

ORIGINAL ARTICLE

No association found between *CYP2D6* genotype and early breast cancer events in tamoxifen-treated patientsANDREA MARKKULA^{1,*}, MARIA HJERTBERG^{1,2,*}, CARSTEN ROSE³,
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Abstract

Background. *CYP2D6* is considered the key enzyme in tamoxifen metabolism. Several studies have investigated the relationship between the *CYP2D6* genotype and tamoxifen treatment outcome, with discrepant results. *CYP2D6* inhibitor use, aromatase inhibitor use, and chemotherapy may account for some of the discrepancies. We examined the association between *CYP2D6* genotype and early breast cancer events in tamoxifen-treated breast cancer patients, in relation to *CYP2D6* inhibitor use, aromatase inhibitor use, and chemotherapy. **Material and methods.** Pre- and postoperative questionnaires on lifestyle and concomitant medications were completed by 634 primary breast cancer patients between 2002 and 2008, among whom 333 patients had ER-positive tumors and received tamoxifen. *CYP2D6**3, *4, *6, *10 and *41 were genotyped. Information on clinical data, breast cancer events, and tumor characteristics was obtained from patients' charts, population registries, the Regional Tumor Registry, and pathology reports. **Results.** Median follow-up was 4.9 years. Neither poor metabolizers (adjusted HR 0.50; 95% CI 0.07–3.82) nor intermediate metabolizers (adjusted HR 1.00; 95% CI 0.47–2.11) had an increased risk of early breast cancer events when compared with extensive metabolizers. *CYP2D6* activity score (taking into account genotype and *CYP2D6* inhibitor use) was not associated with early breast cancer events (LogRank, $P_{\text{trend}} = 0.44$). **Conclusions.** *CYP2D6* genotype was not associated with tamoxifen treatment outcome, even when *CYP2D6* inhibitor use, aromatase inhibitor use, or chemotherapy was taken into account. *CYP2D6* genotype may be of minor importance for tamoxifen-treated patients in Scandinavia.

Breast cancer is the most common cancer among women [1]. Despite an overall five-year relative survival rate of almost 90% for breast cancer patients in Sweden [2], it remains the primary cause of cancer death among women worldwide [1]. Though tamoxifen is an effective anti-estrogen treatment for breast cancer patients with estrogen receptor (ER) positive tumors, around 30% of tamoxifen-treated women relapse despite five years of tamoxifen treatment [3]. Markers of tamoxifen treatment-resistance could allow for more personalized treatment, improving the prognosis for many women [4].

The cytochrome P2D6 (*CYP2D6*) enzyme is considered the key enzyme in transforming tamoxifen into one of its most abundant active metabolites,

endoxifen [5]. Patients with two non-functional *CYP2D6* alleles have lower plasma concentrations of endoxifen than patients with functioning alleles [6,7]. Hence, it has been proposed that *CYP2D6* genotype may be associated with recurrence among tamoxifen-treated breast cancer patients. Several studies have investigated the relationship between the gene encoding cytochrome P450 2D6 (*CYP2D6*) and tamoxifen treatment outcome, with widely heterogeneous results [4,5,8–10].

It has been suggested that *CYP2D6* inhibitor use, aromatase inhibitor use and chemotherapy may account for some of these discrepancies [5]. Therefore, we examined the association between *CYP2D6* genotype and early breast cancer events in tamoxifen-treated

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(Received 27 May 2013; accepted 26 August 2013)

breast cancer patients, in relation to CYP2D6 inhibitor use, aromatase inhibitor use, and chemotherapy in a prospective cohort of tamoxifen-treated breast cancer patients in Sweden.

Material and methods

The design of the study has been described in detail elsewhere [11]. In brief, preoperative questionnaires on lifestyle and concomitant medications were completed by 634 breast cancer patients in Sweden between 2002 and 2008, among whom 333 patients had ER-positive tumors and received tamoxifen

(Figure 1). Follow-up questionnaires were completed up to nine years postoperatively. Information on clinical data, breast cancer events, and tumor characteristics was obtained from patients' charts, population registries, the Regional Tumor Registry, and pathology reports. ER and progesterone receptor (PR) status were obtained from each patient's pathology report. ER and PR status were determined by immunohistochemistry using the Dako LSAB™ kit system (Dako, Glostrup, Denmark) and the antibodies M7047 (ER) and M3569 (PR) (Dako). Tumors with more than 10% positive nuclear staining were considered ER-positive or PR-positive [12].

