

Toll-like receptor 4 as a predictor of clinical outcomes of estrogen receptor-negative breast cancer in Saudi women

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Abstract: The aim of this study was to investigate the association of the common polymorphisms of Toll-like receptor 4 (TLR-4) with breast cancer development in the Saudi Arabian population. Four TLR-4 polymorphisms (rs2770150, rs10759931, rs10759932, and rs4986790) were studied using 127 breast cancer patients and 117 controls. Relative expression of TLR-4 protein in the breast tumor and the matched normal breast tissues was determined in a large cohort of 70 clinical breast samples in a tissue micro-array format by immunohistochemistry using a specific anti-TLR-4 antibody. Our results demonstrated an increase in TLR-4 expression in estrogen receptor (ER)-, postmenopausal breast cancer patients compared to normal. We also demonstrated that the G allele of single-nucleotide polymorphism *rs10759931* was found to be significantly higher in frequency among patients (36.3%) compared to the control group (26.7%), suggesting that this polymorphism is strongly associated with the development of breast cancer in this ethnic population. In addition, the TLR-4 polymorphism *rs2770150* was shown to be highly correlated with breast cancer in patients over 48 years of age. The TLR-4 polymorphism *rs4986790* was also found to be associated with this malignancy in the ER- patient groups. Our results suggested firstly that the variation in TLR-4 gene expression may influence breast cancer development and secondly a closely linked association between TLR-4 gene polymorphism and ER status. Our study provides support for a better understanding of the implication of TLR-4 polymorphism in breast tumorigenesis and for its eventual use as a cancer biomarker.

Keywords: Toll-like receptor 4, single-nucleotide polymorphisms, breast cancer, Saudi population, innate immunity, estrogen receptor

Introduction

Breast cancer is one of the most common cancers that threaten women's lives around the world, with approximately a 3% chance that a woman will die of breast cancer.¹ Dynamic interplay between tumors and the immune system is essential for tumor survival, growth, and metastasis.² Development of an invasive cancer is the result of genetic and epigenetic changes within the host. Studies provide clear evidence that genetic variants could be implicated in increasing breast cancer risk.^{3,4} The immune system is known to play a major role in preventing tumor progression by recognizing tumor antigens, and dysregulation of immune system activity could contribute to tumorigenesis.⁵ A dynamic association between immune response and breast cancer is important for its progression and incidence.⁶⁻⁸ Recent studies have shown that dysregulation of innate immunity receptors such as Toll-like receptors (TLRs) can promote cancer progression.⁹⁻¹² To date, ten functional TLRs have been identified in humans as playing an active role in innate immunity through inflammatory cytokines

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such as interleukin (IL)-1 and IL-8. TLRs are also expressed in many cancer cells and are known to play a major role in tumor progression through regulating cell proliferation and survival.^{13,14} Of this TLR family, TLR-4 is a major TLR that plays an important role in regulating inflammation and immune responses through activating nuclear factor kappa-light-chain enhancer of activated B cells.¹⁵ This Toll protein is a key receptor for lipopolysaccharide (LPS) from Gram-negative bacteria and is crucial for upregulation of mechanisms of defense against bacterial infections. Several other pathogen-associated molecular patterns, including fusion protein from respiratory syncytial virus and envelope protein from mouse mammary tumor virus, can also stimulate TLR-4 signaling.^{16,17} In addition to activating the MyD88-dependent pathway, TLR-4 is the only TLR that can activate the MyD88-independent pathway via its TLR domain-containing adaptor.¹⁸ TLR-4 has received special attention in cancer research due to its role in tumor progression. It has been previously shown that TLR-4 is expressed in many cancer cells such as human melanoma cells,¹⁹ human gastric cancer cells,²⁰ and human head and neck squamous cell carcinoma.²¹ In addition, TLR-4 has also been linked to breast cancer. Previous studies have demonstrated that TLR-4 depletion leads to increased tumor progression and metastasis in a murine model of breast cancer.⁹ There is evidence that genetic single-nucleotide polymorphisms (SNPs) may cause the impairment of immune responses, and consequently, the development of infectious diseases. The association between the development of infections and chronic inflammation could increase cancer risk. Few associations were observed between TLR genes and risk of developing breast cancer. Several studies highlighted the implication of TLR polymorphisms in pathogenesis of tumors. It was demonstrated that polymorphisms in TLR-2 and TLR-4 were associated with gastric cancer.^{22,23} Increasing bodies of evidence have suggested that TLR polymorphism is closely related to inflammation and may increase the risk of developing gastric malignancy.^{22,24,25} TLR-4 polymorphism was also connected with colon cancer²⁶ and hepatitis C virus-induced hepatocellular carcinoma.²⁷ In addition, a polymorphism in TLR-10, TLR-6, TLR-2, and TLR-1 was shown to be associated with increasing susceptibility of prostate cancer.^{28,29} Other studies have also presented the correlation between TLR-2 polymorphism and papillary thyroid cancer in the Korean population.³⁰ Recently, several studies have demonstrated that the presence of the TLR-4 Asp299Gly polymorphism is associated with a higher frequency of prostate cancer in the North Indian population.³¹ It has also been shown that TLRs are implicated in the progression of polyps to tumors

