nutritional status, and reduced overall survival in patients with HCC treated with sorafenib.

Keywords: Hepatocellular carcinoma, Neutrophil-to-lymphocyte ratio, Systemic inflammation, Sorafenib, Survival analysis.

Conflicts of interest: The authors declare that they have no conflicts of interest.

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AN EXPLORATORY GENOMIC ANALYSIS OF GASTRIC CANCER WITH 18F-PSMA UPTAKE

Renata Erbert Contriciani, Barbara Cipriano, Larissa Ariel Oliveira Carrilho, Leo Victor Kim, Fabíola Furtuoso Zarpelão, Sandra Regina Branbilla, Ligia M. Antunes Correa, Caroline Torricelli Corrêa, Natália Tobar Toledo Prudente da Silva, Elba C.S.C. Etchebehere, Luiz Roberto Lopes, Nelson Adami Andreollo, Maria Carolina Santos Mendes, José Barreto Campello Carvalheira

Universidade Estadual de Campinas, Campinas, SP, Brazil

Introduction: Gastric Cancer (GC) presents significant challenges regarding staging and biological heterogeneity. Recently, Prostate-Specific Membrane Antigen (PSMA) expression was identified in the neovasculature of gastric tumors. However, the molecular mechanisms underlying this expression remain poorly understood. This translational cross-sectional study aimed to characterize the biological profile of PSMA-avid tumors by integrating imaging-based metabolic assessment with transcriptomic analysis. **Methodology:** This study analyzed a subgroup of 11 patients with gastric adenocarcinoma treated at the Clinics Hospital of the University of Campinas (HC-UNICAMP). All patients underwent preoperative 18F-PSMA PET/CT and 18F-FDG PET/CT. Tumor gene expression was evaluated using the nCounter® Analysis System with the Tumor Signaling 360™ Panel (NanoString Technologies, a Bruker Company). Differential gene expression was analyzed using R software, and pathway enrichment analysis for up- and down-regulated genes was conducted using the Enrichr software. Clinical and systemic inflammatory data were managed using REDCap. Statistical analyses of clinical variables were performed with Jamovi software (v.2.3.28). The study was approved by the Institutional Review Board (CAAE: 76237023.0.0000.5404). **Results:** Patients were stratified according to PSMA uptake (6 Positive vs. 5 Negative). The PSMA-positive group exhibited a distinct metabolic profile, with 100% of patients showing 18F-FDG avidity compared to only 25% in the negative group ($p = 0.011$). Regarding systemic inflammation, the PSMA-positive group presented significantly higher CRP levels (Median: 8.0 vs. 2.0 mg/L; $p = 0.049$). Gene expression analysis revealed that PSMA positivity was associated with the upregulation of angiogenesis (VEGF signaling) and hypoxia pathways (HIF-1 signaling). Conversely, this group showed downregulation of adaptive immune markers, specifically T-cell receptor (TCR) signaling and Primary Immunodeficiency pathways, suggesting an immune-excluded phenotype. No significant differences were observed regarding demographic characteristics. **Conclusion:** The PSMA-positive group was associated with a distinct phenotype, characterized by tumor neoangiogenesis, increased glucose metabolism, and systemic inflammation. The transcriptomic analysis confirmed that these tumors possess a unique biological profile compared to PSMA-negative lesions. These exploratory findings suggest that PSMA and FDG PET/CT might provide complementary biological information to standard imaging, although further research is needed to fully understand its clinical relevance.

Keywords: Gastric Cancer, 18F-PSMA PET/CT, Radiogenomics, Transcriptomics.

Conflicts of interest: The authors declare that they have no conflicts of interest.

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SEQUENTIAL FDG PET/CT FOLLOW-UP IN A RENAL-TRANSPLANT RECIPIENT WITH MULTIPLE CUTANEOUS SQUAMOUS CELL CARCINOMAS AND POST-TRANSPLANT LYMPHOPROLIFERATIVE DISORDER: SUSTAINED METABOLIC STABILITY WITHOUT PROGRESSION

Barbara Rayne Santos de Alencar, Mariana Maitto, Tomás Agnello, Barbara Juarez Amorim, Elba C.S. Camargo Etchebehere, Allan Oliveira Santos, Celso Dario Ramos, Mariana da Cunha Lopes de Lima

Universidade Estadual de Campinas, Campinas, SP, Brazil

Introduction: Cutaneous squamous cell carcinoma (cSCC) is the most frequent malignancy in solid-organ transplant recipients, promoted by chronic immunosuppression and