

## Is Angiotensin Converting Enzyme Insertion/Deletion (rs1799752) Polymorphism Associated with Breast Cancer Risk in Egyptian Population?

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### Authors' contributions

*This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.*

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### ABSTRACT

**Background:** According to GLOBOCAN estimates, breast cancer was found to be the most often diagnosed cancer in women worldwide, (11.7 %) and the fourth leading cause of cancer mortality (6.9 %).

**Aim:** The purpose of this study is to investigate the role of the Angiotensin I-converting enzyme (ACE) gene polymorphism in breast cancer prediction risk in Egyptian population.

**Methods:** Polymorphism detection analysis was performed on 163 subjects from breast cancer (BC) patients, 79 with Benign Breast Disease group (BBD) patients and 202 controls (C). ACE I/D (rs1799752) polymorphism were detected using polymerase chain reaction (PCR).

**Results:** The observed genotype frequencies were II 10.9%, ID 78.2% and DD 10.9% in healthy control, II 8.6%, ID 79.1% and DD 12.3% in BC patients and II 12.6%, ID 78.4% and DD 9% in BBD patients. There were no association between ACE gene polymorphisms, between the BC or

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BBD groups when compared to the control group ( $OR_{DD} = 1.43$ , 95 % CI= (0.58-3.52),  $P = 0.29$ ) and ( $OR_{DD} = 1.29$ , 95 % CI= (0.57-2.95),  $P = 0.37$ ) respectively. There was no risk estimate in BC or BBD when DD vs II + ID (Recessive) or ID vs II+ DD (Over-dominant) were compared to control. Allele frequencies show the same figure. From the different histological BC hormonal markers the Her2 was showing significant association in ID genotype of ACE I/D (rs1799752) ( $P = 0.04$ ) and dominant model (II vs ID + DD,  $P = 0.03$ ). Concerning different BC prognostic models, the poor prognostic one of Her2 enriched model ( $ER^{-ve} PR^{-ve} Her2^{+ve}$ ) show significant association in ACE genotype ID and dominant model (II vs ID + DD), ( $P = 0.01$ ) when compared to the good prognostic hormonal status.

**Conclusion:** It seems that this is the first study that interested in correlate the ACE gene polymorphisms in different BC variants characters in Egyptian patients. ACE I/D (rs1799752) polymorphism ID genotype have strong association to breast cancer carcinogenesis, poor prognosis and metastasis. It may be used as practical biomarker to guide the BC carcinogenesis and risk process.

**Keywords:** Breast cancer; ACE; polymorphism; genotypes; risk factor.

## ABBREVIATIONS

BC : Breast Cancer  
 BBD : Benign Breast Disease  
 C : Controls  
 PCR : Polymerase Chain Reaction method  
 OR : Odds Ratio  
 CI : 95% Confidence Intervals  
 Her2 : Human epidermal growth factor receptor 2  
 ER : estrogen receptor  
 PR : progesterone receptor  
 RAS : Renin–Angiotensin System  
 ACE : angiotensin converting enzyme  
 SNPs : single nucleotide polymorphism  
 IRB : Institutional Review Board  
 NPI : the Nottingham Prognostic Index  
 GPI : Good Prognostic Index  
 MPI : Moderate Prognostic Index  
 PPI : Poor Prognostic Index  
 TNBC : Triple Negative BC

## 1. INTRODUCTION

Breast cancer (BC) is the most often diagnosed malignancy worldwide. Every year, more than two million new instances of BC are diagnosed, accounting for 11.7 percent of all cancer diagnoses. BC is shown to be the leading cause of death in women, accounting for 6.9% of all cancer fatalities. Female BC death rates were higher in transitioning nations (15.0 to 12.8 per 100,000 cases) than in transitioned countries [1]. Breast cancer is the most common cancer among Egyptian women, accounting for more than (32%), with a three-fold increase expected by 2050, according to the National Cancer Institute (NCI) of Egypt [2]. Egypt has a lower incidence of BC than the United States and other