and that increased metastatic potential of colorectal cancers was correlated with reduced TLR expression.^{31,32} TLR-4 polymorphism rs11536898 has also been shown to be connected with colon cancer.²⁶ The TLR-4 Asp299Gly polymorphism and TLR-2 Thr399Ile polymorphism were also observed to be associated with an increased risk of breast cancer.^{33,34} In addition, TLR-1 and TLR-6 polymorphisms have been linked with increased susceptibility of breast cancer in the African-American population.^{35,36} The present study aims to elucidate the potential correlation of the TLR-4 SNP (*rs2770150*, *rs10759931*, *rs10759932*, and *rs4986790*) with the risk of breast cancer in the Saudi Arabian population.

Materials and methods

Sample collection

Blood samples were collected from 127 subjects with histologically confirmed breast cancer, recruited among patients from King Faisal Medical City (KFMC) in Riyadh, Kingdom of Saudi Arabia (KSA). A detailed description of the breast cancer population is shown in Table 1. All subjects provided written informed consent to participate in the study and to approve the use of their biological samples for genetic analyses. The design of the study was approved by the local Ethics Committee (number 15-089E) from KFMC, Riyadh. Study subjects provided information on their lifestyle habits, diabetes, and family/personal history of cancer via a structured questionnaire in accordance with the guidelines of the Ethics Committee at KFMC in Riyadh, KSA, to determine demographic characteristics and potential risk factors for breast cancer development. The immunohistochemical (IHC) assay was performed on the fresh tissue samples. The genomic DNA was extracted from blood samples for genotyping.

IHC array

IHC was performed on 3- to 5-mm thick sections obtained from formalin-fixed tissue embedded in paraffin. Histopathological

Table 1 Clinical characteristics of study subjects

Variable	Characteristic	Patients	Controls
Total	–	127	116
Age (years)	<48	45	62
(median age, 48±8.2)	>48*	82	54
ER status	ER+	76	–
	ER–	49	–
PR status	PR+	71	–
	PR–	55	–
HER status	HER+	49	–
	HER–	78	–

Note: * χ^2 analysis showed significant difference between cases and controls.

Abbreviations: ER, estrogen receptor; PR, progesterone receptor; HER, human epidermal growth factor receptor.

representative tumor areas were defined on hematoxylin/eosin-stained sections. The array blocks were obtained as described elsewhere.³⁷ About 5- μ m sections from each tumor tissue block were consecutively cut with a microtome (Leica Microsystems GmbH, Wetzlar, Germany). Once the slides were ready, they were incubated for 15–20 minutes in a hot air oven at 60°C. Anti-TLR-4 antibody (H-80, sc-10741; Santa Cruz Biotechnology, CA, USA) was used at 1/100 dilution. Different steps and analyses of IHC were then performed as previously described by Semlali et al.³⁸

DNA extraction

Three hundred microliters of whole blood was used to extract genomic DNA by using DNA Blood Mini Kit (Qiagen, Qilden, Germany) according to the manufacturer's instructions. After equilibration of blood at room temperature with protease, the blood samples were incubated at 56°C for 10 minutes. Appropriate volume of absolute ethanol was added, and the mixture was spun through the column. The column membrane was washed, and the DNA was eluted with 100 μ L elution buffer. The concentration and the purity of DNA were determined by NanoDrop 800 spectrophotometer (Thermo Fisher Scientific).

