MedCrave
Step into the World of Research

Journal of Stem Cell Research & Therapeutics

Research Article

Open Access

The future of early detection for prostate cancer

Abstract

Prostate cancer remains a major global health burden and one of the leading causes of cancer-related death in men worldwide. Early detection continues to be challenging because conventional screening tools, including prostate-specific antigen (PSA) testing and digital rectal examination (DRE), have limited specificity and may lead to inconsistent clinical decision-making. In this context, multiparametric and biparametric MRI have shown promise for improving risk stratification, although their performance may be further enhanced through integration with emerging molecular approaches.

This review examines recent advances in the early detection of prostate cancer, with a focus on novel biomarkers, multi-omics strategies, and artificial intelligence (AI). Emerging biomarkers include molecular, cellular, genetic, and exosomal candidates such as non-coding RNAs, urinary exosomal mRNA, prostate cancer stem cell-related markers, ancestry-associated SNPs, polygenic risk scores, and blood-based tools such as the 4Kscore. These approaches may improve the identification of clinically significant disease and provide more personalized risk assessment.

In parallel, AI-based methods, including machine learning and deep learning, are increasingly being applied to MRI interpretation, biomarker discovery, risk prediction, and multi-omics data integration. Together, these strategies have the potential to support earlier and more precise detection of prostate cancer across diverse populations. However, broader clinical implementation will depend on further validation, standardization, and assessment of their applicability in real-world settings.

Keywords: prostate cancer, early detection, biomarkers, multi-omics, artificial intelligence, prostate-specific antigen, magnetic resonance imaging, polygenic risk score, health disparities

Volume 11 Issue 1 - 2026

Gomez Daniel,[1] Tawil Bill[2]
[1]Department of Biology, California State University Channel Islands, USA
[2]Department of Bioengineering, University of California, USA

Correspondence: Dr. Bill Tawil, Department of Bioengineering, UCLA School of Engineering, 420 Westwood Plaza, Room 5121, Engineering V. P.O. Box 951600, Los Angeles, CA 90095-1600, USA, Fax (310) 794-5956

Received: February 2, 2026 | **Published:** March 17, 2026

Abbreviations: PCa, prostate cancer; ASR, age-standardized rate; BRCA2, breast cancer gene 2; HOXB13, homeobox B13; SNP, single nucleotide polymorphism; AAPI, Alaskan American and pacific islander; PSA, prostate-specific antigen; DRE, digital rectal examination; MRI, magnetic resonance imaging; mpMRI, multiparametric prostate MRI; bpMRI, biparametric MRI; CTCs, circulating tumor cells; CSCs, cancer stem cells; tCECs, circulating endothelial cells; PCSCs, prostate cancer stem cells; ncRNA, non-coding RNA; CRPC, castration-resistant prostate cancer; GS, gleason score; SM, spine metastasis; HS, healthy subjects; BPH, benign prostate hyperplasia; PRS, polygenic risk score; AI, artificial intelligence; TAPG, trans-atlantic prostate group; TURP, transurethral resection of prostate; mRNA, messenger ribonucleic acid; ctDNA, circulating tumor DNA; 4K, four-kallikrein; CI, confidence interval; ML, machine learning; DL, deep learning; GPT, generative pre-trained transformer; TCGA, the cancer genome atlas; TWAS, transcriptome-wide association study; GWAS, genome-wide association study; HDI, histology data integration.

Introduction

Prostate cancer is the second most commonly diagnosed cancer in men worldwide and the fifth leading cause of cancer-related death globally. Although many prostate cancers grow slowly and are considered low risk, early-stage disease is often asymptomatic, which makes timely detection challenging.[1-4] Clinical manifestations usually appear in advanced stages and may include bone pain, anemia, paralysis due to spinal metastases, and renal failure. These limitations highlight the importance of improving early detection strategies beyond conventional screening approaches.

Epidemiology

Since 2022, an estimated 268,490 new cases and 34,500 deaths from prostate cancer have been reported in the United States. Worldwide, more than 1.4 million new cases are diagnosed, with substantial variation in incidence and mortality across countries, as shown in Figures 1 & 2.

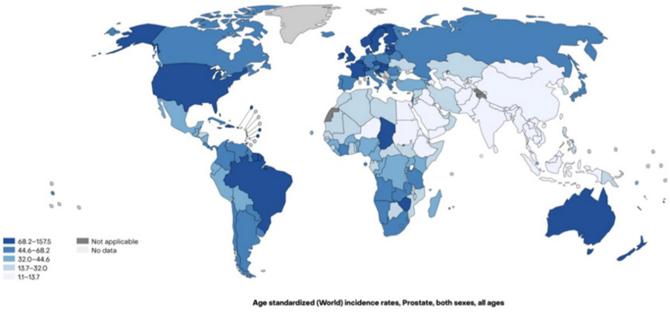

Figure 1 Worldwide age standardized incidence rates for prostate cancer.[3]

This image shows the world where different countries have different rates of incidence for prostate cancer. Examples include North America having a higher rate of incidence while rates of incidence in Asia are low.

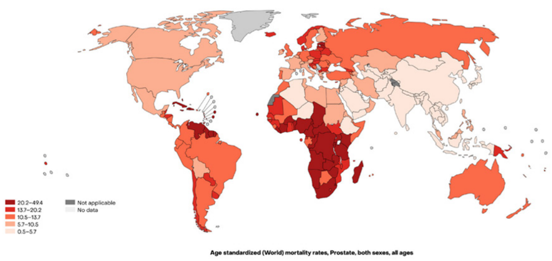

Figure 2 Worldwide age standardized mortality rates for prostate cancer.[3]

This image shows the world where different countries have different rates of mortality for prostate cancer. Examples include countries in Africa having a higher rate of mortality while rates of mortality in Asia are incredibly low.

