



Brief communication

Estrogen receptor alpha gene polymorphisms and breast cancer risk

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Summary

We conducted a hospital-based case-control study to evaluate the association between the *XbaI* and *PvuII* restriction fragment length polymorphisms (RFLPs) in intron 1 of the estrogen receptor α (*ER* α) gene and breast cancer risk. The study population consisted of 205 histologically confirmed incident breast cancer cases and 205 age-matched controls with no present and previous history of cancer. The *PvuII* genotype distribution did not show any difference between cases and controls, but the adjusted odds ratio (OR) for the *XbaI* X allele containing genotypes was 0.4 (95% CI: 0.3–0.6) compared with the xx genotype. The decrease in the OR appeared to be more attributable to the postmenopausal women; the ORs were 0.3 (95% CI: 0.1–0.5) and 0.5 (95% CI: 0.3–0.9) for postmenopausal and premenopausal women, respectively. Our results therefore suggest that the *ER* α *XbaI* polymorphism modifies individual susceptibility to breast cancer in Korean women.

Introduction

Breast cancer is the second most frequent cancer in Korean women and the incidence is increasing [1]. Familial history of breast cancer and reproductive factors are well-established risk factors of breast cancer. However, genetic polymorphisms of genes involved in metabolism of hormones or other carcinogens are evolving as important determinants of breast cancer susceptibility [2].

The estrogen receptor α (*ER* α) is an important mediator of the hormonal response in estrogen-sensitive tissues such as breast, endometrium, and bone. In agreement with this, potentially important polymorphisms in the *ER* α gene have, although inconsistently, been associated with bone density [3] and breast cancer [4–7] and endometrial cancer risks [8].

Most of these studies on *ER* α gene polymorphisms and breast cancer were conducted in western countries. Since oriental women may have different genotype distribution or different level of susceptibility compared with western women, we conducted a hospital-based case-control study to examine this issue further by evaluating the potential association between the genetic polymorphism of intron 1 (*PvuII* and *XbaI*) of *ER* α gene and breast cancer risk in Korean women.

Materials and methods

The study population was selected from three teaching hospitals located in Seoul, South Korea (Seoul National University Hospital, Borame Hospital and Asan Medical Center) between March 1994 and December

2000. Women with a histopathologically confirmed, incident breast cancer were selected as cases. Controls with no present and previous history of cancer were recruited in the same hospital. Most of eligible controls were being treated for gastrointestinal problems such as acute appendicitis, cholecystitis, gall bladder or bile duct stones, hemorrhoid and inguinal hernia. Women with amenorrhea, previous history of hysterectomy, oophorectomy, hormone replacement therapy, hormone-related diseases such as thyroid disease, and systematic diseases such as diabetic mellitus or chronic liver disease were excluded from both groups. Approximately 21% of cases and 6% of controls eligible were excluded from the study participants because of refusal to participate, failure to interview or blood collection.

Three hundred and six cases and 234 controls were eligible for the study. Each case frequency-matched to one control according to age groups as follows: under 29, 30–34, 35–39, 40–54, 55–69, and over 70 years. Finally, study population consisted of 205 cases and their 205 age-matched referents.

Informed consents were obtained at the time of blood sampling. Information on demographic characteristics, education, marital status, family history of breast cancer in first and second degree relatives, reproduction and menstruation, life style habits, and diet were collected by trained interviewer using a questionnaire.

Blood were collected in 10 ml heparinized tubes and DNA was isolated using standard methods. Details of *ERα PvuII* and *XbaI* restriction fragment length polymorphisms (RFLPs) analysis were described in a previous study [9]. Briefly, in the RFLPs analyses the absence and presence of *PvuII* and *XbaI* restriction sites determined the P and X, and p and x alleles, respectively.

Using standard χ^2 -statistics, we tested if allele frequencies deviated from the Hardy–Weinberg equilibrium. Odds ratios (ORs) and 95% confidence intervals (95% CI) were calculated by unconditional logistic regression model after adjustment for age, education level and family history of breast cancer. To evaluate potential interactive effects between genotypes and other risk factors, the product terms of genotypes and alcohol consumption was added in the logistic model for testing the multiplicative interaction effect of these two variables. Interactions between genotypes and reproductive factors such as age at the first full-term pregnancy, age at menarche and the number of full-term pregnancy were also evaluated.

This study was conducted under approval of the Institutional Review Board of Seoul National University Hospital.

