Influence of CYP1A1 gene polymosphisms on recurrence and survival in breast cancer patients

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Introduction

Breast cancer is the first in the ranking of new cases. It is the leading cause of mortality in women and is responsible for 6.9% of cancer deaths worldwide. The enzymes encoded by the Cytochrome P450 superfamily genes play an important role in the xenobiotics metabolism. The CYP1A1*2A and CYP1A1*2C genetic single-nucleotide polymorphisms may be associated with the development of breast cancer.

Objective: To evaluate clinicopathological and epidemiological characteristics of patients with breast cancer and to investigate the association of CYP1A1*2A and CYP1A1*2C polymorphisms

Methods

This is a cross-sectional study, with data collection from medical records of patients diagnosed with breast cancer, at a university reference hospital in the state of São Paulo, Brazil, in the period from 2014 to 2016. Clinical, epidemiological and histopathological data were analyzed according to the following variables: alcohol and tobacco consumption, overweight or obesity, tumor staging and histological characteristics, treatment, presence of metastasis, number of recurrences and death. The inclusion criterion considered primary tumor cases without beginning treatment from women previously genotyped for CYP1A1*2A and CYP1A1*2C polymorphisms by our research group. After data tabulation, descriptive statistical analysis was performed with frequency counts. The Kaplan-Meier method was used to calculate the survival and recurrence rate in relation to the polymorphism genotypes, using GraphPad Prism v.8 software. Values of $p \leq 0.05$ were considered significant.

Results

The study evaluated 218 medical records of women with breast cancer and genotyped for the CYP1A1*2A and CYP1A1*2C polymorphisms. Epidemiological findings revealed a higher prevalence of cancer in nulliparous women (87.15%). Most women (70%) were overweight or obese, not smokers (69.27%) or alcoholics (60.55%). Distance metastasis and regional lymph nodes were diagnosed in approximately 50% of the patients. Of the total patients, 47 had the CYP1A1*2C polymorphism, of which 12.77% presented relapsed of tumor and 2.13% died (Table 1). The CYP1A1*2A polymorphism was identified in 93 patients, of whom 11.83% showed recurrence of disease and 2.15% died (Figure 1). The probability of 100% of survival was the 180 months for CYP1A1*2C (Figure 1) polymorphism and 120 months for CYP1A1*2A (Figure 2). The longest prolongation (180 months) has the lowest chance of occurring (70%).

TABLE 1: Genotyping data for CYP1A1*2C and CYP1A1*2A polymorphisms and association with recurrence and death.

Variáveis	Recidiva	*Óbito*
	Pacientes (n=20)	Pacientes (n=3)
	n (%)	n (%)
CYP1A1*2C		
TT	17 (85%)	2 (66,67%)
TC	5 (25%)	1 (33,33%)
CC	1 (5%)	0
CYP1A1*2A		
TT	12 (60%)	1 (33,33%)
TC	10 (50%)	2 (66,67%)
CC	1 (5%)	0

FIGURE 1 - Survival chart of patients with CYP1A1*2C polymorphism

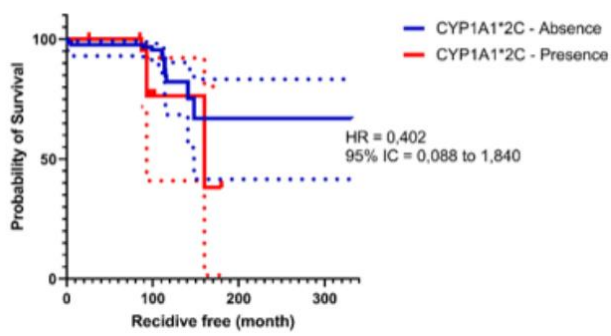
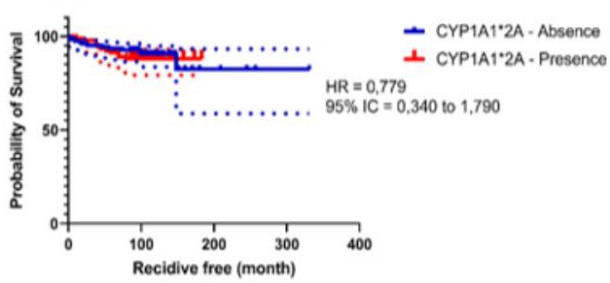


FIGURE 2 - Survival chart of patients with CYP1A1*2A polymorphism



Conclusions

Breast cancer has a higher incidence in nulliparous and obese women. The high survival rate and low percentage of disease recurrence in patients with CYP1A1*2A and CYP1A1*2C polymorphisms shows that these polymorphisms do not contribute to the worsening of disease prognosis and therefore, in this casuistic, these polymorphisms were not considered biomarkers of recurrence/survival.

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Financial and institutional support: PIBIC/Famerp, CNPq productivity (310987/2018-0)