Genotyping

TLR-4 SNPs (*rs2770150*, *rs10759931*, *rs10759932*, and *rs4986790*) were assessed using TaqMan assay as previously described.³⁹ The positional information of the SNPs is described in Table S1. For this purpose, about 10 ng of DNA from each sample was used per reaction with 5.6 μ L of 2X Universal Master Mix and 200 nM primers. All genotypes were determined by using an ABI 7500 real-time PCR machine.

Statistical analysis

As described previously by Semlali et al.,³⁸ genotype and allelic frequencies were compared using Fisher's exact test (two-tailed) to calculate the χ^2 value with Yates corrections, and allelic odds ratios (ORs) with 95% confidence intervals (CIs). Statistical analysis was performed using SPSS (Statistical Package for the Social Sciences) 16.0 software for Windows.

Results

Analysis of clinical data parameters

A total of 127 breast cancer cases and 117 healthy controls were enrolled in the study. The clinical characteristics of the patients, including age, nationality, estrogen receptor (ER) status, family history, and stage of breast cancer, were recorded and compared to the control patients. The study population was divided into two age groups: under 48 years and over 48 years (Table 1).

Evaluation of expression of TLR-4 protein in breast cancer tissues

TLR-4 has been reported as an indicator of various types of cancers. In the present study, we investigated whether the expression of TLR-4 in breast cancer has any prognostic value in the Saudi population and whether TLR-4 expression is related to the TLR-4 polymorphism specially located in the regulatory regions (promoter and 5' upstream). The expression of TLR-4 protein in breast cancer and normal tissues was determined in a large cohort of 70 clinical breast samples in a tissue micro-array format by IHC. As shown in Figure 1, the levels of TLR-4 protein were very low in normal breast tissues. The strength of positive staining gradually increased from ER- premenopausal patients in situ to postmenopausal patients (Figure 1). The expression of TLR-4 was found to be significantly associated with clinical parameters such as ER- pre- or postmenopausal age.

Interaction between TLR-4 polymorphism (*rs2770150*, *rs10759931*, *rs10759932*, and *rs4986790*) and breast cancer risk in the study populations

DNA samples obtained from the blood of 127 breast cancer patients and 117 healthy controls were included in this study. Distribution of TLR-4 SNPs genotype and allele frequencies in breast cancer cases and control population are given in Table 2. Four TLR-4 SNPs (*rs2770150* T/C, *rs10759931* A/G, *rs10759932* T/C, and *rs4986790* A/G) were genotyped and tested for the Hardy-Weinberg equilibrium. The distribution of alleles and genotypes and the association analysis are reported in Table 2. The data for three TLR-4 SNPs, *rs2770150*, *rs10759932*, and *rs4986790*, located in the promoter, did not present any correlation with breast cancer in the Saudi population (Table 2). However, the frequencies of *rs10759931* SNP (Asp299Gly) in breast cancer cases were significantly different from the healthy controls. The G allele was found to be significantly higher in frequency among the patients (36%) compared to the control group (27%) (Table 2). These data suggested that TLR-4 Asp299Gly SNP is strongly associated with increased susceptibility to breast cancer in the Saudi Arabian population.

Link between pre- and postmenopause status and the genotype frequencies of TLR-4 gene polymorphism in breast cancer patients

The analysis of the TLR-4 genotype distribution after correlation with age indicated that the median age of onset of