Western cultures, but Egyptian BC patients have a higher fatality rate. In Egyptian women, BC is the second largest cause of cancer death. Patients with no family history of BC account for 85 percent of all diagnosed BC in Egypt. This could be explained by genetic alterations that develop as a result of ageing or a certain lifestyle, with a proclivity for younger age groups with advanced stages [3- 5]. BC arises as a result of complex interplay between genetic and risk factors. Patients' clinical characteristics, such as tumour size, estrogen receptor (ER), progesterone receptor (PR), and human epidermal growth factor receptor 2 (Her2) status, were assessed using a variety of traditional pathological indicators. A unique diagnostic and therapeutic regimen should be used to identify high-risk patients at the earliest possible time. Increased response to neo-adjuvant and adjuvant chemotherapy has been shown in patients with significant immune infiltration [6,7]. Single nucleotide polymorphism (SNP) is a common genetic variation that has an impact on biological function [8]. The renin–angiotensin system (RAS) regulates sodium balance, extracellular fluid volume, and systemic vascular resistance [9,10], as well as the cardiovascular system and homeostasis. It has been found to be expressed in a variety of cancers, including BC [11,12]. ACE regulates tumour cell proliferation, invasion, angiogenesis, and aggressive behaviour and is variably regulated in a variety of cancers. Overexpression of the ACE gene has been observed in a variety of neoplastic transformations and angiogenesis [13–15].

The ACE, a cell surface zinc metalloenzyme, dipeptidyl carboxypeptidase is considering a member of RAS system. It involves in catalyzing

the conversion of angiotensin I (Ang I) into a physiologically active octa-peptide angiotensin II (Ang II) is another emerging candidate marker for tumorigenesis [16,17]. The ACE gene (Gene ID: 1636; also known as: DCP; ACE1; DCP1; CD143) is localized in human chromosomes 17q23, and composed of 26 exons and 25 introns, spans about 21 kb and more than 13 polymorphisms in this gene have been identified with susceptibility to different disease such as ACE I/D (rs1799752), A240A>T (rs4291), 2350G>A (rs4344), and 17888C>T (rs4359) [18]. The ACE insertion/deletion (I/D) polymorphism is a nonsense and 287 bp Alu repetitive sequence of DNA in the intron 16 of ACE gene, which represented by "Insertion" or "I", and absence of the same denotes "Deletion" or "D" [19]. Thus, patients can be of three genotypes with regard to ACE, namely, II, ID and DD. Homozygotes for the D allele have the greatest ACE plasma levels, followed by ID heterozygotes and homozygotes for the I allele [20,21].

Several research have looked into the link between the ACE I/D polymorphism and the risk of breast cancer. However, due to the small sample size, the results are varied and unclear, with some research finding a significant link while others did not. Therefore, this study is performed to investigate the role of the ACE I/D (rs1799752) gene polymorphism in breast cancer prediction risk in Egyptian population.

## 2. MATERIAL AND METHODS

### 2.1 Patients and Controls

BC female patients 163 the median age = 52.7 years, (age range = 27– 80 years). BC patients are classified by different grading systems which influence different prognosis and for diagnosis characters. Histological appearance is usually used to classify BC according grade, stage, node status and metastasis as well operation site [12]. Tumor size, as well as ER, PR, and Her2 statuses, were determined for each patient, and the BC group was then able to link these individual prognostic variables to the ACE I/D polymorphism genotypes. BC patients group have receives no chemo/radiotherapy involvements. NPI, the mandatory Nottingham prognostic index accurately predicts survival in BC patients [22], was calculated for each BC patient. Three prognostic groups were cut-off points separated. They were (NPI of < 3.4) represent the good prognostic index (GPI), (NPI of 3.41–5.4) was performed as the moderate

prognostic index (MPI) and finally the (NPI of > 5.41) were illustrating the poor prognostic index (PPI). The equation used in NPI quantitation is:

$$\text{NPI} = (0.2 \times \text{tumor size}) + \text{Node status} + \text{Grade status}.$$

Another two groups were recruited, Benign Breast Disease group (BBD) of 79 patients and 202 volunteer of control group (C) were recruited as cancer-free and donors of solid organ from Mansoura University with median age of 45.9 years, (age range 36– 63 years).