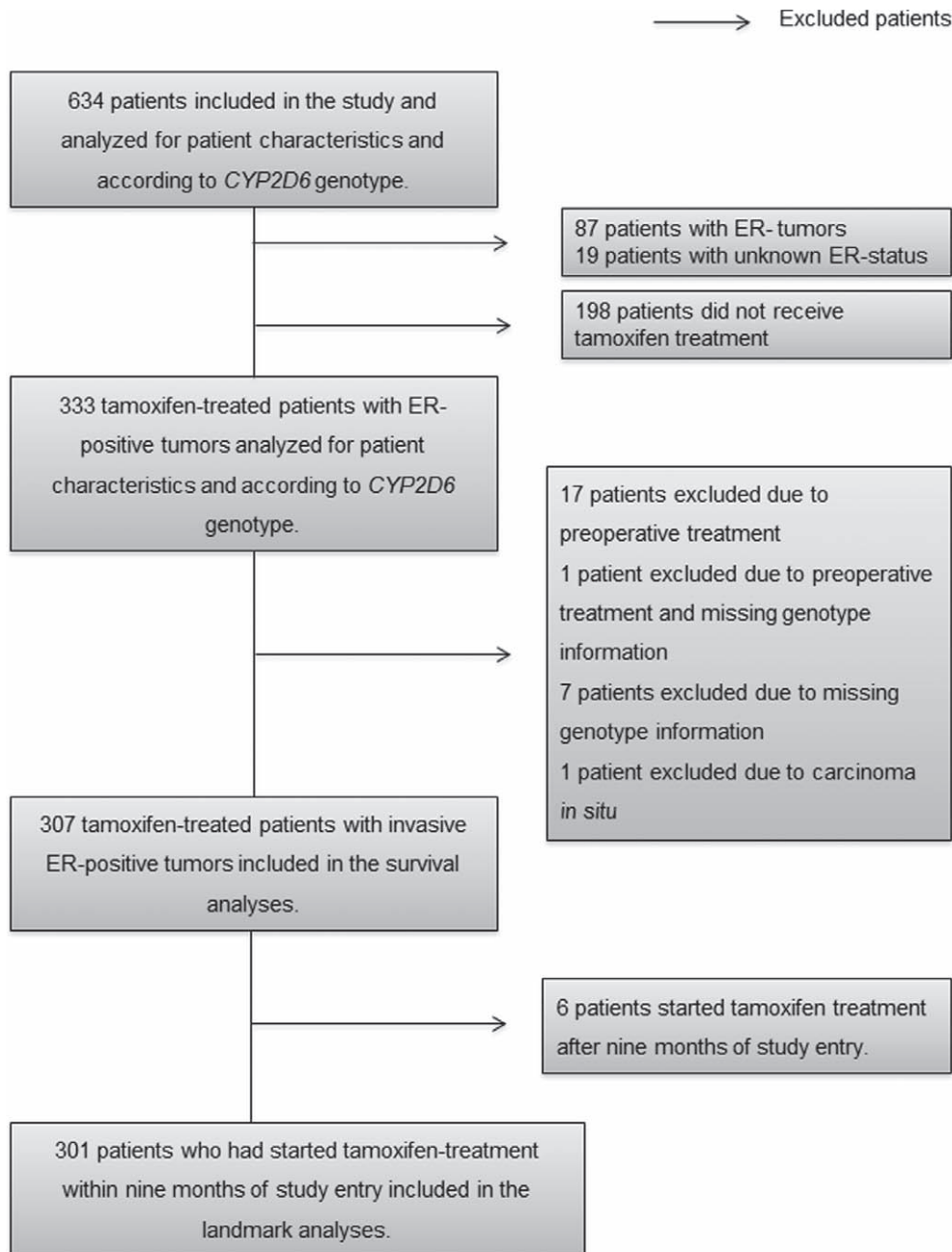


Figure 1. Flow chart of the selection process of patients.