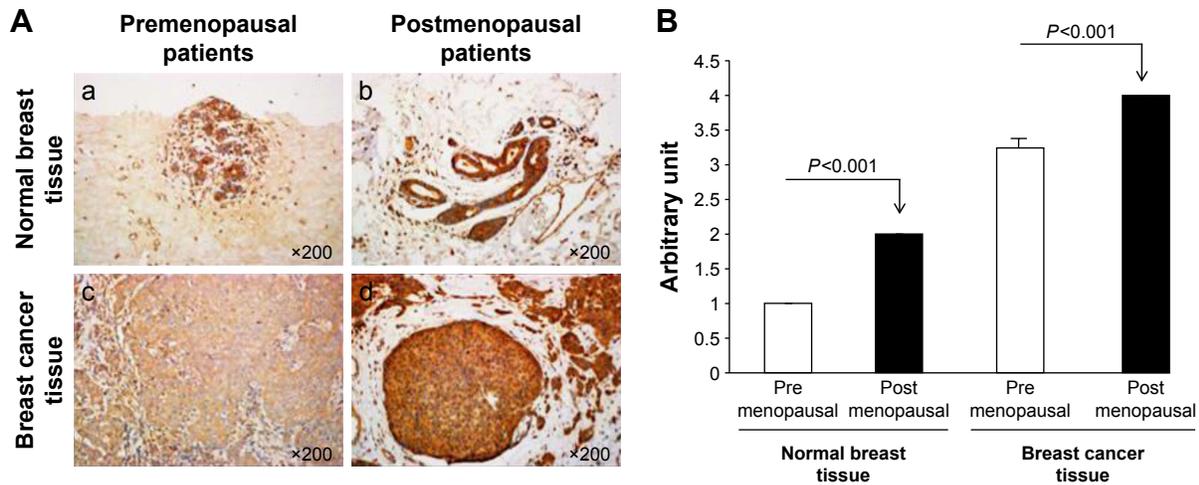


Figure 1 Immunohistochemical determination of TLR-4 protein expression in normal and breast cancer tissues. **(A)** Representative sections ($\times 200$) of positive immunostaining of TLR-4 protein expression in normal breast tissues (a and b) and ER- breast cancer tissues (c and d). The staining of samples from ER- premenopausal patients is illustrated in (a and c) and from ER- postmenopausal patients in (b and d). Tissues were immunostained using specific TLR-4 antibodies. **(B)** TLR-4 positive staining was estimated as follows: 0 point, no positive staining; 1 point, $<20\%$ positive staining; 2 points, $21\%–50\%$ positive staining; 3 points, $51\%–75\%$ positive staining; and 4 points, $>75\%$ positive staining.

Abbreviations: TLR-4, Toll-like receptor 4; ER, estrogen receptor.

breast cancer patients included in the study was 48 years. To investigate the association of TLR-4 SNPs with a younger age at diagnosis of breast cancer, we classified the patients as aged ≤ 48 or >48 years. The genotype distribution for the

individual SNP along with the statistical analysis is given in Tables 3 and 4. Interestingly, patients over 48 years of age showed higher numbers of the C allele of SNP rs2770150 than healthy subjects (43% versus 28%, respectively)

Table 2 Frequencies of TLR-4 gene polymorphism in breast cancer

Polymorphism	Patients	Control	OR	CI	χ^2	P-value
rs2770150						
T	154 (0.62)	87 (0.70)	Ref			
C	96 (0.38)	37 (0.30)	1.466	0.924–2.325	2.65	0.10347
TT	53 (0.42)	32 (0.52)	Ref			
TC	48 (0.38)	23 (0.37)	1.260	0.649–2.445	0.47	0.49409
CC	24 (0.19)	7 (0.11)	2.070	0.801–5.349	2.31	0.12850
TC + CC	72 (0.58)	30 (0.48)	1.449	0.786–2.671	1.42	0.23360
rs10759931						
G	91 (0.36)	62 (0.27)	Ref			
A	161 (0.64)	170 (0.73)	0.645	0.438–0.951	4.92	0.02650*
AA	13 (0.10)	8 (0.07)	Ref			
GA	65 (0.52)	46 (0.40)	0.870	0.334–2.267	0.08	0.77488
GG	48 (0.38)	62 (0.53)	0.476	0.183–1.242	2.37	0.12407
GA + GG	113 (0.90)	108 (0.93)	0.644	0.257–1.615	0.89	0.34496
rs10759932						
T	39 (0.15)	43 (0.19)	Ref			
C	213 (0.85)	179 (0.81)	1.312	0.814–2.113	1.25	0.26348
CC	4 (0.03)	6 (0.05)	Ref			
TC	31 (0.25)	31 (0.28)	1.500	0.385–5.842	0.34	0.55712
TT	91 (0.72)	74 (0.67)	1.845	0.502–6.781	0.87	0.35034
TC + TT	122 (0.97)	105 (0.95)	1.743	0.479–6.343	0.73	0.39396
rs4986790						
A	238 (0.97)	216 (0.94)	Ref			
G	8 (0.03)	14 (0.06)	0.519	0.213–1.260	2.17	0.14099
AA	115 (0.93)	101 (0.88)	Ref			
AG	8 (0.07)	14 (0.12)	0.502	0.202–1.245	2.28	0.13127
GG	0 (0.00)	0 (0.00)	0.879	0.017–44.691	–	1
AG + GG	8 (0.07)	14 (0.12)	0.502	0.202–1.245	2.28	0.13127

Note: *Statistically significant ($P < 0.05$).

