

mm³ (12.8 ± 1.1 days) was longer compared to only NIR-light irradiated (10 ± 4.9 days) or only tracer injected control mice (6.4 ± 1.7 days, P<0.05). In addition, tPDT prolonged survival (defined as tumor growth >1000 mm³, humane endpoint) in treated mice (16 days) compared to the two control groups (12 and 10 days, respectively). **Conclusion:** Here, we demonstrated the feasibility of PSMA-targeted PDT using the newly developed PSMA-N064 multimodal ligand. In the future, this ligand will be used for intra-operative tumor detection and PSMA-tPDT. Use of tPDT during surgery can facilitate removal of unresectable tumor rest and positive surgical margins, potentially leading to improved surgical outcomes of PCa patients. **References:** This work was supported by EKFS (2016-A64) and the Dutch Cancer Society (NKB-KWF 10443/2016-1).

OP-025

Assessment of in vivo biodistribution and treatment efficacy of ¹⁷⁷Lu PSMA-R2 and ¹⁷⁷Lu-PSMA-617 on mice bearing prostate cancer tumors

V. Muzio¹, L. Ravasi¹, L. Sacchetti¹, L. Fugazza¹, S. Bacot², M. Debiossat², M. Ahmadi², C. Montemagno², C. Ghezzi², A. Broisat²;
¹Advanced Accelerator Applications, a Novartis company, Geneva, SWITZERLAND, ²Univ. Grenoble Alpes, Inserm, CHU Grenoble Alpes, Grenoble, FRANCE.

Aim/Introduction: Comparison of the in vivo biodistribution and the treatment efficacy of ¹⁷⁷Lu PSMA-R2 and ¹⁷⁷Lu-PSMA-617 in mice with prostate cancer grafts. **Materials and Methods:** PSMA positive-PC3-PIP were subcutaneously implanted in athymic nude mice in the left flank. A single injection of 111MBq of ¹⁷⁷Lu-PSMA-R2 or ¹⁷⁷Lu-PSMA-617 or of saline was performed approximately two weeks later, concomitantly to randomization into groups of similar average tumor volumes expressed in mm³. SPECT/CT imaging was performed in a subset of 12 mice (6 from ¹⁷⁷Lu-PSMA-R2 group and 6 from ¹⁷⁷Lu-PSMA-617 group). Acquisitions were performed 24h post injection of ¹⁷⁷Lu-PSMA-R2 and ¹⁷⁷Lu-PSMA-617. Tumor volumes were monitored daily and expressed either as absolute values in mm³ or as a volume relative to that measured the day of the ¹⁷⁷Lu-PSMA-R2, ¹⁷⁷Lu-PSMA-617 or saline administration. Tumor growth curves were compared using two-ways ANOVA from the day of first injection to day 14. **Results:** Absolute tumor volumes were significantly reduced in the ¹⁷⁷Lu-PSMA-R2 and ¹⁷⁷Lu-PSMA-617 groups vs control group (p<0.001). Similarly, tumor volumes from ¹⁷⁷Lu-PSMA-R2 and ¹⁷⁷Lu-PSMA-617 groups were significantly reduced in comparison to control group (p<0.001). No differences were observed between the tumor volumes of the treated groups. At later time points (14-36 days), the tumors of the control group started to reach the 1500mm³-limit volume as opposed to those of the treated groups. Control mice were therefore euthanized. Although ¹⁷⁷Lu-PSMA-R2 and ¹⁷⁷Lu-PSMA-617 were no longer administered, a tumor regression was observed in both groups. By day 36th, tumors were no longer detectable in 5 out of 10 tumors from ¹⁷⁷Lu-PSMA-R2 group and 4 out of 10 tumors from ¹⁷⁷Lu-PSMA-617 group. Mean tumor volume was of 13.9±23.6

and 11.1±10.4 in ¹⁷⁷Lu-PSMA-R2 and ¹⁷⁷Lu-PSMA-617 groups, respectively. No statistical differences were found in tumor growth under ¹⁷⁷Lu-PSMA-R2 or ¹⁷⁷Lu-PSMA-617 treatment. SPECT/CT data acquired on 6 mice from each ¹⁷⁷Lu-group showed strong ¹⁷⁷Lu-PSMA-R2 and ¹⁷⁷Lu-PSMA-617 uptakes at tumor level 24h p.i. with very low uptake elsewhere. VOI quantification confirmed visual observation. Interestingly, after 14 days of a single dose of 111 MBq of ¹⁷⁷Lu-PSMA-R2 or ¹⁷⁷Lu-PSMA-617, similar tumor growth was observed between ¹⁷⁷Lu-PSMA-R2 and ¹⁷⁷Lu-PSMA-617 treated mice despite this different tumor uptake at 24h. **Conclusion:** ¹⁷⁷Lu-PSMA-R2 and ¹⁷⁷Lu-PSMA-617 have a similar biodistribution in mice inoculated with PSMA positive-PC3-PIP tumor grafts. Similar significant reduction of tumor size was observed, despite the difference in clearance from tumor tissue. **References:** None.