Although patterns differ by region, areas with high incidence often report lower mortality rates, including the United States, Oceania, Northern Europe, and the Caribbean. In contrast, regions with more limited access to healthcare resources, such as parts of Africa and Latin America, tend to experience higher mortality rates, as summarized in Table 1. These differences may reflect disparities in early detection, access to healthcare, and diagnostic infrastructure. Countries with lower mortality rates generally benefit from more established screening practices and stronger healthcare systems.

Table 1 Estimated global prostate cancer incidence and mortality in 2022[3]

	Number of countries	Cumulative risk of prostate cancer	Incidence rate ASR per 100,000	Rate of death	Mortality rate ASR per 100,000
Africa	54	3.7%	30.3	1.7%	17.3
Asia	47	1.4%	12.6	0.29%	3.8
Europe	40	7.9%	59.9	1.0%	11.2
Latin America and Caribbean	32	7.1%	58	1.1%	13.9
North America	2	9.5%	73.5	0.69%	8.3
Oceania	10	9.1%	71.9	0.83%	11.5

ASR, Age-standardized rate.

Risk factors of prostate cancer

Several factors may increase the likelihood of developing prostate cancer, including age, ethnicity, dietary patterns, environmental exposures, and family history, in addition to other factors summarized in Figures 3-6.

Figure 3 Risk factors of prostate cancer.[6]

This image shows all the possible risk factors that are associated with prostate cancer which are listed are chemicals, hormones, age, ethnicity, geography, genetic changes, family history, and dietary factors.

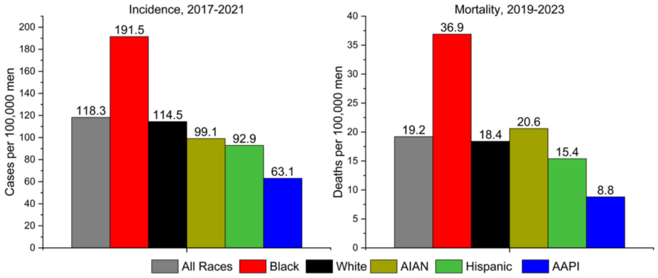

Figure 4 Graphs that compare the incidence and mortality rate among different ethnicities.[8]

In the United States, African American men have the highest rate of incidence and mortality compared to other ethnicities. AAPI (Asian American and Pacific Islander) have the lowest mortality and incidence rates.

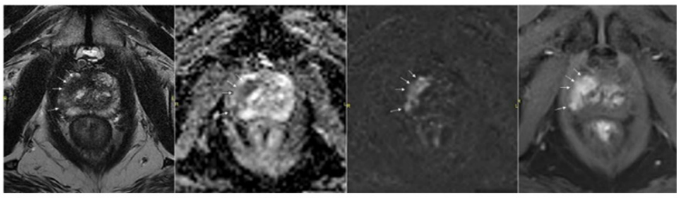

Figure 5 Multiparametric magnetic resonance imaging of a 73-year-old patient with a PSA level of 9.5 ng/mL.[11]

This image shows an example of mpMRI imaging where it displays arrows showing the location of possible carcinoma in the peripheral zone of the mid prostate and right anterior to posterolateral.

Citation: Daniel G, Bill T. The future of early detection for prostate cancer. *J Stem Cell Res Ther.* 2026;11(1):38‒46. DOI: 10.15406/jsrt.2026.11.00217

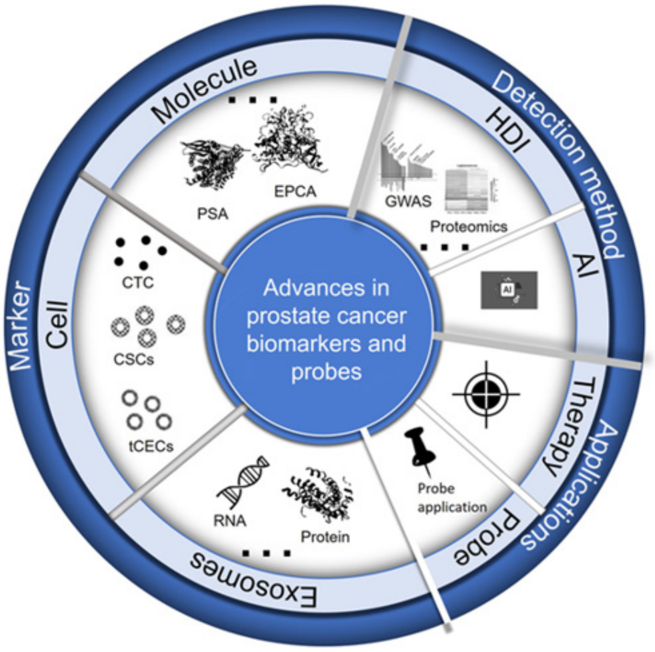

Figure 6 Diagram of advances in prostate cancer biomarkers and probes.[1]

This diagram presents advancements regarding biomarkers and probes. Novel markers include molecular, cellular, and exosomal biomarkers. There are novel detection methods that include Histology data integration (HDI) and Artificial Intelligence (AI). Applications include therapy and probe applications.

Age is one of the strongest risk factors, with incidence rising progressively after 65 years.5 Family history and genetic predisposition also play an important role, particularly through variants such as BRCA2, HOXB13, mutations in DNA repair pathway genes, Lynch syndrome-associated alterations, and more than 260 identified single nucleotide polymorphisms (SNPs) linked to prostate cancer susceptibility.[5-8]

Ethnic disparities are also well recognized. African American men have the highest incidence and mortality rates compared with other ethnic groups, whereas Asian American and Pacific Islander populations show lower rates, as illustrated in Figure 4.[8] In addition, dietary and environmental factors may contribute to these differences. Higher consumption of red meat and lower intake of potentially protective foods such as lycopene-rich products have been associated with increased risk in some populations.[7]

Social determinants of health may further influence prostate cancer risk. For example, neighborhood deprivation has been associated with increased risk among African American men, possibly through stress-related molecular mechanisms identified in prostate tumors.[9] Overall, prostate cancer risk is shaped by the interaction of genetic, environmental, lifestyle, and social factors.

