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# CYP17A1 polymorphism c.-362T>C predicts clinical outcome in metastatic castration-resistance prostate cancer patients treated with abiraterone

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## Abstract

**Background** Abiraterone became a standard hormonal therapy for patients with metastatic castration-resistance prostate cancer (mCRPC). However, patients may experience primary resistance to treatment. To date, few predictive biomarkers of efficacy have been identified. Our aim was to investigate the association between the single nucleotide polymorphism (SNP) c.-362T>C in the CYP17A1 gene, and clinical outcome in mCRPC patients treated with abiraterone.

**Patients and methods** mCRPC patients candidate to receive abiraterone were enrolled in the present retrospective pharmacogenetic study. Based on a literature selection, CYP17A1 rs2486758 (c.-362T>C) was selected and analysed by real-time PCR on genomic DNA extracted from whole blood. Univariate analysis was performed to test the association between the SNP and treatment-related clinical outcomes.

**Results** Sixty mCRPC patients were enrolled in the present study. Patients carrying the mutant CYP17A1 c.-362CT/CC genotypes showed a shorter median progression-free survival (PFS) and prostate-specific antigen-PFS (PSA-PFS) compared to patients carrying the TT genotype (10.7 vs 14.2 months and 8 vs 16 months, respectively;  $p=0.04$ ). No association between the selected SNP and the overall survival was found.

**Conclusions** These findings suggest an association between CYP17A1 c.-362T>C polymorphism and poorer clinical outcome with abiraterone for mCRPC patients. However, further validations on larger cohort of patients are needed to confirm its role as a predictive biomarker for abiraterone resistance.

**Keywords** CYP17A1 · Polymorphism · CRPC · Abiraterone · Pharmacogenetics

## Introduction

Prostate cancer is the most commonly diagnosed cancer among men in Western countries, accounting for 24% of all new cancers diagnosed in 2018, and is considered as the second and third leading cause of cancer death in American and European men, respectively [1–3]. Although the incidence of prostate cancer is high, most of the cases are

detected when the cancer is localised within the prostate, with a 5-year survival rate in USA of 98% [3]. The rate of patients with metastatic prostate cancer at diagnosis is less than 30% and remains low [4]. Metastatic prostate cancer may be present already as a disseminated disease at the time of diagnosis or as a disease recurrence after local therapy [5]. Androgen deprivation therapy (ADT) is the gold standard and the most effective initial treatment; however, after the initial response, almost all patients eventually progress following a median 18–24 months of ADT, to metastatic castration-resistant prostate cancer (mCRPC) [6, 7]. Despite the increasing options in terms of mCRPC treatment, median survival for mCRPC remains in the range of 15–36 months [6, 8]. Docetaxel was the gold standard for mCRPC treatment, being the first and only life prolonging agent until 2010 [5, 9]. However, in the last years, five new drugs have shown efficacy in improving overall survival in mCRPC

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patients. Cabazitaxel, abiraterone, enzalutamide, apalutamide, and radium-223 dichloride became, or will be in the near future, part of CRPC drugs armamentarium [10–12].

Abiraterone is a selective inhibitor of cytochrome P450 17-hydroxylase (CYP17A1) [13, 14] and suppresses the androgen synthesis in adrenal glands, testicles and tumour micro-environment [15, 16]. Although phase III clinical trials demonstrated a clear improvement in progression-free survival (PFS) and overall survival (OS) in patients with mCRPC treated with abiraterone acetate plus prednisone [17, 18], the response to treatment is heterogeneous and about 25–30% of patients experience primary resistance. To date, few predictive biomarkers of efficacy have been identified in mCRPC patients and none of them has been investigated in prospective randomised trials to confirm its predictive role in clinical practice [19]. CYP17A1 is the direct target of abiraterone and, therefore, could be one of the most important biomarkers to predict therapy response/failure. CYP17A1 is located on chromosome 19q23.4, and catalyses key reactions in sex-steroid biosynthesis, mediating 17 $\alpha$ -hydroxylase and 17,20-lyase activities [20]. In vitro study demonstrated that alterations of CYP17A1 activity may play a role in reducing response to treatment [21], and the intratumour overexpression of CYP17A1—detected in prostate cancer tissue biopsies from patients treated with abiraterone—suggests the enzyme upregulation as a key mechanism of resistance to therapy [22]. A published retrospective study demonstrated an association between CYP17A1 copy number variation and shorter PFS in mCRPC patients treated with abiraterone [23], while another study, published by Binder et al., evaluated the predictive role of 4 CYP17A1 single nucleotide polymorphisms (SNPs) (rs2486758, rs4919685, rs17115100 and rs743572) with respect to abiraterone response in 87 CRPC patients [24]. The study showed a relationship between the rs2486758 SNP (c.-362T>C), a worse biochemical response rate and a shorter time to biochemical progression [24]. However, conflicting results concerning any correlation between CYP17A1 polymorphisms and the anti-hormonal agent response have been reported [25]. The aim of the present study was to investigate the correlation between CYP17A1 c.-362T>C polymorphism with clinical outcome, verifying its impact on abiraterone efficacy.