106

Do.MoRe - Rapid Fire Session: Data Analysis

Sunday, October 13, 2019, 8:00 - 9:30

Lecture Hall 112

OP-026

Standardized Radiomics of Clinical Myocardial Perfusion Stress SPECT Images to Determine Coronary Artery Calcification Score

S. Ashrafinia¹, P. Dalaie¹, M. Salehi Sadaghiani¹, T. H. Schindler², M. G. Pomper¹, A. Rahmim³;

¹Johns Hopkins University, Baltimore, MD, UNITED STATES OF AMERICA, ²Washington University at St. Louis, St. Louis, MO, UNITED STATES OF AMERICA, ³University of British Columbia, Vancouver, BC, CANADA.

Aim/Introduction: Myocardial perfusion stress SPECT(MPSS) is an established diagnostic test for patients suspected with coronary-artery-disease(CAD). Meanwhile, coronary-artery calcification(CAC) scoring obtained from diagnostic CT is a highly-specific test, offering incremental diagnosis information in identifying patients with significant CAD yet normal MPSS scan[1]. Nonetheless, CAC scoring is not commonly performed/reimbursed in a wide community setting. Our aim is to quantify heterogeneity of uptake via radiomics of 'normal' MPSS scans to enable prediction of CAC scores, identifying subclinical CAD. **Materials and Methods:** 428 patients were collected with normal (non-ischemic) MPSS (8-30mCi ^{99m}Tc-Sestamibi) with consensus reading. NM physician verified images (iteratively-reconstructed/attenuation-corrected) to be free from fixed perfusion-defect/artifactual attenuation. 3D images were automatically-segmented into 4 regions-of-interest(ROI), including myocardium+3vascular segments (LAD-LCX-RCA). We developed standardized environment for radiomics analysis(SERA)[2] and calculated 215 3D radiomic features in compliance with image-biomarker standardization

initiative (IBSI)[3], ensuring reproducibility of this study. Isotropic-cubic-voxel-ROIs (no resampling/interpolation needed) were discretized using fixed-bin-number discretization into 8 grey-levels (GLs) ($2^2, \dots, 2^9$). We first performed two-phase blind-to-outcome feature-selection: A) Removing: A-1) three smallest GLs (very-low dynamic-range), A-2) two highest-GLs (causing highly-correlated features $\rho > 0.9$), and A-3) GL=128 (indifferent statistical properties), ultimately selecting GL=64, similar to findings from our previous study[4]. B) Post-feature calculation: removing features with B-1) identical values, B-2) very-low dynamic-range, B-3) varieties of higher-order feature-classes, B-4) redundant features ($\rho=1$), and B-5) highly-correlated features (Spearman $\rho > 0.95$). Next, we ran multivariate analysis to predict CAC scores from i) radiomics, ii) clinical-features, iii) radiomics+clinical-features. We performed randomly-selected 60%/25%/15% training/validation/testing. Training started from a constant fit, following iteratively adding/removing features (stepwise-regression) based on sorted univariate-Spearman-correlation with CAC-scores, invoking Akaike-information-criterion (AIC) to discourage overfitting. Validation was run similarly, with the training output-model as initial fit. We shuffled training-validation sets 20 times, then found the best model using log-likelihood to evaluate the test-set. The sensitivity to test-set was further reduced by running the entire operation 50 times, then employing Fisher's method to verify significance of independent tests. **Results:** Feature-selection significantly reduced 8×215 features to 56. Median Absolute Pearson's-correlation coefficient|p-value for 3 feature-pools (radiomics, clinical, combined) were: $(0.15 \pm 0.11, 0.38 \pm 0.08, 0.41 \pm 0.05) | (0.1, 0.001, 0.0006)$, $(0.24 \pm 0.06, 0.35 \pm 0.08, 0.41 \pm 0.05) | (0.05, 0.004, 0.0007)$, $(0.07 \pm 0.05, 0.24 \pm 0.1, 0.28 \pm 0.09) | (0.4, 0.06, 0.02)$ $(0.06 \pm 0.05, 0.16 \pm 0.06, 0.24 \pm 0.06) | (0.4, 0.2, 0.05)$ for Myocardium-LAD-LCX-RCA, respectively. Results demonstrate combined features enhance the significance of CAC score prediction across all segments. **Conclusion:** Our multivariate model enabled the significant prediction of CAC scores at all cardiac segments when combining standardized-radiomics with clinical features, suggesting radiomics adds diagnostic/prognostic value to standard MPSS for wide clinical usage. **References:** [1] Shaw, et-al, Radiology, vol.228, no.3, pp.826-833, 2003. [2] Ashrafinia, PhD Thesis, 2019. [3] Zwanenburg, et-al., arXiv:1612.07005v3. [4] Ashrafinia, et al., Medical Physics. Vol.44. No.6, 2017.

