

Advancing Radioproteomics: Integrating PSMA PET/CT and mpMRI with Localized Proteomic Profiling in Prostate Cancer

Background

Current diagnostic methods for primary prostate cancer (PCa), such as image-guided biopsies, carry risks and may miss tumor heterogeneity. This has driven interest in non-invasive imaging approaches like multiparametric MRI (mpMRI) and PSMA PET/CT, which capture the full tumor burden. This study integrates radiomic features from imaging with histopathology and proteomics from distinct tumor subregions to enhance the molecular interpretation of imaging characteristics in PCa.

Methods

Twenty patients with intermediate- or high-risk PCa underwent preoperative mpMRI and PSMA PET/CT, followed by radical prostatectomy. Imaging and histopathology were co-registered for voxel-based analysis. Proteomic profiling of selected regions was performed using LC-MS/MS, enabling correlation of imaging features with localized protein expression.

Results

Analysis of 77 tumor and adjacent non-malignant tissue samples identified over 2,400 proteins. The maximal standardized uptake values (SUV max) from PSMA PET/CT correlated with PSMA expression, validating the radioproteomic approach. High SUV regions were enriched in proteins related to telomere maintenance and RNA processing, while low SUV regions were associated with extracellular matrix remodeling. MRI-derived apparent diffusion coefficient (ADC) values correlated with proteins involved in cell adhesion and Golgi organization. Distinct proteomic signatures were identified across tumor subregions, revealing potential biomarkers for non-invasive tumor characterization and risk stratification.

Conclusion

By integrating advanced imaging with proteomic profiling, this study highlights molecular correlates of imaging features in PCa. These insights support the development of imaging-based biomarkers and personalized therapeutic strategies, bridging non-invasive diagnostics with tumor biology.

Preferred type of presentation

Poster Presentation only

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