Common evaluation methods

Traditional evaluation methods for prostate cancer include prostate-specific antigen (PSA) testing and digital rectal examination (DRE). PSA is a protein produced by the prostate gland that is primarily found in semen, although small amounts can also be detected in blood.10 Serum PSA levels between 4 and 10 ng/mL have been associated with an approximately 25% probability of prostate cancer, whereas levels above 10 ng/mL may increase that probability to nearly 50%.[10] However, PSA has limited specificity because both benign and malignant prostate conditions can elevate serum levels, which may result in false-positive findings, unnecessary biopsies, and overdiagnosis.[11]

DRE is a physical examination used to detect prostate abnormalities through the rectal wall, including nodules or induration that may suggest malignancy. Although DRE may provide additional clinical information, it has limited diagnostic performance when used alone and is therefore often combined with PSA testing.[10]

Because of the limitations of PSA and DRE, magnetic resonance imaging (MRI)-based approaches have become increasingly important in prostate cancer evaluation. Multiparametric MRI (mpMRI), illustrated in Figure 5, has improved sensitivity and specificity while helping reduce the detection of indolent disease.[11,12] Although mpMRI is currently considered the standard imaging approach in prostate cancer diagnosis, biparametric MRI (bpMRI) has emerged as a shorter and less costly alternative with potential to increase scanner throughput and improve accessibility.[13,14]

Overall, while conventional and imaging-based methods have improved prostate cancer assessment, their limitations continue to support the need for more precise and integrated diagnostic strategies.

Prostate cancer biomarkers

Biomarkers

A wide range of novel biomarkers has been investigated for prostate cancer and can be broadly classified as molecular, cellular, and exosomal biomarkers, as summarized in Figure 6.[1] Their identification has been facilitated by histology data integration (HDI) and multi-omics approaches, including genomics, transcriptomics, proteomics, and metabolomics, which enable large-scale characterization of tumor-associated features within a histomic framework. These biomarkers have significant potential to improve early detection, diagnosis, and prognosis, particularly as part of more integrated and precise strategies for prostate cancer assessment.[15]

Molecular biomarkers

Molecular biomarkers in prostate cancer mainly include nucleic acids and proteins, such as BRCA1/2 genes involved in DNA damage repair, prostate-specific antigen (PSA), and B7-H4, an immune regulatory protein.[1] Among these, germline alterations in BRCA1 and BRCA2 have been extensively studied because of their association with hereditary prostate cancer risk, particularly in men with a positive family history.[2] Molecular biomarkers can be obtained from serum, urine, or tissue samples, allowing both non-invasive and invasive approaches for analysis, as illustrated in Figure 7.[14,15] Their assessment may support earlier detection, improve risk stratification, and contribute to more timely therapeutic intervention in prostate cancer.

Cellular biomarkers

Cellular biomarkers in prostate cancer mainly include circulating tumor cells (CTCs), cancer stem cells (CSCs), and tumor-associated circulating endothelial cells (tCECs), which may help monitor disease progression, identify potential therapeutic targets, and support non-invasive detection, as summarized in Figure 8.[1,15] Among these, CTCs are considered valuable biomarkers in cancer diagnostics and therapeutics, particularly in the context of personalized medicine and precision oncology.[16]

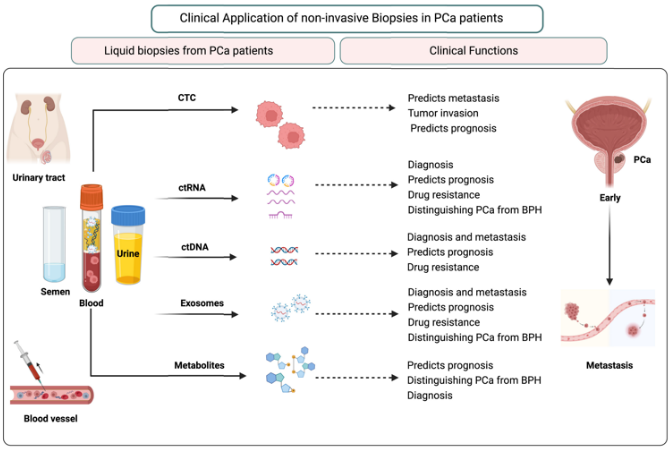

Figure 7 The clinical applications of non-invasive biopsies for prostate cancer patients.[15]

Samples obtained from semen, blood, and urine will contain biomarkers such as CTC, ctDNA, exosomes, and metabolites which will be analyzed for potential prediction of tumor metastasis, prognosis, drug resistance, and accurate diagnosis for early detection of prostate cancer.

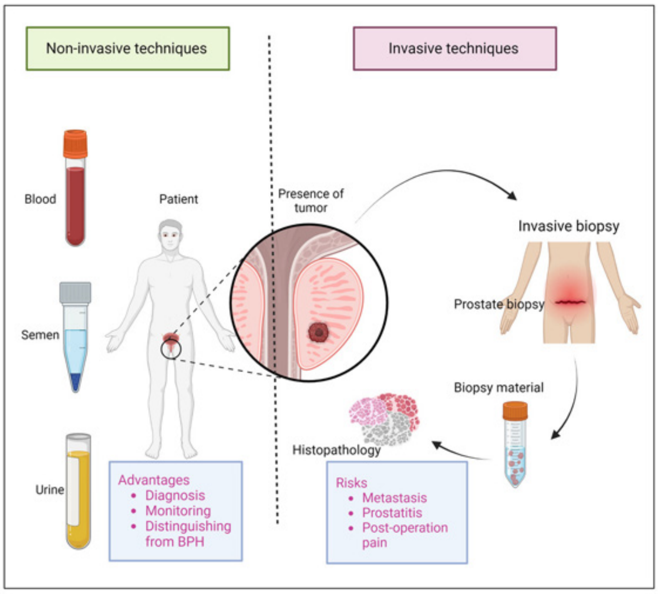

Figure 8 Non-invasive techniques vs invasive techniques.[15]

A brief overview on how non-invasive techniques can provide an advantage for early detection while invasive techniques can provide better analysis for early detection but are riskier since it could introduce issues to patients such as metastases, prostatitis, and post-operation pain.