All tumors were analyzed at the Department of Pathology at Skåne University Hospital in Lund. Written informed consent was obtained from all patients. The study was approved by the Ethics Committee of the Lund University (Dnr 75-02 and 37-08).

*CYP2D6**3,*4,*6,*10, and *41 were analyzed using Genomic deoxyribonucleic acid (DNA) extracted from the leukocyte portion of whole blood. The SNPs were genotyped with custom TaqMan® assay (*CYP2D6**3), TaqMan® Drug Metabolism Genotyping Assays (*CYP2D6**4,*6,*10), and iPLEX reagents (*CYP2D6**41) at Region Skåne Competence Centre (RSKC Malmö), Malmö University Hospital, Malmö, Sweden, using methods previously described [11]. Over 10% of the samples were run in duplicate with a concordance of 100%. *CYP2D6* inhibiting drugs were classified in accordance with Flockhart et al. [13]. Only the use of the strongest inhibitor was considered. Patients with ER-negative tumors who had received tamoxifen treatment were excluded. Each patient received a *CYP2D6* genotype activity score and a *CYP2D6* activity score [14,15], and was then categorized as poor (PM), intermediate (IM), and extensive metabolizer (EM) (activity scores 0, 0.5–1.5, 2, respectively) [14].

Breast cancer-free survival was calculated from the pre-operative visit to the last follow-up visit or a non-breast cancer-related death or to a diagnosis of a breast cancer event prior to January 1, 2012. Survival analyses were performed using Kaplan-Meier and Cox regression models. Patients who had received pre-operative treatment (n = 17), patients with carcinoma in situ (n = 1), patients who lacked *CYP2D6* genotype information (n = 7), and patients who both received pre-operative treatment and lacked *CYP2D6*

genotype information (n = 1) were excluded from the survival analyses. Survival in relation to combined tamoxifen and *CYP2D6* inhibitor use was assessed through landmark analyses (landmark set as treatment initiation of tamoxifen and *CYP2D6* inhibitors within nine months of study entry). A p-value of <0.05 was taken to be significant. All p-values were two-sided.

Results

Patient characteristics for all 634 patients, and for the 333 tamoxifen-treated patients with ER-positive tumors, are presented in Table I. The median follow-up was 4.9 years. Frequency of the *CYP2D6* genotypes, with and without stratification according to *CYP2D6* genotype activity score and *CYP2D6* activity score, is presented in Table II. Among the 307 tamoxifen-treated patients with invasive ER-positive tumors and *CYP2D6* genotype information, 31 breast cancer events were observed. There was no association between early breast cancer events and *CYP2D6* genotype metabolizer category (Figure 2a). Excluding chemotherapy-treated patients (Figure 2b) and patients who had received either chemotherapy and/or aromatase inhibitors (Figure 2c) generated similar results. Neither PM, nor IM were associated with early breast cancer events in a multivariable model compared to EM [adjusted hazard ratio (HR_{PM}) 0.50; 95% CI 0.07–3.82; p = 0.50], [adjusted (HR_{IM}) 1.00; 95% CI 0.47–2.11; p = 1.00], adjusting for invasive tumor size (> 20 mm, or muscular or skin involvement), any axillary lymph node involvement, age at diagnosis, and histological grade III.

Table I. Patient characteristics for all 634 patients, and for the 333 tamoxifen-treated patients with ER-positive tumors (in gray).