### 2.2 DNA Extraction and ACE (rs1799752) gene I/D Polymorphism Genotyping

EDTA containing tubes were used to collect blood samples. DNA was extracted from puffy coats. Puffy coats were collected after spin at 2500 g for 9 min at RT from the intermediate layer in-between plasma and red blood cells. DNA extraction was performed according to the commercial kit procedure Promega DNA extraction kit (Promega. USA. A1120).

The ACE I/D (rs1799752) genotypes were determined using the polymerase chain reaction method (PCR) according to the method of Rigat et al., [21]. The sequences of the sense (F) and antisense (R) primers were 5'-CTG GAG ACC ACT CCC ATC CTT TCT-3' and 5'-GAT GTG GCC ATC ACA TTC GTC AGA T-3', respectively prepared by (Eurofins, genomics, Germany). PCR was performed in a final volume of 20 µl that contained 10 µl 2X ViRed Taq Master Mix (vivantis, Malaysia), ≈500 ng of genomic DNA, 12.5 pmol of each primer and 5% dimethylsulphoxide (DMSO). Amplification was performed using a Gene Amp PCR system (Thermo Scientific ARKTIK thermal cycler). Samples were denatured for 7 minute at 94°C and then cycled 30 times through the following steps: 45 seconds at 94°C, 1 minute at 62°C, and 1 minute at 72°C. PCR products (490-bp insertion and 190-bp deletion) were visualized on a 1.5 % agarose- gel containing GelStar™ Nucleic Acid Gel Stain (LONZA, Rockland, ME, USA, Cat No: 50535) (Fig. 1a).

A second PCR amplification was performed for each DD type with a primer pair that recognizes an insertion-specific sequence (sense and antisense primers were 5'- TGG GAC CAC AGC GCC CGC CAC TAC-3'; 5'-TCG CCA GCC CTC CCA TGC CCA TAA-3' respectively), with identical PCR conditions except for an annealing

temperature of 67°C and the absence of 5% DMSO. The PCR product was detected at 330-base pair (Fig. 1b). The consistency and reproducibility of the test were checked by randomly selecting 15% of the DNA samples to repeat the PCR for a second time and confirming that there were no errors in genotyping. The results were completely consistent with the previous ones.

### 2.3 Statistics

Allelic frequencies were calculated using the gene counting approach in all of the study participants. The genotypes and allele frequencies of ACE I/D (rs1799752) in BC patients were compared to BBD and controls using the chi-square test. Odds ratios (OR) and 95 percent confidence intervals were used to assess relative illness risk (CI). The same procedures were used to evaluate the correlation values of histological and clinical data with the ACE I/D (rs1799752) genotypes in BC patients. Using a two-tailed Student's t-test, NPI was quantitatively compared to the ACE I/D (rs1799752) genotypes. At the  $P < 0.05$  level, statistical significance was assumed. The statistical analysis was performed using the SPSS statistical software package version 21.0 for Windows (Chicago, Illinois, USA).

## 3. RESULTS

### 3.1 Distribution of ACE I/D Genotypes (rs1799752) in Different Studied Groups

A total of 242 female breast patients were participated in the study in addition to 202 healthy unrelated individuals from the same locality. The amplified PCR product for ACE I/D (rs1799752) were detected at 490- base pair for insertion and 190- base pair for deletion as shown in (Fig. 1), second PCR amplification was performed for each DD genotype with an insertion-specific sequence detected at 330-base pair (Fig. 2). Based on these results, in different studied groups, the genotypes and the alleles of the ACE I/D genes polymorphism were determined and evaluated in comparison with their respective healthy controls. Results shown in (Table 1), pointed out the frequencies of different genotypes as well as different genetic models which revealed the same frequencies in different genotypes (II, ID and DD) within different studied groups (BC, BBD and C). These frequencies were  $C_{II}$  (10.9%),  $C_{ID}$  (78.2%) and  $C_{DD}$  (10.9%);  $BC_{II}$  (8.6%),  $BC_{ID}$  (79.1%) and

$BC_{DD}$  (12.3%) and  $BBD_{II}$  (12.6%),  $BBD_{ID}$  (78.4%) and  $BBD_{DD}$  (9%). Similarly, the allele frequencies also have the same figure in different studied groups  $C_I$  (50%) and  $C_D$  (50%);  $BC_I$  (48.2%) and  $BC_D$  (51.8%) and  $BBD_I$  (51.9%) and  $BBD_D$  (48.1%).