Abbreviations: TLR-4, Toll-like receptor 4; OR, odds ratio; CI, confidence interval; Ref, reference.

Table 3 Genotype frequencies of TLR-4 in breast cancer patients aged <48 years versus control

Polymorphism	Patients	Control	OR	CI	χ^2	P-value
rs2770150						
TT	22 (0.51)	32 (0.52)	Ref			
TC	17 (0.40)	23 (0.37)	1.075	0.469–2.464	0.03	0.86410
CC	4 (0.09)	7 (0.11)	0.831	0.217–3.184	0.07	0.78709
TC + CC	21 (0.49)	30 (0.48)	1.018	0.468–2.217	0.00	0.96380
T	61 (0.71)	87 (0.70)	Ref			
C	25 (0.29)	37 (0.30)	0.964	0.527–1.763	0.01	0.90438
rs10759931						
AA	6 (0.14)	5 (0.08)	Ref			
GA	21 (0.48)	25 (0.40)	0.700	0.187–2.623	0.28	0.59564
GG	17 (0.39)	32 (0.52)	0.443	0.118–1.665	1.50	0.22104
GA + GG	38 (0.86)	57 (0.92)	0.556	0.158–1.950	0.86	0.35400
G	33 (0.38)	35 (0.28)	Ref			
A	55 (0.63)	89 (0.72)	0.655	0.366–1.173	2.03	0.15402
rs10759932						
CC	0 (0.00)	4 (0.07)	Ref			
TC	11 (0.25)	13 (0.22)	7.667	0.372–158	3.02	0.08226
TT	33 (0.75)	41 (0.71)	7.265	0.378–139.78	3.09	0.07868
TC + TT	44 (1.00)	54 (0.93)	7.349	0.38–140.18	3.16	0.07554
T	11 (0.13)	21 (0.18)	Ref			
C	77 (0.88)	95 (0.82)	1.547	0.703–3.406	1.19	0.27574
rs4986790						
AA	41 (0.93)	53 (0.85)	Ref			
AG	3 (0.07)	9 (0.15)	0.431	0.110–1.694	1.52	0.21775
GG	0 (0.00)	0 (0.00)	1.289	0.025–66.34	–	1
AG + GG	3 (0.07)	9 (0.15)	0.431	0.110–1.694	1.52	0.21775
A	85 (0.97)	115 (0.93)	Ref			
G	3 (0.03)	9 (0.07)	0.451	0.119–1.716	1.43	0.36680

Abbreviations: TLR-4, Toll-like receptor 4; OR, odds ratio; CI, confidence interval; Ref, reference.

(OR 1.985; 95% CI 1.177–3.346 and $P=0.00956$). The prevalence of the homozygous CC of the same SNP was also significantly increased in the patient group compared to the control group (24% versus 2%, respectively) (Table 4). However, we did not find any association between this SNP and the subpopulation of patients <48 years of age (Table 3). Additionally, no significant difference in the distribution of genotypes between patients and healthy controls for both subpopulations was observed ($P>0.05$) for the other three SNPs (*rs10759931*, *rs10759932*, and *rs4986790*; Tables 3 and 4).

Association between the genotype frequencies of TLR-4 gene polymorphism and ER status

We next wanted to evaluate the association of breast cancer risk with the individual SNPs based on the patient's ER status. The genotype distributions in the ER+ and the ER– breast cancer patient groups were compared with those of the ER+ and ER– control subjects, respectively (Tables 5 and 6). Interestingly, in the ER– group, the AA genotype of

SNP *rs4986790* presented a frequency that was significantly higher in the patients than in the controls (98% versus 88%, respectively). Similarly, the genotype AG was significantly less frequent in the cases compared to the controls (2% versus 12%, respectively) (OR 0.16; 95% CI 0.020–1.257 and $P=0.04860$) (Table 5). However, this SNP was not associated with breast cancer in the ER+ group (Table 6). For SNPs *rs2770150*, *rs10759931*, and *rs10759932*, no significant difference in the distribution of genotypes between affected and non-affected ER+ and ER– status was observed ($P>0.05$) (Tables 5 and 6).