CSCs are also of particular interest because they may give rise to a distinct subpopulation known as prostate cancer stem cells (PCSCs), which have the capacity for self-renewal and differentiation and are associated with tumorigenicity and drug resistance. For this reason, PCSC-related molecular markers may offer promising targets for novel therapeutic strategies.[17] In addition, tCECs have emerged as potential blood-based biomarkers and may help reduce overdiagnosis by up to 40%.1 Endothelial cells also appear to play a role in prostate cancer metastasis through specific non-coding RNAs, such as miR-1246, which can promote the activation of epithelial-mesenchymal transition (EMT)-related genes involved in tumor progression.[18]

Exosomal biomarkers

Exosomal biomarkers include RNAs, proteins, DNA, and lipids, all of which can mediate intercellular communication in prostate cancer. These biomarkers have been investigated for their potential roles in cancer detection, metastatic regulation, and prognostic assessment. Exosomes are released through exocytosis from multivesicular bodies and serve as carriers of biologically active molecules.[1]

Among exosomal components, non-coding RNAs (ncRNAs) have attracted particular interest because of their role in the dysregulation of cellular processes involved in prostate cancer development and progression. This makes ncRNAs promising biomarkers for diagnosis, disease monitoring, and prediction of clinical outcomes.[19] Table 2 summarizes several ncRNAs associated with prostate cancer initiation, growth, progression, and therapy resistance, while Figure 9 illustrates the overall mechanisms mediated by ncRNAs in prostate cancer.[18]

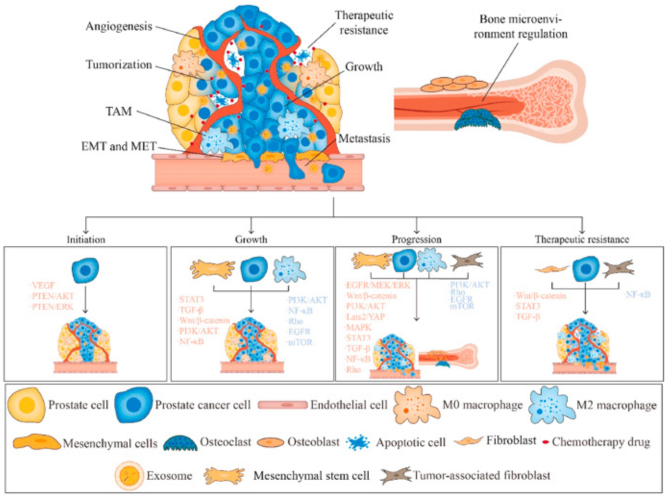

Figure 9 Mechanisms of exosomal ncRNA in prostate cancer.[18]

Various ncRNA are responsible for modulating expression of downstream genes, signaling pathways, and target mRNAs which eventually promotes a variety of pathological events that are associated with prostate cancer such as angiogenesis, migration, microenvironment, and therapeutic resistance.

Citation: Daniel G, Bill T. The future of early detection for prostate cancer. *J Stem Cell Res Ther.* 2026;11(1):38‒46. DOI: 10.15406/jsrt.2026.11.00217

Table 2 Exosomal ncRNAs of prostate cancer that are biomarkers[18]

Biomarker type	Role	Source: urine	Source: plasma	Source: serum
Diagnostic Biomarkers	Distinguish PCa from HS	miR-19b, miR-21, miR-141-5p, miR-375, miR-486-5p, miR-451a, miR-486-3p, miR-196a-5p, miR-501-3p, let-7c, miR-574-3p and miR-2909	miR-125a-5p, miR-141-5p and lncAY927529	miR-141, miR-212, HIPK3 and circ_0044516
	Distinguish PCa from BPH	miR-145, miR-1290, miR-2909 and lncRNA-p21	miR-21-5p [53] and miR-200c-3p	
	Distinguish PCa from negative prostate biopsy	PCA3 and MALAT1		
Staging and Grading Biomarkers	Identify metastatic PCa	miR-375 and miR-1290		miR-141 and circ_0081234
	Distinguish treatment-naïve PCa from CRPC		miR-423-3p	
	Distinguish PCa with different GS	miR-145, PCA3 and MALAT1	let-7a-5p	
	Identify metastatic PCa after radial prostatectomy			miR-141, miR-375 and miR-1246
Prognostic Biomarkers	Associated with poor overall survival		miR-375 and miR-1290	

PCa, prostate cancer; CRPC, castration-resistant prostate cancer; GS, Gleason score; SM, spine metastasis; HS, healthy subjects; BPH, benign prostatic hyperplasia.

One relevant example is the overexpression of exosomal miR-27a-3p, identified in the PC-3 prostate cancer cell line, which promotes angiogenesis by inhibiting tissue factor pathway inhibitor (TFPI) and thereby affecting VEGFR2 phosphorylation and VEGF-related signaling. Despite their clinical potential, exosomal biomarker analyses still face important limitations, including the lack of standardized analytical protocols and the high cost of large-scale implementation.[20] In addition, Table 2 includes other potential exosomal ncRNA biomarkers from different sources that may be relevant for current and future studies, as described by Li et al.[18]

Histology data integration (HDI)

Given the complexity of prostate cancer histology and its interaction with multiple biological and environmental factors, histology data integration (HDI) supported by multi-omics approaches has become increasingly valuable for understanding disease mechanisms and identifying potential biomarkers.[1] These integrated strategies may contribute to a more comprehensive characterization of prostate cancer and support the development of improved approaches for early detection, diagnosis, and prognosis.