The data shows no significant differences in BC or BBD groups in different genetic models of ACE I/D (rs1799752) genotype when compared to control group or when both groups were compared together (Table 1). This observation was seen in all genetic models (II vs ID, II vs DD; Co-dominant), (DD+ID vs II; Dominant), (ID vs II + DD; Over-dominant) as well as (DD vs II + ID; Recessive). All these models shows the same OR (95% CI) within different studied groups which gives no significant probability (P) which reveals the lack of the ACE I/D (rs1799752) genes polymorphism in the development of breast cancer.

### 3.2 Distribution of ACE I/D Genotypes (rs1799752) in Different Variant of BC Group

The demographic, clinicopathological, and biomarker parameters of research participants were acquired from patients' medical records and displayed in the graph (Table 2, First Column). Different features listed in the table represent the number and percentage of each variant in relation to the BC group, among these features the predominant cancer stage was stage II (67.5%), node status was N0 (34.4%), cancer grade was grade II (71.2%), tumor size was  $\geq 2$  cm- 5 cm (74.2%), NPI was  $>3.4$ - 5.4 (74.2%), positive ER was (79.9%), positive PR was (76.1%), negative Her2/neu expression was (56.4%), negative metastasis was (85.3%) and left operated breast was (61.3%). Different ACE I/D (rs1799752) genotypes in BC group was 14 (8.6%), 129 (79.1%) and 20 (12.3%) for II, ID and DD genotype respectively.

The distribution of different genotype of ACE I/D (rs1799752) gene in different variables of tumor in breast cancer patients (163 Patients) were detailed in (Table 2). among the predominant of these features ID genotype show the most prevalence genotype in cancer stage was in stage T2 (67.4%), in node status was N0 (37.2%), in cancer grade was grade II (71.3%), in tumor size was (2- 5cm, 73.6%), in NPI was ( $>3.4$ - 5.4, MPI) (73.6%), in positive ER was (82.1%), in positive PR was (76.7%), in negative Her2/neu expression was (56.6%), in negative metastasis was (84.5%) and right operated

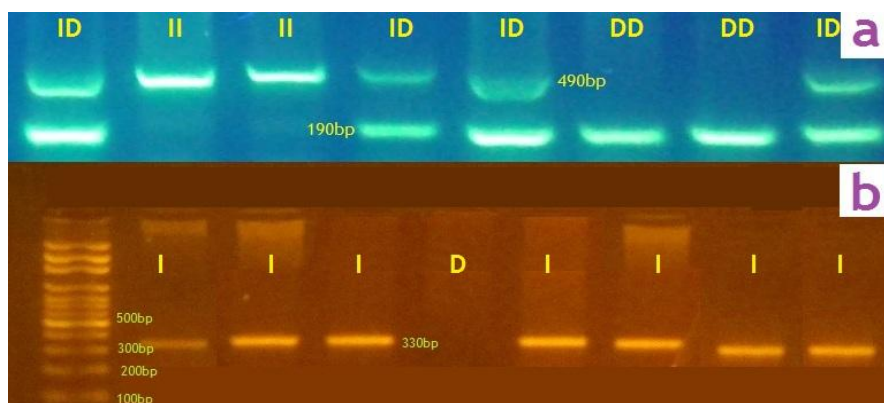
breast was (62%). The II and DD genotypes show mostly the same presentation in different BC characteristic variables of the tumor. II genotype tends to be predominant in the worse variable of T3, N3, G3, negative ER and PR, positive Her2neu, (2- 5cm) tumor size and PPI. Inversely, DD genotype tends to be predominant in the initial variable of T1, N1, G1 tumor size (<2cm) and MPI. Detailed distribution of different genotype of ACE I/D (rs1799752) gene in different variables of tumor in breast cancer patients (163 Patients) were presented in (Table 2).