Results

The characteristics of the study populations were similar to those reported in previous studies [10]. The distributions of education, age at full-term pregnancy (FFTP), family history of breast cancer, and alcohol consumption were significantly different between cases and controls (data not shown).

The distribution of *ERα PvuII* and *XbaI* genotypes are shown in Table 1. The *PvuII* and *XbaI* genotype in controls agreed with those previously observed in Korean women [11], but were significantly different from the frequencies observed in a Swedish study [8]: where the prevalence of XX genotype in controls was about 3-fold (10.2%), and the prevalence of PP genotype 2-fold (29.9%) compared with the respective values (3.6 and 13.3%) in our study controls. Allele frequencies of *PvuII* and *XbaI* genotype of controls were not deviated from the Hardy–Weinberg equilibrium.

The *PvuII* genotype distribution did not show any difference between cases and controls, but the *XbaI* X allele containing genotypes showed decreased risk of breast cancer (OR: 0.4, 95% CI: 0.3–0.6) compared with the xx genotypes. This decrease was more attributable to postmenopausal breast cancer risk (OR: 0.3, 95% CI: 0.1–0.5). Combined with *XbaI* and *PvuII*, ORs were 2.4 (95% CI: 1.4–3.9) for xxPP or xxPp genotypes and 2.5 (95% CI: 1.5–4.0) for xxpp genotype compared with genotypes containing X allele, and their increased risks were statistically significant (p for trend <0.001).

When data were stratified by known breast cancer risk factors, nulliparous women or women with first full-term pregnancy at over 30 years of age and with xx genotype were at about 4-fold risk (OR: 4.0, 95% CI: 1.9–8.8) compared to women with X allele containing genotypes and first full-term pregnancy before 29 years (Table 2). No statistically significant multiplicative interaction, however, was observed between the *XbaI* genotypes and age at first full-term pregnancy. The xx genotype carrying drinkers who drink more than once in a week also showed an increased risk of breast cancer (OR: 3.8, 95% CI: 1.9–7.6), but no significant multiplicative interaction was observed.

Table 1. Frequency of *ERα* *XbaI* and *PvuII* genotypes in the study populations

Genotype	All women			Premenopausal women			Postmenopausal women		
	Cases (%) (n = 201)	Controls (%) (n = 195)	Adjusted OR (95% CI)*	Cases (%) (n = 122)	Controls (%) (n = 109)	Adjusted OR (95% CI)*	Cases (%) (n = 79)	Controls (%) (n = 81)	Adjusted OR (95% CI)*
<i>XbaI</i>									
xx	130 (64.7)	86 (44.1)	1.1 (0.4–2.9)	77 (63.1)	52 (47.7)	1.0	53 (67.1)	32 (39.5)	1.0
Xx	60 (29.8)	102 (52.3)	0.4 (0.2–0.6)	39 (32.0)	54 (49.5)	0.8 (0.2–3.4)	21 (26.6)	46 (56.8)	0.2 (0.1–0.4)
XX	11 (5.5)	7 (3.6)	0.9 (0.3–2.6)	6 (4.9)	3 (2.8)	0.4 (0.1–1.7)	5 (6.3)	3 (3.7)	1.1 (0.2–5.0)
xx	130 (64.7)	86 (44.1)	1.0	77 (63.1)	52 (47.7)	1.0	53 (67.1)	32 (39.5)	1.0
XX or Xx	71 (35.3)	109 (55.9)	0.4 (0.3–0.6)	45 (36.9)	57 (52.3)	0.5 (0.3–0.9)	26 (32.9)	49 (60.5)	0.3 (0.1–0.5)
<i>PvuII</i>									
PP	35 (17.4)	26 (13.3)	1.0	21 (17.2)	18 (16.5)	1.0	14 (17.7)	8 (9.9)	1.0
Pp	91 (45.3)	105 (53.9)	0.6 (0.4–1.2)	56 (45.9)	58 (53.2)	0.9 (0.4–1.8)	35 (44.3)	45 (55.5)	0.4 (0.2–1.2)
pp	75 (37.3)	64 (32.8)	0.9 (0.5–1.7)	45 (36.9)	33 (30.3)	1.2 (0.6–2.7)	30 (38.0)	28 (34.6)	0.7 (0.2–1.9)
PP or Pp	126 (62.7)	131 (67.2)	1.0	77 (63.1)	76 (69.7)	1.0	49 (62.0)	53 (65.4)	1.0
pp	75 (37.3)	64 (32.8)	1.3 (0.8–1.9)	45 (36.9)	33 (30.3)	1.4 (0.8–2.4)	30 (38.0)	28 (34.6)	1.3 (0.7–2.6)
Combined genotypes									
<i>XbaI</i> <i>PvuII</i>									
XX, Xx	71 (35.4)	109 (55.8)	1.0	45 (36.9)	57 (52.2)	1.0	26 (32.9)	49 (60.4)	1.0
xx	64 (31.8)	43 (22.1)	2.4 (1.4–3.9)	37 (30.3)	26 (23.9)	1.8 (0.9–3.5)	27 (34.2)	16 (19.8)	3.8 (1.7–8.8)
xx	66 (32.8)	43 (22.1)	2.5 (1.5–4.0)	40 (32.8)	26 (23.9)	1.9 (1.0–3.6)	26 (32.9)	16 (19.8)	3.9 (1.7–9.1)
p for trend			<0.001			<0.05			<0.001