Among these approaches, genomics-transcriptomics combines genomic and transcriptomic analyses to identify abnormal RNA modifications and transcriptional interactions that may reveal novel biomarkers with diagnostic, therapeutic, and prognostic relevance in prostate cancer. Proteomics-metabolomics integrates protein and metabolite profiling from prostate cancer tissue samples to determine molecular alterations associated with tumor biology and pathology. In turn, transcriptomics-metabolomics combines gene expression and metabolic profiling to identify metabolite-related abnormalities while also clarifying the transcriptional mechanisms underlying altered metabolism in prostate cancer.[1]

Overall, HDI and multi-omics approaches provide a broader framework for biomarker discovery and continue to be explored for their potential clinical application in prostate cancer.

Current research for early detection of prostate cancer

Current research on the early detection of prostate cancer includes a broad range of analytical approaches based on emerging biomarkers, multi-omics strategies, and advanced diagnostic methods. These approaches aim to improve the identification of clinically significant prostate cancer and to overcome the limitations of conventional screening tools.

Applying PRS and PSA to predict prostate cancer death in men

Santiago et al. evaluated the use of polygenic risk score (PRS) and prostate-specific antigen (PSA), together with Gleason score and artificial intelligence (AI), to predict prostate cancer-specific mortality in men from the TAPG-TURP cohort with intermediate-aggressive disease.[21] The aim was to identify which patients were more likely to die from prostate cancer. PRS reflects the cumulative contribution of multiple single nucleotide polymorphisms (SNPs) associated with prostate cancer risk and may improve risk prediction beyond conventional clinical parameters.[22] The Gleason score, in turn, is widely used to assess tumor aggressiveness based on prostate biopsy findings.

As shown in Figure 10, Santiago and colleagues applied machine learning classifiers to distinguish between healthy and cancer patients using PRS and to integrate PRS, PSA, Gleason score, and AI-based analysis for the assessment of prostate cancer aggressiveness, particularly in patients with Gleason scores of 6 or 7.[21] This approach highlights the potential value of combining genetic risk, clinical biomarkers, and AI-assisted models to improve mortality prediction in intermediate-risk patients. However, further studies remain necessary, particularly in more diverse populations, including African American men.

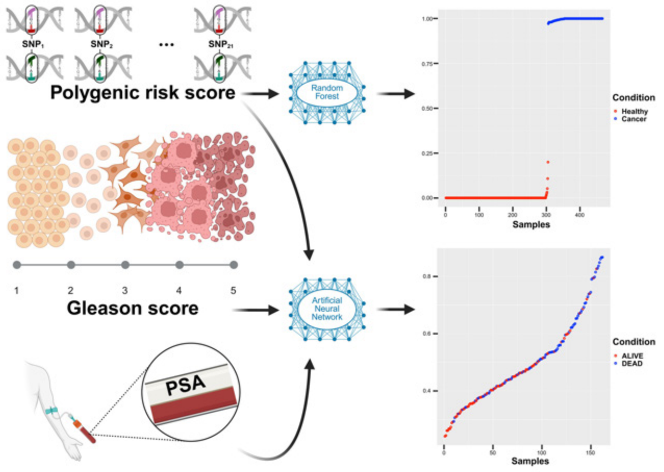

Figure 10 Two AI classifiers were used for detection of prostate cancer and prediction of aggressiveness with mortality.[21]

Two machine learning classifiers that were used are called the rain forest model for PRS of healthy and cancer patients while the second model combines PRS, PSA, Gleason, and AI to determine the aggressiveness of prostate cancer for patients with a Gleason score of 6 or 7 in order to predict mortality among intermediate risk individuals. This provides potential clinical applications.

Applying urinary exosomalm RNA for early detection of prostate cancer

Yu et al. investigated urinary exosomal mRNA profiling as a potential strategy to improve the early detection of prostate cancer, with particular focus on RAB5B and WWP1.[23] Exosomes are extracellular vesicles measuring approximately 30-150 nm that carry nucleic acids, proteins, and lipids. Because they are relatively stable and protected from external degradation, they have emerged as promising tools for liquid biopsy and as potential biomarkers for the diagnosis and management of prostate cancer.[24]

In this study, next-generation sequencing was used to analyze exosomal RNAs, including RAB5B, WWP1, HIST2H2BF, ZFY, MARK2, PASK, RBM10, and NRSN2, in individuals with prostate cancer and healthy controls. The findings were further validated by qPCR, revealing distinct mRNA expression signatures associated with prostate cancer. Figure 11 presents a microarray of the analyzed mRNAs.[23,24] Overall, urinary exosomal mRNA profiling appears to be a promising non-invasive approach for improving early detection of prostate cancer.

KScore used for improved calibration for African American men

Hougen et al. evaluated the 4Kscore by incorporating a prespecified coefficient for African American race in order to improve its calibration and clinical utility in this population.[25] The 4Kscore combines four blood kallikrein markers-total PSA, free PSA, intact PSA, and human kallikrein 2-with clinical variables such as digital rectal examination (DRE), age, and prior negative biopsy to estimate the probability of detecting Grade Group 2 or higher prostate cancer.[26]

Using this adjusted model, Hougen and colleagues increased the representation of African American men in the cohort from 25% to 37%, and the modified 4Kscore maintained good discriminatory performance while showing improved calibration in this population, as presented in Table 3. These findings suggest that population-specific refinement of biomarker-based algorithms may enhance early detection and risk stratification in groups that have historically been underrepresented in predictive models. However, further research is still needed, particularly through the incorporation of additional genetic markers.[25]

