LETTER to the EDITOR **Editorial Process:** Submission:20/03/2026 Acceptance:22/09/2026 Published:25/09/2026

miR-126 and miR-143/145 Polymorphisms in Prostate Cancer: Clinical and Methodological Perspectives

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Dear Editor

We read with great interest the study by Bahari et al. evaluating miR-126 and miR-143/145 polymorphisms in prostate cancer (PCa) [1]. In this single-center case-control study, 185 patients with PCa and 220 age-matched controls were genotyped utilizing PCR-RFLP and T-ARMS PCR methodologies. The authors showed that different miRNA variants and haplotypes were linked to a lower risk of prostate cancer in several genetic models. However, there were no strong links found with clinical and pathological factors such as PSA level, Gleason score, pathological stage, perineural invasion, or surgical margin status. These results provide initial insights into possible genetic susceptibility factors in PCa.

Nonetheless, several methodological and interpretative factors necessitate additional scrutiny. Firstly, the study was performed at a single center and confined to an Iranian population, thereby limiting its external validity. The established influence of ethnic and genetic diversity on prostate cancer biology and miRNA polymorphisms highlights the need for validation in independent and multiethnic cohorts to enhance the generalizability of the findings [2].

Secondly, while essential clinical data such as PSA, Gleason score, and pathological stage were documented, they were not included in recognized risk stratification frameworks (e.g., ISUP Grade Groups or EAU/NCCN risk categories). Integrating such frameworks could improve the clinical interpretability of the reported associations.

Thirdly, while the study examines potential prognostic implications, it did not evaluate long-term oncological outcomes. Endpoints such as biochemical recurrence, progression, metastasis, or survival were not assessed. Thus, the results are better understood as indicators of disease susceptibility rather than having prognostic value [3].

In addition, the absence of functional validation limits the biological interpretation of the results. Additional research into the impact of these polymorphisms on miRNA expression and subsequent molecular pathways may clarify their potential mechanistic roles.

In conclusion, this study provides substantial hypothesis-generating evidence regarding the association between miR-126 and miR-143/145 polymorphisms and prostate cancer risk in an Iranian cohort. Nonetheless, further multicenter and prospective trials involving diverse populations, uniform risk stratification, functional evaluations, and longitudinal outcomes are essential prior to the application of these findings in clinical practice.

References

1. Bahari G, Rahimi N, Hashemi M, Siri MA, Narouie B. Association of miR-126 and miR-143/145 Gene Polymorphisms with the Risk and Clinicopathological Features of Prostate Cancer. Asian Pac J Cancer Prev. 2025;26(12):4339-47. https://doi.org/10.31557/apjcp.2025.26.12.4339.
2. Zhu Y, Mo M, Wei Y, Wu J, Pan J, Freedland SJ, et al. Epidemiology and genomics of prostate cancer in Asian men. Nat Rev Urol. 2021;18(5):282-301. https://doi.org/10.1038/s41585-021-00442-8.
3. Sauerbrei W, Taube SE, McShane LM, Cavenagh MM, Altman DG. Reporting recommendations for tumor marker prognostic studies (remark): An abridged explanation and elaboration. J Natl Cancer Inst. 2018;110(8):803-11. https://doi.org/10.1093/jnci/djy088.

Akif Erbin*, Serbay Arslan

*Health Science University, Basaksehir Çam Sakura City Hospital, Department of Urology, Istanbul, Turkiye. *For Correspondence: akiferbin@hotmail.com*