

The Evolution of ctDNA as a Predictive Biomarker of Response in Metastatic Castration Resistance Prostate Cancer Therapy

Huber IMT^{1*}, Carvalho MDB², Pelloso SM³ and Ruppen IC⁴

¹MSc, Clinical Oncologist at the Center of Excellence in Oncology, Coordinator of the Medicine Course at the Inga University Center, Maringá, PR, Brazil

²Director of Pedagogical Supervision at Inga University Center, Maringá, PR, Brazil

³Postgraduate Director at Inga University Center, Maringá, PR, Brazil

⁴Student at school of medicine at Inga University Center, Maringá, PR, Brazil

*Corresponding author:

Isabella Morais Tavares Huber, MSc,
Medical Oncologist at Center of Excellence in
Oncology, Coordinator at School of Medicine
at Inga University Center, Maringá, PR, Brazil

Received: 15 Apr 2023

Accepted: 20 May 2023

Published: 16 Sep 2023

J Short Name: COO

Copyright:

©2023 Huber IMT, This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and build upon your work non-commercially.

Citation:

Huber IMT, The Evolution of ctDNA as a Predictive Biomarker of Response in Metastatic Castration Resistance Prostate Cancer Therapy. Clin Onco. 2023; 6(23): 1-4

1. Abstract

Circulating tumor DNA (ctDNA) is an emerging biomarker in cancer research and has shown promise in predicting response to therapy in several malignancies, including metastatic castration-resistant prostate cancer (mCRPC). In mCRPC, ctDNA has the potential to identify patients who are more likely to respond to specific therapies based on the detection of specific genetic alterations. However, the use of ctDNA as a biomarker has several limitations, including the sensitivity of ctDNA detection and the subjectivity of clonal evolution. Future research in ctDNA analysis should focus on developing standardized methods for ctDNA analysis, identifying additional genetic alterations associated with treatment response, and integrating ctDNA analysis with imaging and other biomarkers. Despite these limitations, the potential of ctDNA as a biomarker highlights the importance of precision medicine in prostate cancer treatment, where personalized treatment strategies can be tailored to the specific genetic profile of the patient's tumor. Further investigation of ctDNA as a biomarker in prostate cancer will be critical to advancing personalized medicine and improving the lives of those living with mCRPC.

2. Introduction

Metastatic castration-resistant prostate cancer (mCRPC) is a lethal disease with limited treatment options. Androgen deprivation therapy (ADT) is the initial standard of care, but patients often progress to mCRPC. Although chemotherapy, radiotherapy, and

androgen receptor (AR) pathway inhibitors have been approved for mCRPC treatment, the response to therapy varies significantly among patients, and there is a significant need for predictive biomarkers to identify patients who will benefit most from therapy.

Circulating tumor DNA (ctDNA) is an emerging biomarker in cancer research, and its potential to predict response to therapy has been explored in several malignancies, including prostate cancer. ctDNA refers to fragments of tumor DNA that circulate in the bloodstream of cancer patients. Several studies have suggested that ctDNA may serve as a predictive biomarker of response to therapy in mCRPC.

Wyatt et al. showed that the presence of ctDNA was associated with worse overall survival (OS) and progression-free survival (PFS) in mCRPC patients. Annala et al. demonstrated that the presence of ctDNA was associated with worse OS and PFS in mCRPC patients treated with abiraterone or enzalutamide. Scher et al. reported that the presence of AR gene alterations detected in ctDNA was associated with a lower likelihood of response to therapy and worse PFS and OS in mCRPC patients treated with AR-targeted therapy. Similarly, Conteduca et al. found that the presence of ctDNA mutations in genes involved in DNA repair was associated with a higher likelihood of response to therapy and better PFS and OS in mCRPC patients treated with abiraterone or enzalutamide. Carreira et al. demonstrated that the presence of ctDNA mutations in genes involved in DNA repair was associated

with a higher likelihood of response to therapy and longer PFS in mCRPC patients treated with the PARP inhibitor olaparib.

In this article, we will provide an in-depth review of the role of ctDNA as a predictive biomarker of response in mCRPC therapy, exploring the latest findings and highlighting the limitations and potential future directions for the use of ctDNA in clinical practice.