OP-027

A novel myocardial perfusion phantom: performing 'ground truth' flow measurements to evaluate accuracy of flow quantification with SPECT

M. E. Kamphuis¹, G. de Vries¹, M. Saaltink², J. Verschoor², A. Agoor², M. J. W. Greuter^{3,1}, C. H. Slump¹, R. H. J. A. Slart^{3,1};

¹University of Twente, Enschede, NETHERLANDS,

²Ziekenhuisgroep Twente, Hengelo, NETHERLANDS, ³University Medical Center Groningen, Groningen, NETHERLANDS.

Aim/Introduction: Quantitative PET myocardial perfusion imaging (MPI) can standardize detection of coronary artery

disease and improve diagnostic accuracy in patients with balanced ischemia. Emerging SPECT technology may enable quantitative evaluation as well, but proof hereof is still in its infancy. We aim to contribute to 'ground truth' validation of quantitative SPECT-MPI by evaluating the accuracy of flow quantification using a novel myocardial perfusion phantom. **Materials and Methods:** The in-house built perfusion phantom mimics the anatomy and (patho-) physiology of left ventricular first-pass perfusion. Pumped continuous flow is conducted through a 3D printed left ventricle and aorta, which branches into coronary arteries that are connected to three myocardial modules. These represent the microcirculation of the main coronary territories. The modules are interchangeable and can consist of different tissue fillings. Flow sensors are incorporated into the setup as 'ground truth' flow measure. Flow distribution is controlled by adjustable end-resistances, which also enables simulation of local perfusion deficits. As with patients, a radioactive tracer is administered and a dynamic myocardial perfusion scan is started simultaneously to monitor tracer distribution. The resulting time activity curves (TACs) serve as input for myocardial blood flow quantification. The absolute difference between measured and computed flow (in mL/min/g) is used as measure of accuracy. In the phantom experiments, we used standard clinical protocols for SPECT-MPI (D-SPECT, Spectrum Dynamics) and subsequent flow quantification (4DM Corridor software). We injected 500 MBq ^{99m}Tc-tetrafosmin at an aorta flow of 2-5L/min. The flow into the individual myocardial modules varied between 20-100mL/min and module fillings varied (e.g. different types of sponge materials). **Results:** The obtained TACs inside the simulated left ventricle match physiological values. The area under the curve remains the same for the different aortic flow rates, but the maximum of the curve goes down and smears out over a longer period when lowering the flow. The TACs corresponding to myocardial tissue segments have a relatively fast washout of less than 20s. An aortic and myocardial flow of 2 and 100mL/min, respectively, resulted in the longest washout time. **Conclusion:** This study highlights the design and realization of a novel myocardial perfusion phantom to contribute to ground truth validation of quantitative SPECT-MPI. First testing showed promising results, as both geometry and tracer distribution resemble left ventricular microcirculation. Subsequent evaluation of quantitative SPECT-MPI accuracy is in progress. **References:** None.

OP-028

Initial evaluation of an automated high temporal resolution data-driven motion correction for rubidium cardiac relative perfusion PET

I. Armstrong¹, C. Hayden², P. Arumugam¹;

¹Manchester University NHS Foundation Trust, Manchester, UNITED KINGDOM, ²Siemens Medical Solutions USA, Inc., Knoxville, TN, UNITED STATES OF AMERICA.

Aim/Introduction: Vasodilator stress, due to predominantly respiratory side effects, can introduce varying degrees of patient