Discussion

TLR-4 activation has been previously shown to promote tumor progression and chemoresistance in breast cancer,^{40,41} whereas impairment of the TLR-4 signaling pathway can reduce breast cancer growth and prolong survival.⁹ Our hypothesis is that TLR-4 plays an important role in activating innate immune system and that dysregulation of this receptor compromises the immune surveillance leading to breast cancer progression and metastasis. Using a Saudi

Table 4 Genotype frequencies of TLR-4 in breast cancer patients aged >48 years versus control

Polymorphism	Patients	Control	OR	CI	χ^2	P-value
rs2770150						
TT	31 (0.38)	25 (0.46)	Ref			
TC	31 (0.38)	28 (0.52)	0.893	0.429–1.860	0.09	0.76214
CC	20 (0.24)	1 (0.02)	16.129	2.022–128.63	10.86	0.00098*
TC + CC	51 (0.62)	29 (0.54)	1.418	0.707–2.847	0.97	0.32487
T	93 (0.57)	78 (0.72)	Ref			
C	71 (0.43)	30 (0.28)	1.985	1.177–3.346	6.71	0.00956*
rs10759931						
AA	7 (0.09)	3 (0.06)	Ref			
GA	44 (0.54)	21 (0.39)	0.898	0.211–3.824	0.02	0.88421
GG	31 (0.38)	30 (0.56)	0.443	0.105–1.874	1.27	0.25966
GA + GG	75 (0.91)	51 (0.94)	0.630	0.156–2.552	0.42	0.51459
G	58 (0.35)	27 (0.25)	Ref			
A	106 (0.65)	81 (0.75)	0.609	0.355–1.046	3.26	0.07113
rs10759932						
CC	4 (0.05)	2 (0.04)	Ref			
TC	20 (0.24)	18 (0.34)	0.556	0.091–3.405	0.41	0.52111
TT	58 (0.71)	33 (0.62)	0.879	0.153–5.059	0.02	0.88489
TC + TT	78 (0.95)	51 (0.96)	0.765	0.135–4.329	0.09	0.76106
T	28 (0.17)	22 (0.21)	Ref			
C	136 (0.83)	84 (0.79)	1.272	0.684–2.367	0.58	0.44696
rs4986790						
AA	74 (0.94)	48 (0.91)	Ref			
AG	5 (0.06)	5 (0.09)	0.649	0.178–2.360	0.44	0.50871
GG	0 (0.00)	0 (0.00)	0.651	0.013–33.359	–	1
AG + GG	5 (0.06)	5 (0.09)	0.649	0.178–2.360	0.44	0.50871
A	153 (0.97)	101 (0.95)	Ref			
G	5 (0.03)	5 (0.05)	0.660	0.186–2.338	0.42	0.52871

Note: *Statistically significant ($P < 0.05$).

Abbreviations: TLR-4, Toll-like receptor 4; OR, odds ratio; CI, confidence interval; Ref, reference.

Table 5 Genotype frequencies of TLR-4 in ER– breast cancer patients versus control