## Patients and methods

### Patient selection

The study is a mono-institutional pharmacogenetic study that enrolled mCRPC patients receiving abiraterone acetate as per approved label. Inclusion criteria allowed the enrolment of patients with histologically or cytologically confirmed prostate adenocarcinoma, a castration-resistance state

as defined per current clinical guidelines (castrate serum testosterone <50 ng/dL or 1.7 nmol/L plus either biochemical progression, which consists in 3 consecutive rises in PSA 1 week apart resulting in two 50% increases over the nadir, and a PSA >2 ng/mL or, radiological progression, that is, the appearance of new lesions on bone scan or CT scan), with documented metastases confirmed by CT and/or technetium-99 bone scan and/or 18F-fluorocholine PET-CT, and patients had to be eligible for receiving abiraterone acetate as per current clinical guidelines.

The study was approved by the Ethics Committee of Pisa University Hospital and conducted in accordance with the principles of the Declaration of Helsinki. All patients gave their signed informed consent before blood collection and data analysis.

### Blood sample collection, DNA isolation, and SNP genotyping

Blood samples were collected in tubes containing EDTA and stored at –80 °C until analysis. Genomic DNA was extracted from 200  $\mu$ l of whole blood using QIAamp DNA Blood Mini kit (Qiagen, Valencia, CA) following the manufacturer's protocol. The analysis of the CYP17A1 SNP (rs2486758) c.-362T>C was conducted on a Quantstudio Dx (Applied Biosystem, Foster City, CA) by using the TaqMan<sup>®</sup> SNP Genotyping Assay (Assay ID: C\_\_15807798\_10) according to the manufacturer's standard protocol.

### Statistical analysis

Categorical data were described by absolute and relative frequencies, whereas quantitative data were reported as mean and standard deviation. PFS was defined as the length of time from starting abiraterone treatment to radiological progression of disease or death. OS was defined as the length of time from starting abiraterone treatment to death for any cause. PSA-PFS was defined as the presence of two consecutive total serum PSA increases  $\geq$ 50%, at least 2 weeks apart. The Kaplan–Meier method was used to create PFS curves and log-rank test was used to evaluate the differences between curves. Hazard ratio was calculated to compare cumulative risks. Univariate and multivariate analyses were performed to evaluate the correlation between clinical parameters and the CYP17A1 SNP. The frequency of CYP17A1 c.-362T>C polymorphism in our cohort was compared to the worldwide population and Hardy–Weinberg equilibrium was assessed. Allelic frequencies were determined by dbSNP short genetic variations. Statistical significance was defined by a *p* value of 0.05 or lower. Analyses were performed using MedCalc version 14.8.1.