3. Role of ctDNA as a Predictive Biomarker of Response in Metastatic Castration-Resistant Prostate Cancer Therapy

Circulating tumor DNA (ctDNA) is a promising biomarker in cancer research. ctDNA refers to fragments of tumor DNA that circulate in the bloodstream of cancer patients. ctDNA can be detected and quantified in the plasma or serum of patients using various techniques, including polymerase chain reaction (PCR), next-generation sequencing (NGS), and digital droplet PCR (ddPCR). ctDNA has several advantages over traditional tissue biopsies as a biomarker. ctDNA is less invasive than tissue biopsies and can provide a more comprehensive picture of the tumor's genetic profile as it reflects the heterogeneity of the tumor. In prostate cancer, ctDNA has shown promise as a predictive biomarker of response to therapy in metastatic castration-resistant prostate cancer (mCRPC).

The potential of ctDNA as a prognostic biomarker in prostate cancer was first demonstrated in a study by Wyatt et al. The authors analyzed ctDNA in 514 patients with mCRPC and found that the presence of ctDNA was associated with worse overall survival (OS) and progression-free survival (PFS) compared to patients with undetectable ctDNA. The study also showed that the number of genomic alterations detected in ctDNA was associated with worse OS and PFS. A similar study by Annala et al. analyzed ctDNA in 171 patients with mCRPC treated with abiraterone or enzalutamide and found that the presence of ctDNA was associated with worse OS and PFS compared to patients with undetectable ctDNA. The study also showed that the change in ctDNA levels after therapy was a significant predictor of OS and PFS, with patients with a decrease in ctDNA levels showing a better response to therapy.

4. ctDNA as a Predictive Biomarker of Response to AR-Targeted Therapy

AR-targeted therapy, such as abiraterone and enzalutamide, has been approved for the treatment of mCRPC. However, the response to therapy varies significantly among patients, and there is a significant need for predictive biomarkers to identify patients who will benefit most from therapy. Several studies have explored the potential of ctDNA as a predictive biomarker of response to AR-targeted therapy in mCRPC.

Scher et al. analyzed ctDNA in 142 patients with mCRPC treated with abiraterone or enzalutamide and showed that the presence of AR gene alterations detected in ctDNA was associated with a lower likelihood of response to therapy and worse PFS and OS

compared to patients without AR gene alterations. Similarly, Wyatt et al. analyzed ctDNA in 67 patients with mCRPC treated with docetaxel chemotherapy and found that the presence of ctDNA alterations in the AR gene was associated with a lower likelihood of response to therapy and worse PFS and OS compared to patients without AR gene alterations.

Conteduca et al. analyzed ctDNA in 73 patients with mCRPC treated with abiraterone or enzalutamide and found that the presence of ctDNA mutations in genes involved in DNA repair (such as BRCA2, ATM, or CHEK2) was associated with a higher likelihood of response to therapy and better PFS and OS compared to patients without these mutations. The authors suggested that the detection of these mutations in ctDNA may identify patients who will benefit from treatment with AR-targeted therapy and PARP inhibitors.

5. ctDNA as a Predictive Biomarker of Response to PARP Inhibitors

PARP inhibitors are a novel class of drugs that have shown promising results in the treatment of mCRPC. PARP inhibitors target DNA repair mechanisms and are particularly effective in tumors with defects in DNA repair pathways, such as those with mutations in BRCA1, BRCA2, ATM, or PALB2 genes. Carreira et al. analyzed ctDNA in 97 patients with mCRPC treated with the PARP inhibitor olaparib and found that the presence of ctDNA mutations in genes involved in DNA repair (such as BRCA1, BRCA2, ATM, or PALB2) was associated with a higher likelihood of response to therapy and longer PFS compared to patients without these mutations.

The detection of ctDNA mutations in genes involved in DNA repair may also identify patients who are more likely to benefit from combination therapy with PARP inhibitors and AR-targeted therapy. In a study by Goodall et al., the authors analyzed ctDNA in 49 patients with mCRPC treated with the combination of olaparib and abiraterone or enzalutamide. The study showed that the detection of ctDNA mutations in genes involved in DNA repair was associated with a higher likelihood of response to combination therapy and longer PFS compared to patients without these mutations.

6. Limitations of ctDNA as a Biomarker

Despite the potential benefits of ctDNA as a biomarker, it has several limitations that must be considered. These limitations include:

1. Sensitivity of ctDNA detection: The sensitivity of ctDNA detection can vary between patients and can be influenced by several factors, including the tumor burden, the tumor's location, and the patient's treatment history. Consequently, false-negative results may occur, leading to an underestimation of disease burden and potential treatment response.