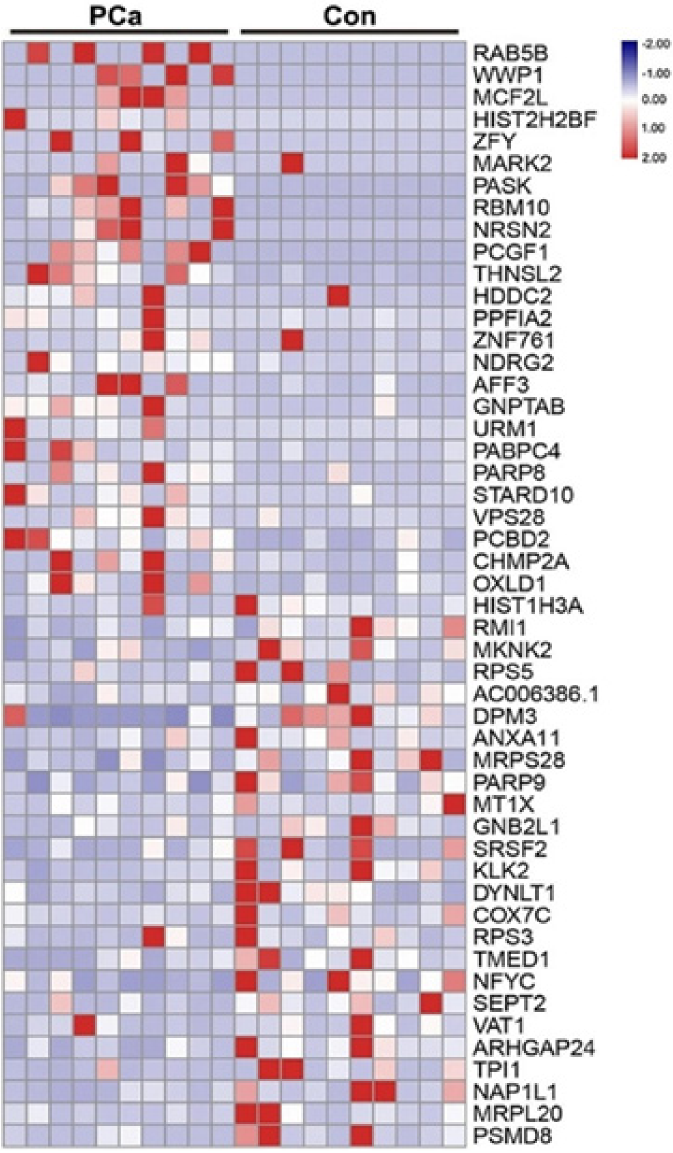

Figure 11 Microarray for urinary exosomes mRNAs heatmap.[22]

This image shows a heatmap that visualizes 50 upregulated mRNAs but it was discovered that 10 specific mRNA (candidate genes) are associated with prostate cancer which are *RAB5B*, *WWP1*, *MCF2L*, *HIST2H2BF*, *ZFY*, *MARK2*, *PASK*, *RBM10*, *NRSN2*, and *PCGF1*.

Analysis of rs7824364 from 8q24 locus in African American men

Gu et al., investigated the SNP rs7824364, derived from West African ancestry, located within the 8q24 locus, a genomic region that contains several variants associated with prostate cancer and other diseases.[27] Variants within this locus have also been reported in other populations; for example, rs16901979A, rs629242T, and rs1447295A have been associated with prostate cancer risk in Saudi Arabian men.[28]

Table 3 4Kscore analysis - comparison between race-stratified probability vs observed results for African American men with GG2=5 prostate cancer[25]

	Categorized 4Kscore					
	0-9.99% (95% CI)	10-19.99% (95% CI)	20-29.99% (95% CI)	30-39.99% (95% CI)	40-49.99% (95% CI)	>=50% (95% CI)
African American men						
Biopsy Grade Group ≥2	3.3% (0.58%, 13%)	18% (8.7%, 33%)	26% (14%, 42%)	41% (24%, 61%)	57% (35%, 76%)	67% (57%, 76%)
4Kscore with Race	5.4%	15%	25%	35%	45%	77%
Non-African American men						
Biopsy Grade Group ≥2	5.2% (3.4%, 7.7%)	19% (14%, 25%)	26% (19%, 35%)	43% (32%, 55%)	48% (34%, 62%)	66% (57%, 73%)
4Kscore with Race	4.7%	14%	24%	35%	45%	74%

CI, Confidence interval.

In this study, rs7824364 was evaluated as a predictor of positive prostate biopsy in African American and Puerto Rican men, given its strong association with prostate cancer risk. African American men with PSA levels of 2.5 ng/mL or higher or abnormal digital rectal examination (DRE) findings were genotyped for this SNP. The results showed that rs7824364 was predictive of positive prostate biopsy in African American men undergoing prostate cancer screening.[27]

This study highlights the potential value of incorporating ancestry-associated SNPs into risk assessment models for prostate cancer. It also supports continued investigation of variants within the 8q24 locus to improve the identification of clinically relevant genetic markers that may contribute to earlier and more precise detection strategies.

Future of artificial intelligence

Overview of artificial intelligence

In recent years, artificial intelligence (AI) has shown considerable potential to improve biomedical research and clinical decision-making. In prostate cancer, AI is particularly useful for addressing complex questions that involve large and heterogeneous datasets, including genomic, proteomic, imaging, and clinical data.[1,29] Through these integrated approaches, AI may contribute to a better understanding of molecular mechanisms and support the development of more precise strategies for early detection, diagnosis, and patient management.

As shown in Figure 12, AI mainly includes two major approaches: machine learning (ML) and deep learning (DL). ML uses engineered features to analyze large amounts of data, whereas DL, a subfield of ML, applies neural network architectures, such as convolutional neural networks, to identify more complex patterns.[30] In prostate cancer, one of the most relevant applications of DL has been in MRI interpretation, where AI-assisted models may improve the automatic detection, localization, and characterization of suspicious lesions.[31]

AI has also shown potential in several aspects of prostate cancer care, including diagnosis, treatment planning, and disease management.[32,33] Some currently available AI-based tools can assist in determining Gleason score and in predicting the potential benefit of androgen deprivation therapy in patients receiving radiation therapy.[34] In addition, AI may facilitate the integration of genomic and clinical data to support more personalized approaches to care.[29] Figure 13 illustrates how AI models may contribute to clinical decision-making and precision treatment strategies.[35]

Despite these advances, the broader implementation of AI in routine clinical practice remains limited. Further progress will depend on interdisciplinary collaboration, prospective multicenter validation studies, and closer alignment with regulatory standards to support the safe integration of ML models into clinical settings.[33] More recently, generative AI tools such as ChatGPT have also been proposed as supportive resources in prostate cancer management, for example by helping simplify pathology reports and other complex medical information for patients.[35] Overall, AI represents a promising component of future prostate cancer care, particularly when integrated with biomarkers, multi-omics strategies, and advanced imaging approaches.