Polymorphism	Patients	Control	OR	CI	χ^2	P-value
rs2770150						
TT	23 (0.47)	32 (0.52)	Ref			
TC	18 (0.37)	23 (0.37)	1.089	0.481–2.465	0.04	0.83819
CC	8 (0.16)	7 (0.11)	1.590	0.505–5.008	0.63	0.42612
TC + CC	26 (0.53)	30 (0.48)	1.206	0.569–2.553	0.24	0.62478
T	64 (0.65)	87 (0.70)	Ref			
C	34 (0.35)	37 (0.30)	1.249	0.709–2.201	0.59	0.44120
rs10759931						
AA	5 (0.10)	8 (0.07)	Ref			
GA	26 (0.53)	46 (0.40)	0.904	0.268–3.052	0.03	0.87128
GG	18 (0.37)	62 (0.53)	0.465	0.135–1.596	1.53	0.21603
GA + GG	44 (0.90)	108 (0.93)	0.652	0.202–2.102	0.52	0.47117
G	36 (0.37)	62 (0.27)	Ref			
A	62 (0.63)	170 (0.73)	0.628	0.380–1.039	3.31	0.06899
rs10759932						
CC	1 (0.02)	6 (0.05)	Ref			
TC	12 (0.24)	31 (0.28)	2.323	0.252–21.372	0.58	0.44610
TT	36 (0.73)	74 (0.67)	2.919	0.339–25.162	1.04	0.30897
TC + TT	48 (0.98)	105 (0.95)	2.743	0.321–23.415	0.92	0.33752
T	14 (0.14)	43 (0.19)	Ref			
C	84 (0.86)	179 (0.81)	1.441	0.748–2.779	1.20	0.27328
rs4986790						
AA	45 (0.98)	101 (0.88)	Ref			
AG	1 (0.02)	14 (0.12)	0.160	0.020–1.257	3.89	0.04860*
GG	0 (0.00)	0 (0.00)	2.231	0.044–114.18	–	1
AG + GG	1 (0.02)	14 (0.12)	0.160	0.020–1.257	3.89	0.04860*
A	91 (0.99)	216 (0.94)	Ref			
G	1 (0.01)	14 (0.06)	0.170	0.022–1.308	3.70	0.07686

Note: *Statistically significant ($P < 0.05$).

Abbreviations: TLR-4, Toll-like receptor 4; ER, estrogen receptor; OR, odds ratio; CI, confidence interval; Ref, reference.

Table 6 Genotype frequencies of TLR-4 in ER+ breast cancer patients versus control

Polymorphism	Patients	Control	OR	CI	χ^2	P-value
rs2770150						
TT	30 (0.41)	32 (0.52)	Ref			
TC	29 (0.39)	23 (0.37)	1.345	0.642–2.819	0.62	0.43208
CC	15 (0.20)	7 (0.11)	2.286	0.819–6.378	2.56	0.10973
TC + CC	44 (0.59)	30 (0.48)	1.564	0.792–3.090	1.67	0.19662
T	89 (0.60)	87 (0.70)	Ref			
C	59 (0.40)	37 (0.30)	1.559	0.940–2.586	2.97	0.08483
rs10759931						
AA	8 (0.11)	8 (0.07)	Ref			
GA	38 (0.51)	46 (0.40)	0.826	0.283–2.408	0.12	0.72614
GG	29 (0.39)	62 (0.53)	0.468	0.160–1.370	1.98	0.15965
GA + GG	67 (0.89)	108 (0.93)	0.620	0.222–1.731	0.84	0.35839
G	54 (0.36)	62 (0.27)	Ref			
A	96 (0.64)	170 (0.73)	0.648	0.417–1.009	3.71	0.05419
rs10759932						
CC	3 (0.04)	6 (0.05)	Ref			
TC	18 (0.24)	31 (0.28)	1.161	0.258–5.219	0.04	0.84527
TT	54 (0.72)	74 (0.67)	1.459	0.349–6.096	0.27	0.60244
TC + TT	72 (0.96)	105 (0.95)	1.371	0.332–5.662	0.19	0.66126
T	24 (0.16)	43 (0.19)	Ref			
C	126 (0.84)	179 (0.81)	1.261	0.728–2.184	0.69	0.40678
rs4986790						
AA	68 (0.91)	101 (0.88)	Ref			
AG	7 (0.09)	14 (0.12)	0.743	0.285–1.936	0.37	0.54160
GG	0 (0.00)	0 (0.00)	1.482	0.029–75.574	–	1
AG + GG	7 (0.09)	14 (0.12)	0.743	0.285–1.936	0.37	0.54160
A	143 (0.95)	216 (0.94)	Ref			
G	7 (0.05)	14 (0.06)	0.755	0.298–1.917	0.35	0.55367

Abbreviations: TLR-4, Toll-like receptor 4; ER, estrogen receptor; OR, odds ratio; CI, confidence interval; Ref, reference.