**Table 1** Patient characteristics

Baseline characteristics	N=60
Age—median (range)	74 (54–86)
ECOG performance status, number (%)	
0	34 (56)
1	25 (42)
2	1 (2)
Tumour stage at diagnosis, number (%)	
T1/2 N0 M0	3 (5)
T3/4 N0 M0	15 (25)
Any T N1 M0	13 (22)
Any T any N M1	22 (36)
Unknown	7 (12)
Gleason score at diagnosis, number (%)	
≤7	23 (38)
>7	33 (55)
Unknown	4 (7)
Presence of bone metastases	
No	11 (18)
Yes	49 (82)
Presence of lymph node metastases	
No	26 (43)
Yes	34 (57)
Presence of visceral (lung and/or liver) metastases	
No	17 (28)
Yes	43 (72)
Lung	1 (2)
Liver	5 (12)
Volume of disease at diagnosis (according to CHAARTED criteria)	
Low	42 (70)
High	14 (23)
Unk	4 (7)
High-/Low-risk according to LATITUDE criteria	
High	12 (20)
Low	48 (80)
No. of previous chemotherapeutic regimens (%)	
0	23 (38)
1	21 (35)
2	16 (27)
Baseline total PSA level (ng/mL), median (range)	25.32 (0.35–4581)

**Results**

The study included a total of 60 mCRPC patients treated between 2012 and 2019 at the University Hospital of Pisa (Italy), with abiraterone acetate plus prednisone as per clinical practice. The main characteristics of patients are reported in Table 1. The majority of patients had a good performance status (0–1, 98%), high Gleason score (≥ 7, 55%) and locally advanced (N1) or metastatic (M1) disease at diagnosis (58%). Twenty-three percent of patients had a high volume of disease at diagnosis of metastatic disease according to CHAARTED criteria [26] or a high-risk disease according to Latitude criteria [27].

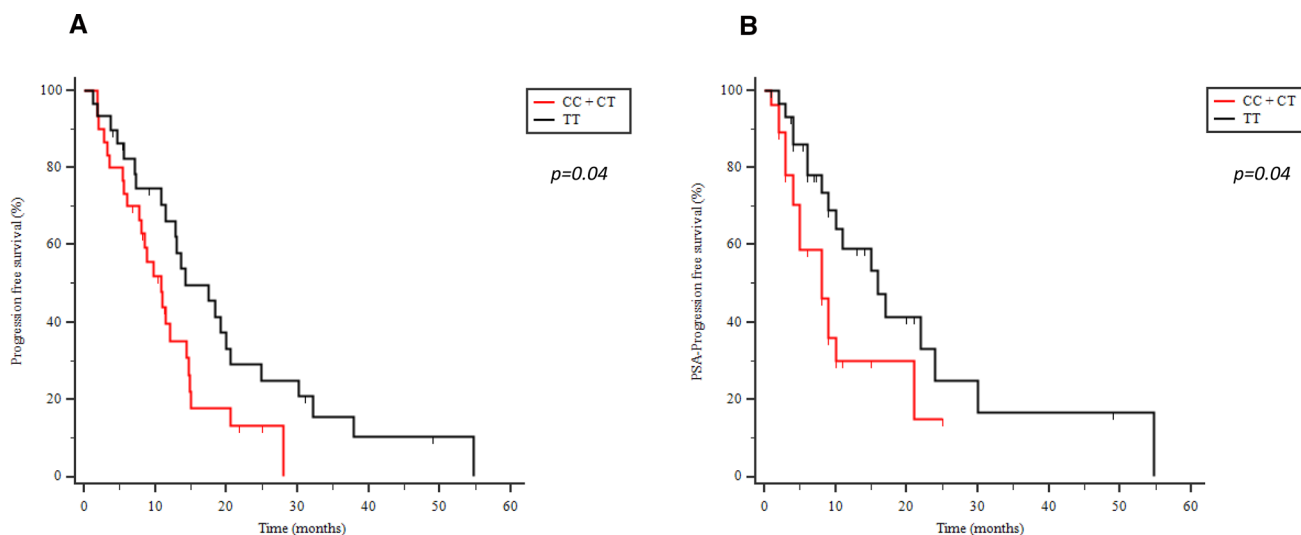
After treatment with abiraterone acetate, the majority of patients (52%) received a subsequent chemotherapy regimen. In particular, 35% and 17% received docetaxel and cabazitaxel, respectively. Seven (11.7%) patients had a partial response (PR), 28 (46.7%) patients achieved a stable disease (SD), and 14 (23.3%) had a progressive disease (PD). In 11 patients (18.3%), it was not possible to assess tumour response. Median PFS on abiraterone treatment was 10.8 months (95% CI 7.9–13 months) and median OS was 21 months (95% CI 13–29.4 months).