N=	All patients		Tamoxifen treated patients	
	Median (IQR) of %	Missing	Median (IQR) or %	Missing
	634		333	
Age at diagnosis, yrs	59.6 (51.1–66.1)	–	59.3 (50.7–65.3)	–
Weight, kgs	68 (61–76)	2	68 (62–76)	2
Height, m	1.66 (1.62–1.70)	1	1.66 (1.62–1.70)	1
BMI, kgs/m ²	24.6 (22.3–27.8)	3	24.5 (22.4–27.4)	3
Waist-hip ratio	0.84 (0.78–0.89)	4	0.84 (0.78–0.89)	2
Age at menarche, yrs	13 (12–14)	5	13 (12–14)	3
Parous, %	84.7	–	83.5	–
Smoker at baseline*, %	21.3	–	19.5	–
Ever use of HRT, %	45.3	1	45.5	1
Antidepressant use at baseline, %	10.7	–	10.8	–
Strong <i>CYP2D6</i> -inhibitor use**, %	2.7	1	3.9	–
Intermediate <i>CYP2D6</i> -inhibitor use**, %	3.3	1	3.3	–
Ever received chemotherapy, %	21.9	–	15.6	–
Ever received aromatase inhibitors, %	33.6	–	42.0	–

*Regular smoker or party smoker at baseline.

**Use of *CYP2D6* inhibitors within landmark set at nine months of study entry.

Table II. Frequency of the *CYP2D6* genotypes in all patients (n = 634), and for the 333 tamoxifen-treated patients with ER-positive tumors (in gray) with and without stratification according to *CYP2D6* genotype activity score and *CYP2D6* activity score. *CYP2D6* genotype was missing for 18 of the 634 patients.

<i>CYP2D6</i> genotypes in the study population (n = 634)	Number of patients with the <i>CYP2D6</i> genotypes (%)	<i>CYP2D6</i> genotype activity score based on genotype only ¹	<i>CYP2D6</i> genotypes in the tamoxifen treated study population (n = 333)	Number of tamoxifen treated patients with the <i>CYP2D6</i> genotypes (%)	<i>CYP2D6</i> genotype activity score among tamoxifen treated patients based on genotype only ¹
*1/*1	299 (47.2)	0	*1/*1	164 (49.2)	0
*1/*4	159 (25.1)	0.5	*1/*4	84 (25.2)	0.5
*1/*41	67 (10.6)	1	*1/*41	29 (8.7)	1
*4/*4	28 (4.4)	1.5	*4/*4	16 (4.8)	1.5
*4/*41	14 (2.2)	2	*4/*41	7 (2.1)	2
*1/*3	12 (1.9)		*1/*3	4 (1.2)	
*4/*10	6 (0.9)	Missing 18 (2.8)	*4/*10	4 (1.2)	Missing 8 (2.4)
*3/*4	6 (0.9)		*3/*4	5 (1.5)	
*3/*41	5 (0.8)	<i>CYP2D6</i> activity score based on genotype and the use of <i>CYP2D6</i> inhibitors ²	*3/*41	0	<i>CYP2D6</i> activity score among tamoxifen treated patients based on genotype and the use of <i>CYP2D6</i> inhibitors ²
*1/*6	5 (0.8)		*1/*6	4 (1.2)	
*1/*10	5 (0.8)		*1/*10	3 (0.9)	
*4/*6	4 (0.6)	0	*4/*6	1 (0.3)	0
*10/*10	2 (0.3)	0.5	*10/*10	1 (0.3)	0.5
*10/*41	2 (0.3)	1	*10/*41	2 (0.6)	1
*6/*6	1 (0.2)	1.5	*6/*6	0	1.5
*6/*41	1 (0.2)	2	*6/*41	1 (0.3)	2
Missing	18 (2.8)	Missing 19 (3.0)	Missing	8 (2.4)	Missing 8 (2.4)

¹Points assigned per allele: 1 point for major alleles (*1), 0.5 points for variant alleles (*10, *41), and 0 points for null alleles (*3, *4, *6) according to Blake et al.

²Points deducted from the *CYP2D6* genotype activity score according to Rae et al.: -2 points for the use of strong inhibitors and 1 point for the use of moderate *CYP2D6* inhibitors during at least one study visit within a landmark of nine months after baseline. Zero points were deducted for the use of weak *CYP2D6* inhibitors. If the patient reported use of several *CYP2D6* inhibitors, only the use of the strongest inhibitor was considered.

