less by AI than by the semiautomatic method, especially in patients with advanced disease. **Conclusion:** The determination of whole-body metabolic tumor burden on 18F-FDG PET/CT with artificial intelligence software is challenging because of the physiologic bowel activity. However, deep learning may have the ability to overcome these challenges and may therefore improve the primary staging of rectal cancer.

Keywords: 18F-FDG PET/CT, Artificial intelligence., Rectal cancer.

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SYNTHESIS, CHARACTERIZATION, AND RADIOLABELING OF MODIFIED PEPTIDE FRAGMENTS TARGETING AVB3 INTEGRIN ADHESION MOLECULE OVEREXPRESSED IN TUMORS

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Introduction/Justification: Peptides are biomolecules that have been associated with various physiological responses and have great potential for the diagnosis or treatment of diseases, including various types of tumors. Several studies have shown that biologically active peptides containing the RGD domain have a high affinity with the $\alpha v\beta 3$ integrin adhesion molecule overexpressed in tumor cells, assisting in molecular imaging or targeted radionuclide therapy (TRT) as an anti-tumor agent. **Objectives:** To obtain an anti-integrin peptide fragment modified by incorporating two spacers — hexa-aminocaproic acid (C6) or dodeca-aminocaproic acid (C12) — and by adding the chelating agent DOTA for subsequent radiolabeling with yttrium-86 (86Y). **Materials and Methods:** The modified peptides were synthesized by the solid-phase peptide synthesis method using the Fmoc/tBut strategy. In this strategy, the Fmoc group removal step was carried out with 20% 4-methylpiperidine / 80% DMF, and the amino acid coupling step is usually performed with the diisopropylcarbodiimide/1-hydroxybenzotriazole (DIC/HOBt) acylation mixture. In this step, an excess of Fmoc-amino acids and acylating agents of 2.5 times were used relative to the synthesis scale utilized in mmol/g. Peptide cleavage from the resin and removal of side chain protecting groups were carried out using a mixture containing a high concentration of TFA (reagent K). After synthesis and cleavage, the peptides underwent characterization and purification process through high-performance liquid chromatography (HPLC) and mass spectrometry. The radiolabeling process was conducted utilizing cyclotron-produced 86Y, employing a NaOAc buffer (pH = 5.5). The radiochemical reaction was performed at 95°C for 30 min, followed by filtration through a Sep-Pak C18 cartridge for purification and determination of the radiolabeling yield. **Results:** The DOTA-C6-anti-integrin and DOTA-C12-anti-integrin peptides were efficiently synthesized, and the yields obtained were approximately 12.7% and 26.4%, respectively. Chromatographic analyses obtained by HPLC, as well as mass spectrometry, showed that the entire synthesis, cleavage, and characterization process were carried out properly with visualization of profiles and molecular masses of 1165.3 g/mol and 1249.1 g/mol for the DOTA-C6-anti-integrin and DOTA-C12-anti-integrin peptides, respectively. After the purification process, 14.6 mg and 66.2 mg of pure peptides were obtained. The preliminary 86Y-labeling data indicated a radiochemical yield of approximately 97% for both peptides. **Conclusion:** The proposed modified anti-integrin peptides were efficiently synthesized, characterized, and purified. Preliminary radiolabeling studies with 86Y demonstrated a high radiochemical yield, paving the way for further exploration in radiochemical studies and assays of affinity to tumor cells.

Keywords: Anti-integrin peptides, Tumor cells, Yttrium-86, $\alpha v\beta 3$ integrin.

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AVALIAÇÃO DA BIODISTRIBUIÇÃO DO RADIOFÁRMACO 177LU-PSMA I&T EM ANIMAIS COM MODELO TUMORAL.

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