The calculation of Hardy–Weinberg equilibrium was performed and the CYP17A1 polymorphism was found to be in equilibrium (Table 2). The association between CYP17A1 (rs2486758) c.-362T>C and PFS and OS was evaluated. PFS was longer in patients carrying the wild-type TT genotype compared to patients carrying at least one mutant allele TC/CC (median 14.2 vs 10.7 months, *p*=0.04; Fig. 1a). The PSA-PFS was also longer in patients carrying the TT vs CT/CC genotypes (8 vs 16 months, *p*=0.04) (Fig. 1b). A difference was observed in the OS analysis: median OS was 32 months for the TT genotype vs 21.6 months for the TC/CC genotypes, although it was not statistically significant (*p*=0.14). No association was found between CYP17A1 c.-362T>C and biochemical response to abiraterone (*p*>0.05).

Cox proportional hazard ratios were used to assess the effect of CYP17A1 c.-362T>C polymorphism on the prediction of time-to-event outcomes. In the univariate model, the polymorphism showed to significantly influence

**Table 2** Allele and genotype frequencies of CYP17A1 SNP (SNPs single nucleotide polymorphisms, N number of patients)

SNP	Allele	Allele frequency		P value	Genotypes	Genotype frequency		HWE (p <sub>HWE</sub> )
		Case series	Population			Observed numbers	Expected numbers	
CYP17A1 c.-362T>C	T	71.7	78.7	0.323	TT	30	30.8	0.27 (0.60)
	C	28.3	21.3		CT	26	24.4	
					CC	4	4.8	



**Fig. 1** a, b Kaplan–Meier curves for progression-free survival (PFS) (a) and PSA-progression-free survival (PSA-PFS) (b) in patients treated with abiraterone stratified by CYP17A1 c.-362T>C genotypes

abiraterone PFS (OR = 0.54, CI 95%, 0.29–0.99;  $p = 0.04$ ), together with previous use of docetaxel (32/60 patients; OR = 2.23 CI 95%, 1.21–4.1;  $p = 0.01$ ). Clinical characteristics of patients and known risk factors for disease progression, such as age, higher Gleason score ( $\leq 7, > 7$ ) and high volume/high-risk metastatic disease at diagnosis, were also analysed (Table 3). In the multivariate model, only previous use of docetaxel was confirmed as an independent predictor of PFS (OR 2.17 CI 95%, 1.17–4.01;  $p = 0.02$ ).

Biochemical or radiographic PFS to first-line taxane chemotherapy did not differ significantly depending on CYP17A1 c.-362T>C genotype ( $p > 0.05$ ): median PFS was 6 months in patients carrying TC/CC genotypes (95% CI 4.03–6.30 months) and 5.9 months in patients carrying TT genotype (95% CI 5.03–7.7 months).

**Discussion**

Genotyping analysis of genes involved in prostate cancer carcinogenesis, progression and treatment could help us to better understand the behaviour of CRPC and, consequently, patient outcomes [28]. It has been demonstrated that epigenetic markers and genetic alterations are able to predict clinical outcome in CRPC patients treated with new hormonal therapy [29–31]. However, few studies have investigated the effect of polymorphisms on outcome prediction [19, 23, 25, 32], and the majority of published studies show conflicting results. Since CYP17 is involved in step regulation in the biosynthesis of testosterone and is, therefore, the target of abiraterone, its genetic characterisation could facilitate the understanding of patients’

**Table 3** Univariate and multivariate analysis of clinical variables influencing PFS

Variable	Univariate		Multivariate	
	OR (95% CI)	<i>p</i> value	HR (95% CI)	<i>p</i> -value
Age (< 75, ≥ 75)	1.21 (0.68–2.16)	0.51	–	–
Gleason Score (≤ 7; > 7)	1.17 (0.62–2.19)	0.63	–	–
High-volume metastatic disease at diagnosis (yes; no)	1.01 (0.51–2.02)	0.97	–	–
High-risk metastatic disease at diagnosis (yes; no)	0.99 (0.49–1.98)	0.98	–	–
Prior use of docetaxel (yes; no)	2.23 (1.21–4.1)	0.01	2.17 (1.17–4.01)	0.02
CYP17A1 rs2486758 (TT; TC/CC)	0.54 (0.29–0.99)	0.04	0.58 (0.31–1.06)	0.08