Among the 301 genotyped tamoxifen-treated patients with invasive ER-positive tumors who had started tamoxifen treatment within nine months of study entry, 11 also reported use of strong *CYP2D6* inhibitors, and 11 reported use of intermediate *CYP2D6* inhibitors within nine months of study entry. Six of the tamoxifen-treated patients commenced tamoxifen after nine months, none of which had a breast cancer event. Two patients commenced strong *CYP2D6* inhibitors use, and three patients commenced intermediate *CYP2D6* inhibitors use after nine months but before five years past study entry; none of these five patients had a breast cancer event.

In the landmark analyses, *CYP2D6* activity score (which takes both genotype and *CYP2D6* inhibitor use into account) was not associated with early breast cancer events in the univariable (LogRank, $p_{\text{trend}} = 0.44$) or in the multivariable model. Tamoxifen treatment duration was not associated with *CYP2D6* genotype, age, aromatase inhibitor or chemotherapy treatment.

Discussion

In this prospective cohort of tamoxifen-treated breast cancer patients in Sweden, there was no evidence that poor *CYP2D6* metabolizers had an impaired tamoxifen treatment outcome. In accordance with several previous studies of breast cancer patients in Scandinavia [10,16,17], neither *CYP2D6* genotype nor *CYP2D6* inhibitor use was associated with early events.

The present study has several strengths. It is population-based [11] and uses Swedish population registries for optimal follow-up. All polymorphisms were analyzed from germline DNA, and multiple polymorphisms were included. Also, blood for genotyping was collected at study entry, and *CYP2D6* inhibitor use was collected for the entire cohort of 634 patients. A total number of 38 patients (6%) used either strong or intermediate *CYP2D6* inhibitors, which is comparable to a previous publication [18]. The main limitation of the study is the

