Chirurgia (Bucur). 2025;120(3):265-274
http://dx.doi.org/10.21614/chirurgia.3151

Toward Personalized Surgery in Advanced Prostate Cancer: Stratification by PTEN, AR-V7, TP53, TMPRSS2-ERG, and ERBB2 Genetic Alterations

Cristina Anita Ionescu (Mitu)[1,2], Georgeta Camelia Cozaru[3,4,5], Mariana Aşchie[4,5], Nicoleta Leopa[6], Bogdan Cîmpineanu[2], Felix Voinea[2,7], Elena Matei[3], Anca Mitroi[3,4], Mariana Deacu[2,4], Ionuț Iorga[2,7], Mihaela Pundiche[2,6]

[1]Department of Genetics, Prof. Dr. Alexandru Trestioreanu Institute of Oncology, Bucharest, Romania
[2]Ovidius University, Faculty of Medicine, Constanta, Romania
[3]Center for Research and Development of the Morphological and Genetic Studies of Malignant Pathology, Ovidius University, Constanta, Romania
[4]Department of General Surgery, Cai Ferate Clinical Hospital Constanta, Romania
[5]Academy of Romanian Scientists, Bucharest, Romania
[6]Department of General Surgery, Emergency County Hospital, Constanta, Romania
[7]Department of Urology, Emergency County Hospital, Constanta, Romania

Abstract

Background: Advanced prostate cancer is a biologically heterogeneous disease often marked by multiple genetic and epigenetic alterations that influence tumor progression, treatment resistance, and prognosis. Among the most frequently altered genes are PTEN, AR-V7, TP53, TMPRSS2-ERG, and ERBB2, each with potential relevance for stratifying risk and guiding targeted therapy.

Methods: This retrospective study included 43 patients with advanced prostate cancer who underwent radical prostatectomy. Tumor specimens were analyzed using fluorescence in situ hybridization (FISH) to assess the mutational status of the five markers. Clinicopathological parameters, including PSA levels, Gleason score, tumor stage, and invasion status, were correlated with molecular alterations using multinomial logistic regression.

Results: The most common isolated alteration was PTEN loss (20.9%), followed by TP53 amplification (16.3%), TMPRSS2-ERG fusion (13.9%), AR-V7 expression (11.6%), and ERBB2 amplification (7%). Combined alterations were also observed, with dual or triple marker expression in select aggressive cases. PTEN- and AR-V7+ were associated with low PSA values despite aggressive pathology, while ERBB2+ correlated with high PSA levels and high Gleason scores. TP53+ and ERBB2+ were also significantly associated with high-grade tumors (Gleason >7). AR-V7+ was the only marker significantly associated with seminal vesicle invasion. Younger age was weakly correlated with AR-V7+ and TP53+ status.

Conclusions: The molecular profile defined by PTEN, AR-V7, TP53, and ERBB2 identifies distinct biological subtypes in advanced prostate cancer, each with specific prognostic and therapeutic implications. Integration of these biomarkers into routine clinical assessment may improve treatment personalization and risk stratification. Validation in larger, prospective cohorts is warranted.

Keywords: prostate cancer, genetic profile, personalized surgery, biomarkers, prognosis