response/resistance to abiraterone therapy. The present study evaluated the impact of the CYP17A1 c.-362T>C SNP (rs2486758) on clinical outcome in 60 mCRPC patients treated with abiraterone, showing a significant relationship between the mutant genotype and a shorter radiological PFS. In the multivariate analysis, prior use of docetaxel was confirmed as an independent predictor of PFS, accordingly to a previous study [9]. However, only 32 patients have been treated in first line with docetaxel, suggesting a possible limit of the study. Indeed, in the univariate model, CYP17A1 c.-362T>C polymorphism was shown to significantly influence abiraterone PFS, confirming its potential role in drug resistance.

Binder et al. already evaluated the predictive role of 4 CYP17A1 SNPs (rs2486758, rs4919685, rs17115100 and rs743572) and their association with response to the anti-hormonal agents in 87 mCRPC patients [24]. Of the analysed SNPs, only the c.-362T>C (rs2486758) was associated with a worse biochemical response rate to abiraterone and a shorter abiraterone biochemical progression [24]. These results highlight that germinal polymorphisms of target genes are likely to be included between the most important sources of individual variability in drug efficacy [33].

CYP17A1 overexpression suggested the enzyme upregulation as a key mechanism of resistance to hormonal therapy and its association with outcome (median PFS and OS) of mCRPC patients treated with abiraterone [22, 23, 32]. The c.-362T>C polymorphism represents a variant of the CYP17A1 gene located in the 5' promoter region [34]. The minor C-allele seems to be associated with an increased expression of CYP17 gene, by affecting gene splicing and transcription factor binding or the sequence of noncoding RNA [35]. Abiraterone is a potent inhibitor of the steroidogenic enzyme CYP17A1 and its increased transcriptional activity in the presence of C allele may be associated with the mechanism of resistance, due to a decreased target occupancy and inhibition. Intriguingly, another work by Bremmer et al. showed that when androgen signalling is impaired, i.e. by RNA interference with androgen receptor (AR) expression by specific siRNA, the same resistance effect becomes evident [36]. Therefore, CYP17A1 upregulation is indicative for an androgen signalling impairment, which may be not limited to abiraterone treatment and may represent a negative feedback loop upon the same pathway [37]. Therefore, variations of key genes involved in androgen biosynthesis and metabolism have been also evaluated as candidate biomarkers for prostate cancer susceptibility. A possible association of c.-362T>C polymorphism with prostate cancer risk has been reported by Wang et al. [38]. Again, the hypothesis could lie in the CYP17A1 overexpression, which is able to increase the testosterone synthesis, allowing the risk of prostate cancer development. However,

well-designed epidemiologic studies are necessary to confirm this association.

Even if the present study analysed only one selected SNP, with a high probability of being correlated with abiraterone activity [24], other polymorphisms in genes involved in steroidogenesis or drug metabolism are worth being evaluated, including TSPYL, which was previously shown to be associated with regulation of CYP17A1 and CYP3A4 expression [39]. Polymorphisms affecting SULT2A1 and CYP3A4 genes, involved in abiraterone metabolism, could be also evaluated to identify a possible influence in pharmacokinetics and drug exposure [40].

With the limitation of the retrospective nature of the study and the relatively small sample size, our analysis revealed a possible association between CYP17A1 c.-362T>C germinal polymorphism and abiraterone resistance, based on PFS and PSA-PFS.

We found no association with overall survival; however, such negative finding might be explained by the subsequent therapies that the vast majority of patients received. The administration of a chemotherapy regimen, which is unaffected by CYP17A1 alteration, might have mitigated the effect of this molecular characteristic on the final outcome. Indeed, it is necessary to validate this result in a larger and independent validation cohort. Moreover, the current approach to correlate PFS and PSA-PFS to a single SNP may be replaced by a comprehensive genetic analysis to evaluate the interaction between different SNPs (i.e. haplotype) and survival. Further studies of larger case series are needed to better investigate the therapeutic window of the drug and the potential impact of germinal SNPs.

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## Compliance with ethical standards

**Conflict of interest** :The authors declare no conflict of interest.

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