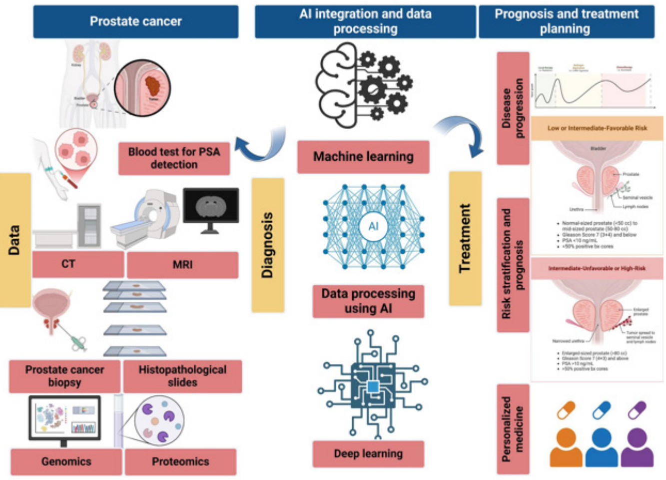

Figure 12 Integration of AI and processing data to be applied to diagnosis and treatment of prostate cancer for improvements.

This image shows the general overview on how the use of machine learning, data processing, and deep learning with AI models can be used to improve diagnosis and treatments for prostate cancer which AI can be implemented to various features such as biopsy analysis, MRI, multi-omics, and personalized medicine.

Applications for artificial intelligence

Wu et al. developed a gene expression-based model to identify genes associated with prostate cancer in men of European ancestry, training its performance using data from The Cancer Genome Atlas (TCGA).[36] TCGA has characterized 333 primary prostate cancers across seven genomic platforms, providing important insight into the molecular and genetic heterogeneity of the disease and contributing to a molecular taxonomy of prostate cancer.[37]

The study by Wu et al., used a transcriptome-wide association study (TWAS) approach, which is designed to identify disease susceptibility genes by integrating gene expression data with findings from genome-wide association studies (GWAS).[38] This strategy improves the ability to detect genes associated with disease risk and progression. Through this approach, the authors identified 14 genes whose silencing reduced the viability of prostate cancer cells, supporting the value of AI- and data-driven models for identifying clinically relevant cancer-associated genes.[39-41]

Overall, this study illustrates the potential of artificial intelligence and integrative genomic analysis to improve the identification of molecular targets relevant to prostate cancer biology. In the context of early detection and precision medicine, these approaches may contribute to more accurate risk assessment and the development of more personalized strategies for patient care.

Conclusion and potential methods for the future of early detection

Prostate cancer remains a major challenge in men's health, particularly in populations with a disproportionate disease burden such as African American men. While conventional tools such as PSA and DRE continue to play an important role, their limitations have driven the development of more accurate strategies for early detection. Emerging biomarkers, multi-omics approaches, advanced imaging, and artificial intelligence are collectively shaping a more precise and integrated model for prostate cancer assessment.

Although these approaches show considerable promise, their routine clinical implementation will require further validation, standardization, and evaluation across diverse populations. In the near future, the most realistic progress will likely come from the gradual incorporation of these tools into more individualized and clinically applicable risk assessment frameworks.

Funding sources

There is no funding to report for this study.

Acknowledgements

Daniel Gomez expresses appreciation to Professor Bill Tawil for overseeing the framework of this review, and for the insightful lectures and advice concerning cell and molecular biology, which contributed to the development of this paper.

Conflicts of interest

The authors declare that there are no conflicts of interest.