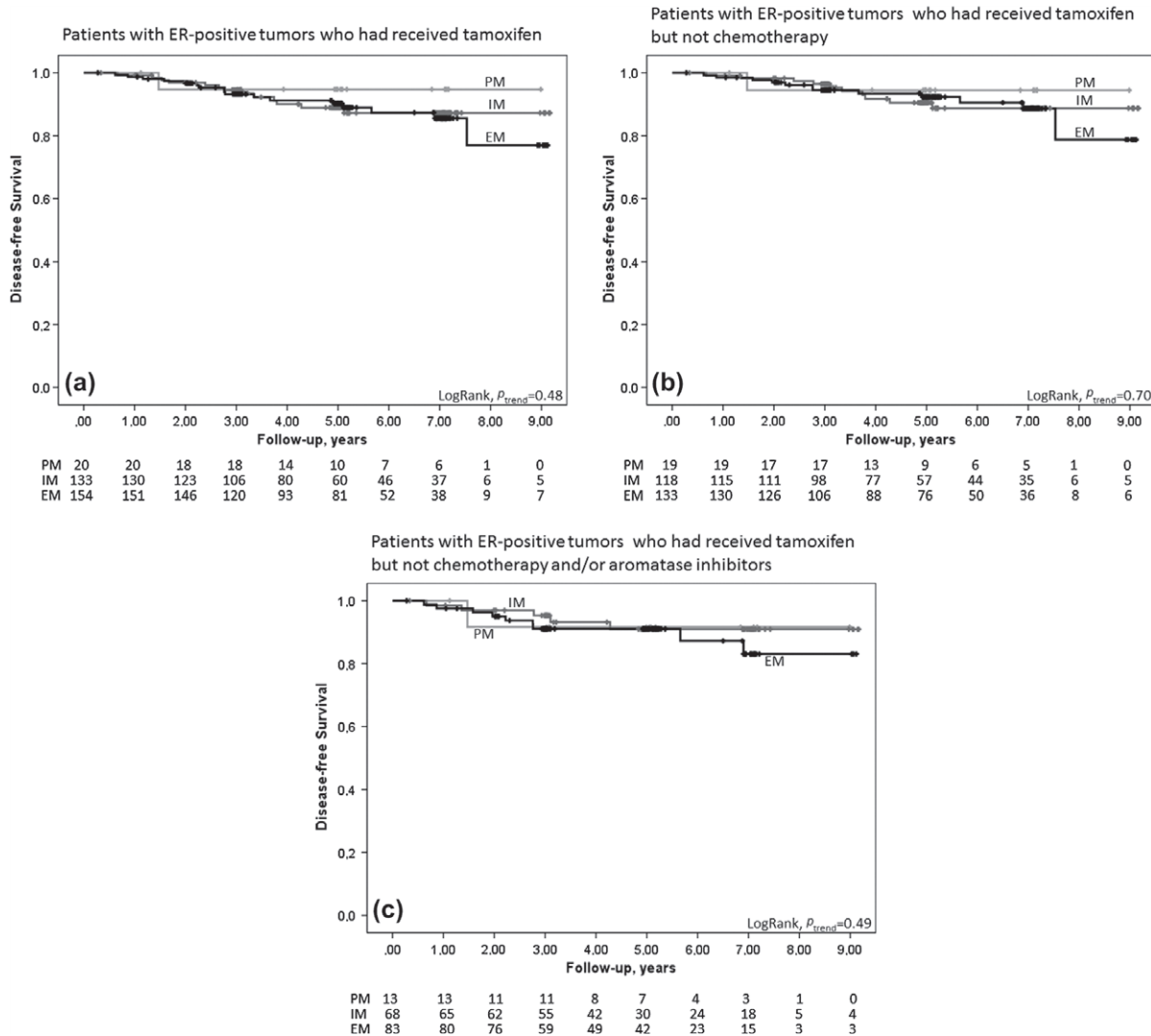


Figure 2. Kaplan-Meier estimate of breast cancer-free survival in relation to *CYP2D6* genotype activity score. a) among tamoxifen-treated patients with invasive ER-positive tumors (LogRank, $p_{trend} = 0.48$). Adjusted HR_{PM} (0.50; 95% CI 0.07–3.82; $p = 0.50$) and adjusted HR_{IM} (1.00; 95% CI 0.47–2.11; $p = 1.00$) compared with EMs. b) among tamoxifen-treated patients with invasive ER-positive tumors who had not received chemotherapy (LogRank, $p_{trend} = 0.70$). c) among tamoxifen-treated patients with invasive ER-positive tumors who had not received chemotherapy and/or aromatase inhibitors (LogRank, $p_{trend} = 0.49$).

sample size. The number of tamoxifen monotherapy-treated patients was relatively small, but the lack of association between *CYP2D6* genotype and disease-free survival seen in the present study has also been reported from previous studies conducted in larger cohorts [5,19].

CYP2D6 inhibitor use, chemotherapy, or aromatase inhibitor therapy did not account for the absence of an association between *CYP2D6* genotype and tamoxifen treatment outcome in this study. Many antidepressants are metabolized by enzymes other than *CYP2D6* that are involved in tamoxifen metabolism, such as *CYP2C19* [20] and *CYP2C8/9* [6,21]. This could in part explain the association between antidepressant use and breast cancer-free survival found in previous studies [6,22]. Other

genetic variants [10,23,24], and lifestyle factors such as a high coffee intake, [25] have been associated with survival among tamoxifen-treated breast cancer patients in Sweden. *CYP2D6* may be of minor importance for prediction of tamoxifen response in Scandinavia [9,10,16,17].

Acknowledgments

We wish to thank our research nurses: Anette Ahlin Gullers, Monika Meszaros, Maj-Britt Hedenblad, Karin Henriksson, Anette Möller, and Linda Ågren. We thank Sol-Britt Olsson, Nils-Gunnar Lundin, and Kristina Lövgren for taking care of blood samples. We also wish to thank Erika Bågeman, Maria Simonsson, and Maria Henningson for taking

care of blood samples and data entry, and Dr Eric Dryver for proofreading.

Declaration of interest: The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper. This work was supported by grants from The Swedish Cancer Society CAN 2011/497, the Medical Research Council K2012-54X-22027-01-3 (PI H Jernström), the Medical Faculty at Lund University, the Mrs. Berta Kamprad Foundation, the Gunnar Nilsson Foundation, the Swedish Breast Cancer Group (BRO), the South Swedish Health Care Region (Region Skåne ALF), Konung Gustaf V:s Jubileumsfond, and the Lund Hospital Fund.

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