2. Clonal evolution: The genetic profile of ctDNA can differ from the primary tumor, as ctDNA may only reflect a subset of genetic mutations or rearrangements present in the tumor. Furthermore,

ctDNA is subject to clonal evolution, meaning that genetic alterations detected in ctDNA may not reflect the entire tumor's genomic profile, leading to incomplete or inaccurate information.

3. Technical challenges: ctDNA analysis requires specialized equipment and expertise, which may limit its widespread use in clinical practice. Furthermore, the quality and quantity of ctDNA may be affected by sample collection, handling, and storage, making standardization of methods challenging.

4. False-positive results: The detection of genetic alterations in ctDNA does not always reflect the presence of viable tumor cells or indicate disease progression. False-positive results may occur due to technical issues, benign conditions, or the presence of other malignancies.

5. Limited validation: The validation of ctDNA as a biomarker in clinical trials is still limited, and further research is needed to confirm its utility in clinical practice.

Overall, the limitations of ctDNA as a biomarker must be considered when interpreting results and making clinical decisions. Further research is needed to optimize ctDNA analysis and improve its sensitivity and specificity in identifying disease burden and treatment response. Despite these limitations, ctDNA holds significant potential as a non-invasive biomarker for cancer diagnosis and monitoring, and its continued investigation may lead to new insights into cancer biology and personalized therapy.

7. Future Directions

The use of ctDNA as a predictive biomarker of response in metastatic castration-resistant prostate cancer therapy is still in its early stages, and further research is needed to optimize its use in clinical practice. Here are some potential future directions for ctDNA as a biomarker in mCRPC:

1. Development of standardized methods for ctDNA analysis: The development of standardized methods for ctDNA analysis will ensure that the results obtained from different laboratories are comparable and reproducible. This will facilitate the integration of ctDNA analysis into clinical practice and accelerate the development of ctDNA-based biomarkers.

2. Identification of additional genetic alterations associated with treatment response: The identification of additional genetic alterations associated with treatment response will expand the utility of ctDNA as a biomarker in mCRPC. This will require the use of large-scale genomic analysis to identify new targets for therapy.

3. Integration of ctDNA analysis with imaging and other biomarkers: The integration of ctDNA analysis with imaging and other biomarkers will provide a more comprehensive picture of the tumor's biology and the patient's response to therapy. This will enable clinicians to tailor treatment strategies to individual patients and improve treatment outcomes.

4. Development of liquid biopsy platforms: The development of

liquid biopsy platforms that are simple, affordable, and widely available will facilitate the widespread use of ctDNA as a biomarker in clinical practice. These platforms will allow clinicians to monitor treatment response and disease progression in real-time, without the need for invasive procedures.

5. Validation of ctDNA as a surrogate endpoint in clinical trials: The validation of ctDNA as a surrogate endpoint in clinical trials will accelerate the development of ctDNA-based biomarkers and facilitate the approval of new therapies. This will require large-scale clinical trials to demonstrate the predictive value of ctDNA in treatment response.

The potential of ctDNA as a biomarker highlights the importance of precision medicine in prostate cancer treatment, where personalized treatment strategies can be tailored to the specific genetic profile of the patient's tumor. Further studies are needed to validate the use of ctDNA as a predictive biomarker in clinical practice and to identify the most effective methods for ctDNA analysis. The development of liquid biopsy platforms and the improvement of ctDNA detection sensitivity may facilitate the widespread use of ctDNA as a biomarker in clinical practice.

8. Conclusion

In conclusion, circulating tumor DNA (ctDNA) is an emerging biomarker in cancer research, and its potential to predict response to therapy has been explored in several malignancies, including prostate cancer. In metastatic castration-resistant prostate cancer (mCRPC), ctDNA has shown promise as a predictive biomarker for response to therapy, with the detection of specific genetic alterations in ctDNA identifying patients who are more likely to respond to specific therapies. However, the use of ctDNA as a biomarker has several limitations that need to be considered, including the sensitivity of ctDNA detection and the subjectivity of clonal evolution.

Despite its limitations, the potential of ctDNA as a biomarker highlights the importance of precision medicine in prostate cancer treatment, where personalized treatment strategies can be tailored to the specific genetic profile of the patient's tumor. Future research in ctDNA analysis should focus on the development of standardized methods for ctDNA analysis, identification of additional genetic alterations associated with treatment response, integration of ctDNA analysis with imaging and other biomarkers, development of liquid biopsy platforms, and validation of ctDNA as a surrogate endpoint in clinical trials.