References

1. Li K, Wang Q, Tang X, et al. Advances in prostate cancer biomarkers and probes. *Cyborg Bionic Syst*. 2024;5;0129.
2. Leslie SW, Soon–Sutton TL, Sajjad H, et al. Prostate cancer. In: StatPearls. StatPearls Publishing. 2023.
3. Vieira B, Pekala KR, Matsoukas K, et al. SIU–ICUD epidemiology of prostate cancer. *Soc Int Urol J*. 2025;6(3):44.
4. Schafer EJ, Laversanne M, Sung H, et al. Recent patterns and trends in global prostate cancer incidence and mortality: an update. *Eur Urol*. 2024;87(3):302–313.
5. Bergengren O, Pekala KR, Matsoukas K, et al. 2022 update on prostate cancer epidemiology and risk factors: a systematic review. *Eur Urol*. 2023;84(2):191–206.
6. Elancheran R, Maruthanila VL, Kumar M, et al. Strategy towards diagnosis and treatment for prostate cancer. 2017.
7. Johnson JR, Mavingire N, Woods–Burnham L, et al. The complex interplay of modifiable risk factors affecting prostate cancer disparities in African American men. *Nat Rev Urol*. 2024;21(7):422–432.
8. Kratzer TB, Mazzitelli N, Star J, et al. Prostate cancer statistics, 2025. *CA Cancer J Clin*. 2025;75(6):485–497.
9. Boyle J, Yau J, Slade JL, et al. Neighborhood disadvantage and prostate tumor RNA expression of stress–related genes. *JAMA Netw Open*. 2024;7(7):e2421903.
10. American Cancer Society. Prostate cancer screening tests. American Cancer Society. 2023.
11. Albers P, Franiel T, Kötter T, et al. The early detection, diagnostic evaluation, and local treatment of prostate cancer: a paradigm shift. *Dtsch Arztebl Int*. 2025.
12. Launer BM, Ellis TA, Scarpato KR. A contemporary review: mpMRI in prostate cancer screening and diagnosis. *Urol Oncol*. 2024;43(1):15–22.
13. Ng ABCD, Asif A, Agarwal R, et al. Biparametric vs multiparametric MRI for prostate cancer diagnosis: the PRIME diagnostic clinical trial. *JAMA*. 2025;334(13):1170–1179.
14. Kral M, Kurfurstova D, Zemla P, et al. New biomarkers and multiplex tests for diagnosis of aggressive prostate cancer and therapy management. *Front Oncol*. 2025;15:1542511.
15. Alahdal M, Perera R, Moschovas MC, et al. Current advances of liquid biopsies in prostate cancer: molecular biomarkers. *Mol Ther Oncolytics*. 2023;30:27–38.
16. Rapanotti MC, Cenci T, Scioli MG, et al. Circulating tumor cells: origin, role, current applications, and future perspectives for personalized medicine. *Biomedicines*. 2024;12(9):2137.
17. Liang H, Zhou B, Li P, et al. Stemness regulation in prostate cancer: prostate cancer stem cells and targeted therapy. *Ann Med*. 2024;57(1):2442067.
18. Li Y, Tang X, Wang B, et al. Current landscape of exosomal non–coding RNAs in prostate cancer: modulators and biomarkers. *Noncoding RNA Res*. 2024;9(4):1351–1362.
19. Cong G, Shao J, Xiao F, et al. The role of endothelial cell–related gene COL1A1 in prostate cancer diagnosis and immunotherapy: insights from machine learning and single–cell analysis. *Biol Direct*. 2025;20(1):3.
20. Salciccia S, Frisenda M, Bevilacqua G, et al. Exosome analysis in prostate cancer: how they can improve biomarkers' performance. *Curr Issues Mol Biol*. 2023;45(7):6085–6096.
21. Santiago LR, Ladoukakis E, Scibior–Bentkowska D, et al. Polygenic risk score and prostate specific antigen predict death from prostate cancer in men with intermediate aggressive cancer. *Int J Cancer*. 2025.
22. Schaffer KR, Shi M, Shelley JP, et al. A polygenic risk score for prostate cancer risk prediction. *JAMA Intern Med*. 2023;183(4):386–388.
23. Yu J, Yu C, Jiang K, et al. Urinary exosomal mRNAs as non–invasive biomarkers for early prostate cancer diagnosis. *BMC Urol*. 2024;24(1).
24. Qiu A, Luo Z, Liu X, et al. Exosomes: a promising tool for liquid biopsy in prostate cancer. *Cancer Screen Prev*. 2025;4(1):53–60.
25. Hougen HY, Sjoberg DD, Thomas J, et al. Adding a coefficient for race to the 4Kscore improves calibration for Black men. *J Urol*. 2024;211(3):392–399.
26. Scuderi S, Tin A, Gandaglia G, et al. Implementation of 4Kscore as a secondary test before prostate biopsy. *Eur Urol Open Sci*. 2023;52:1–3.

27. Gu J, Chery L, Nogueras GM, et al. A West African ancestry–associated SNP on 8q24 predicts a positive biopsy in African American men. *Prostate*. 2024;84(7):694–705.

28. Osman AE, Alharbi S, Ahmed AA, et al. Single nucleotide polymorphism within chromosome 8q24 is associated with prostate cancer development in Saudi Arabia. *Asian J Urol*. 2022;11(1):26–32.

29. Ejaz ZH, Shaikh RH, Fatimi AS, et al. Artificial intelligence, machine learning and deep learning to combat therapeutic resistance in metastatic castration–resistant prostate cancer. *Ecancermedicalscience*. 2025;19:1953.

30. Vidiyala N, Parupathi P, Sunkishala P, et al. Artificial intelligence: a new era in prostate cancer diagnosis and treatment. *Int J Pharm*. 2025;683:126024.

31. Molière S, Hamzaoui D, Ploussard G, et al. Diagnostic accuracy of deep learning models for detection of clinically significant prostate cancer on MRI. *Eur Urol Oncol*. 2024;8(4):1182–1202.

32. Hasan MR, Ibraheem N, Rahman ME, et al. Artificial intelligence across the prostate cancer pathway: screening, imaging, pathology, and biomarkers. *Cureus*. 2025;17(11):e96226.

33. Gu S, Chen J, Fan C, et al. Algorithms on the rise: a machine learning–driven survey of prostate cancer literature. *Front Oncol*. 2025;15:1675459.

34. Riaz IB, Harmon S, Chen Z, et al. Applications of artificial intelligence in prostate cancer care. *ASCO Educ Book*. 2024;44.

35. Zhu L, Pan J, Mou W, et al. Harnessing artificial intelligence for prostate cancer management. *Cell Rep Med.* 2024;5(4):101506.

36. Wu L, Wang J, Cai Q, et al. Identification of novel susceptibility loci and genes for prostate cancer risk. *Cancer Res*. 2019;79(13):3192–3204.

37. Cancer Genome Atlas Research Network. The molecular taxonomy of primary prostate cancer. *Cell*. 2015;163(4):1011–1025.

38. Liu D, Zhu J, Zhou D, et al. Transcriptome–wide association study identifying candidate susceptibility genes for prostate cancer risk. *Int J Cancer*. 2021;150(1):80–90.

39. Sequeira JP, Salta S, Freitas R, et al. Biomarkers for pre–treatment risk stratification of prostate cancer patients: a systematic review. *Cancers*. 2024;16(7):1363.

40. Chen H, Pang B, Zhou C, et al. Prostate cancer–derived small extracellular vesicle proteins in diagnosis and prognosis. *J Nanobiotechnol*. 2023;21(1).

41. Horasan A, Güneş A. Advancing prostate cancer diagnosis: a deep learning approach for enhanced detection in MRI images. *Diagnostics*. 2024;14(17):1871.