*OR were adjusted for age, education level and family history of breast cancer.

Table 2. Association between *XbaI* genotypes of *ERα* and risk of breast cancer stratified by selected risk factors

Stratified variables	<i>XbaI</i>		<i>p</i> for interaction
	XX, Xx	xx	
	Adjusted OR (95% CI)* (cases/controls)	Adjusted OR (95% CI)* (cases/controls)	
Alcohol consumption			
<1/month	1.0 (reference) (54/91)	2.3 (1.4–3.6) (96/71)	0.97
≥1/month	1.6 (0.8–3.3) (17/18)	3.8 (1.9–7.6) (34/15)	
Age at first full-term pregnancy (years)			
Under 29	1.0 (reference) (58/99)	2.3 (1.5–3.6) (103/75)	0.59
Nulliparous or over 30	2.2 (0.9–5.4) (13/10)	4.0 (1.9–8.8) (26/11)	

*Adjusted for age, education, and family history of breast cancer.

Discussion

Our study indicates the *ERα XbaI* genotype may modify individual breast cancer risk in Korean women, especially in postmenopausal women, whereas *PvuII* genotypes appear not to have any significant role in this context. Our findings agree with a Norwegian case-control study where women with the x allele showed a tendency of increased breast cancer risk [4], while no effect was seen for the *PvuII* genotypes. Similar findings to the Norwegian study arose in another Scandinavian (Swedish) case-control study on the association between endometrial cancer risk and *ERα* polymorphisms [8].

The most interesting finding in this study was that increased risk was observed prominently in postmenopausal women, suggesting that *XbaI* polymorphism may be associated with the breast cancer of late-onset or of onset after menopause. These findings were consistent with a previous study showing the possible linkage of the *ERα* gene polymorphism and late-onset breast cancer [12].

In a Japanese study evaluating the association between *XbaI* and *PvuII* polymorphic sites and bone mineral density in postmenopausal women, Px haplotype of *ERα* intron 1 site was related with low bone mineral density [3]. Because the *XbaI* and *PvuII* polymorphic sites are not located in the coding region of the *ERα* gene, they are not anticipated to have direct functional significance in the respective enzyme activity. However, these polymorphisms may act in several other ways. For instance, receptor function could be affected through differential splicing of mRNA [13, 14]. It is also possible

that they are in linkage disequilibrium with other yet unknown regions in the gene responsible for the disease susceptibility.

A recent study suggested that the age of menarche delayed in women with the XX genotype [15]. This finding is consistent with the epidemiological features of breast cancer, because the age of menarche is related with cumulative lifetime estrogen exposure. Women who experienced menarche before 14 years old had increased risk of breast cancer up to 2.5-folds compared with those who have their menarche after 17 years old in Korean studies [16]. Another study suggested that women with the PP genotype had earlier onset of menopause than women with the pp genotype [17]. So the *ERα* polymorphisms may influence the breast cancer development *via* regulating the time of menarche or menopause. But in our study, there was no difference in the age at menarche or menopause between genotypes.

To conclude, our data provided support to the suggestion that *ERα* gene variants may modify individual breast cancer susceptibility. We are currently seeking for novel *ERα* gene polymorphisms. Future association studies with larger sample size and looking at these newly identified polymorphisms will further strengthen the understanding on *ERα* polymorphism and breast cancer risks.

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