population, we demonstrated that TLR-4 is overexpressed in ER–, postmenopausal breast cancer patients compared to normal controls. Thus, an increase in TLR-4 could be seen as a biological indicator of potential cancer in ER–, postmenopausal patients. Interestingly, the presence of a higher level of TLR-4 protein in breast cancer tissue supports previous studies reporting an overexpression of TLR-4 in various types of cancers, including gastric cancer,⁴² breast cancer,^{40,41,43} colon cancer,^{38,43} and ovarian cancer.⁴⁴ Higher TLR-4 expression was also shown to be significantly associated with invasive ductal carcinoma, one of the most common types of breast cancer.⁴⁵ Evidence has demonstrated that TLR-4 activation promotes tumor cell adhesion and metastasis.^{46,47} Injection of 4T1 tumor cells into TLR-4–/– mice leads to increased tumor volume and lung metastasis.⁹ In agreement with these studies, we suggest that high activation of TLR-4 in breast cancerous tissues may promote tumor growth and resistance to apoptosis.

Genetic alterations in the TLR pathway are also known to be associated with an increased risk of developing breast cancer.⁴⁸ This is the first study investigating the role of several common TLR-4 polymorphisms in susceptibility to

breast cancer in Saudi Arabia. We identified that the TLR-4 polymorphism *rs10759931* could be a risk factor for this disease in the Saudi Arabian population. This polymorphism affects the population regardless of ER status or age group. In contrast, the TLR-4 polymorphism *rs2770150* is correlated with breast cancer in patients 48 years and older, which is in agreement with the decreased levels of female sex hormones during the postmenopausal period. However, Marino⁴⁹ has linked the crucial role of estrogen and progesterone in protecting against colon cancer particularly in women patients.^{49–52} Our previous study showed that TLR-4 *rs2770150* is associated with colon cancer in postmenopausal Saudi women.³⁸ The *TLR-4* polymorphism *rs4986790* is associated with this malignancy in the ER– patient groups. These two SNPs were shown to be strongly associated with prostate cancer⁵³ and gastric cancer⁵⁴ in other studies and in other populations. TLR-4 *rs4986790* is the most common polymorphism, which causes an amino acid exchange (aspartate to glycine) at position 299 (Asp200Gly) located within the extracellular domain of the receptor. This polymorphism causes a significant local conformational change at the D299G site,⁵⁵ which may abolish ligand binding,

and consequently, impair the TLR-4 signaling response to LPS.⁵⁶ This polymorphism was also shown to be associated with an increased risk of breast cancer.³³ Recently, we have demonstrated that these same TLR-4 SNPs were associated with TLR-4 expression and colon cancer susceptibility in Saudi patients.³⁸ Because TLR-4 plays an active role in the innate immune system, the loss of function of this protein may lead to a depressed immune response, thus promoting cancer development.

In conclusion, our study shows for the first time that TLR-4 polymorphism *rs10759931* is strongly associated with risk of breast cancer in the Saudi population. Our data suggest that genetic variation in TLR-4 may influence the development of this disease. We believe that our study provides support for a better understanding of the implication of TLR-4 polymorphism in breast tumorigenesis and for its eventual use as a cancer biomarker.

Abbreviations

CI, confidence interval; ER, estrogen receptor; IHC, immunohistochemistry; IL, interleukin; KFMC, King Faisal Medical City; KSA, Kingdom of Saudi Arabia; LPS, lipopolysaccharide; OR, odds ratio; SNP, single-nucleotide polymorphism; TLR, Toll-like receptor.

Acknowledgment

This project was supported by the Research Group Program (number RGP-VPP-260) in the KSA.

Disclosure

The authors report no conflicts of interest in this work.

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Supplementary material

Table S1 Characteristics of selected TLR-4 polymorphisms

SNP	Chr/position	Nucleotide change	Region
rs2770150	Chr 9/117700861	-3612T > C	5' upstream
rs10759931	Chr 9/117701869	-2604G > A	Promoter
rs10759932	Chr 9/120465144	-1607T > C	Promoter
rs4986790	Chr 9/117713024	8552A > G	Exon
Asp299Gly			

Abbreviations: TLR-4, Toll-like receptor 4; SNP, single-nucleotide polymorphism; Chr, chromosome.

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