Overall, the use of ctDNA as a predictive biomarker in mCRPC therapy has the potential to improve treatment outcomes and quality of life for patients by enabling clinicians to select the most effective treatments and avoid those that are unlikely to work. As such, the continued investigation of ctDNA as a biomarker in prostate cancer will be critical to advancing personalized medicine and improving the lives of those living with mCRPC.

References

1. Wyatt AW, Annala M, Aggarwal R, Beja K, Feng F, Youngren J, et al. Concordance of Circulating Tumor DNA and Matched Metastatic Tissue Biopsy in Prostate Cancer. *J Natl Cancer Inst.* 2017; 109(5).
2. Annala M, Vandekerckhove G, Khalaf D, Taavitsainen S, Beja K, Warner EW, et al. Circulating Tumor DNA Genomics Correlate with Resistance to Abiraterone and Enzalutamide in Prostate Cancer. *Cancer Discov.* 2018; 8(3): 444-57.
3. Scher HI, Graf RP, Schreiber NA, Jayaram A, Winkquist E, McLaughlin B, et al. Assessment of the Validity of Nuclear-Localized Androgen Receptor Splice Variant 7 in Circulating Tumor Cells as a Predictive Biomarker for Castration-Resistant Prostate Cancer. *JAMA Oncol.* 2018; 4(5): 1179-86.
4. Conteduca V, Wetterskog D, Sharabiani MTA, Grande E, Fernandez-Perez MP, Jayaram A, et al. Androgen receptor gene status in plasma DNA associates with worse outcome on enzalutamide or abiraterone for castration-resistant prostate cancer: a multi-institution correlative biomarker study. *Ann Oncol.* 2017; 28(2): 150-6.
5. Carreira S, Romanel A, Goodall J, Grist E, Ferraldeschi R, Miranda S, et al. Tumor clone dynamics in lethal prostate cancer. *Sci Transl Med.* 2014; 6(254): 254ra125.
6. Goodall J, Mateo J, Yuan W, Mossop H, Porta N, Miranda S, et al. Circulating Cell-Free DNA to Guide Prostate Cancer Treatment with PARP Inhibition. *Cancer Discov.* 2017; 7(1): 100-13.
7. Sumanasuriya S, Davies AH, Tindall EA, et al. Clinical utility of circulating tumour DNA in prostate cancer: a systematic review. *J Cancer Res Clin Oncol.* 2019; 145(10): 2655-76.
8. Sundaresan TK, Sequist LV, Heymach JV, Riely GJ, Jänne PA, Koch WH, et al. Detection of T790M, the Acquired Resistance EGFR Mutation, by Tumor Biopsy versus Noninvasive Blood-Based Analyses. *Clin Cancer Res.* 2016; 22(5): 1103-10.
9. Abbosh C, Birkbak NJ, Wilson GA, Jamal-Hanjani M, Constantin T, Salari R, et al. Phylogenetic ctDNA analysis depicts early-stage lung cancer evolution. *Nature.* 2017; 545(7655): 446-51.
10. Hong DS, Choe JH, Na JO, et al. Usefulness of circulating tumor DNA for the detection of pancreatic cancer. *Oncotarget.* 2016; 7(33): 40153-64.
11. Li BT, Janku F, Jung B, Hou C, Madwani K, Alden R, et al. Ultra-Deep Next-Generation Sequencing of Plasma Cell-Free DNA in Patients With Advanced Lung Cancers: Results From the Actionable Genome Consortium. *Oncologist.* 2016; 21(8): e684-91.
12. Garcia-Murillas I, Schiavon G, Weigelt B, Ng C, Hrebien S, Cutts RJ, et al. Mutation tracking in circulating tumor DNA predicts relapse in early breast cancer. *Sci Transl Med.* 2015; 7(302): 302ra133.
13. Ulz P, Thallinger GG, Auer M, Graf R, Kashofer K, Jahn SW, et al. Inferring expressed genes by whole-genome sequencing of plasma DNA. *Nat Genet.* 2016; 48(3): 127-31.
14. Perkins G, Yap TA, Pope L, Cassidy AM, Dukes JP, Riisnaes R, et al. Multi-purpose utility of circulating plasma DNA testing in patients with advanced cancers. *PLoS One.* 2012; 7(11): e47020.
15. Chen H, Hardy RW, Hall WA, et al. Blood biomarkers for cancer detection: biomarker discovery strategies and challenges. *Biomark Res.* 2017; 5: 8.