### 3.3 Association of ACE I/D Genotypes (rs1799752) in Response to Hormonal Status of BC Group

By comparing the different models of ACE I/D (rs1799752) genotype as a risk estimate with different variables of tumor in BC group, results revealed no association with ER, PR, metastasis or operation site (Supplement Tables, (ER) 1, (PR) 2 and (Metastasis) 3). While a significant association in the host ACE I/D (rs1799752) genotype with Her2/neu expression marker, in the co-dominant model (II vs. ID,  $P= 0.04$ , II vs. DD,  $P= 0.07$ ) as well as dominant model (II versus ID+DD,  $P= 0.03$ ) with the negative Her2/neu expression marker, (Table 3). Same figure was noted when look at the Operation Site, where significant association in the host ACE I/D

(rs1799752) genotype with Lt MRM the co-dominant model (II vs. ID,  $P= 0.05$ , II vs. DD,  $P= 0.02$ ) as well as dominant model (II versus ID+DD,  $P= 0.04$ ) (Table 4).

When testing the host ACE I/D (rs1799752) genotype in different BC prognostic models (Salimifard et al., 2020) the very poor prognostic model (Triple -ve model) which show negative expression for different hormonal status (10 cases) as well as other poor prognostic model of luminal B model, ( $ER^{+ve} PR^{+ve} Her2^{+ve}$ ) of hormonal status (55 cases), we found no statistical significant differences within different host ACE I/D (rs1799752) genotype when compared to the good prognostic model (64 cases) hormonal status luminal A model, ( $ER^{+ve} PR^{+ve} Her2^{-ve}$ ), (Supplement Tables 4 and 5) respectively. The same figure with no association of ACE I/D (rs1799752) genotype was noted when Triple -ve model was compared to the poor prognostic hormonal status Her2 enriched model ( $ER^{-ve} PR^{-ve} Her2^{+ve}$ ) model (14 cases), (Supplement Table 6). While a significant association in the host ACE I/D (rs1799752) genotype was noted in the co-dominant model (II vs. ID,  $P= 0.01$ ) as well as dominant model (II versus ID+DD,  $P= 0.02$ ) when the poor prognostic hormonal status Her2 enriched model ( $ER^{-ve} PR^{-ve} Her2^{+ve}$ ) model (14 cases) compared to the good prognostic hormonal status luminal A model, ( $ER^{+ve} PR^{+ve} Her2^{-ve}$ ), (Table 5).



**Fig. 1.** Agarose gel electrophoresis of the ACE I/D (rs1799752) polymorphism showing different ACE genotypes which representative by 1.5 % agarose gel stained with GelStar™ Nucleic Acid Gel Stain and photographed under ultraviolet trans-illumination after PCR amplification with specific primers, a) ACE1, The upper band of 490 bp is representing the (I) allele and the lower band of 190 bp is representing the (D) allele. The II genotype is shown as a single upper band, the DD genotype as a single lower band, and the DI type as a double band. b) ACE2, shows the results of different samples from the 1<sup>st</sup> PCR identified as DD genotype, by using an insertion-specific primer to differentiate if it is real DD or mis-genotype from ID. The sample in lane 1 is the Ladder, the band of 330bp present the I allele in the former mis-typed DD, while the true DD genotype show no band

### 3.4. Distribution of ACE I/D (rs1799752) Genotype According NPI in BC Group

Regarding NPI, the frequency among different ACE I/D (rs1799752) genotype was listed in (Table 6). The significant differences have been noted within different genotypes when using student t- Test. The different NPI were ( $5.05 \pm 0.2$  for II,  $4.68 \pm 0.07$  for ID and  $4.49 \pm 0.16$  for DD) respectively and the significant were ( $P= 0.10$  for II vs ID,  $P= 0.03$  for II vs DD and  $P= 0.3$  for ID vs DD) respectively. When ACE I/D (rs1799752) genotype where tested in response to different hormonal markers, no significance differences were noted in NPI in both ER and PR (Supplement Tables (ER) 7, (PR) 8). While in Her2/neu expression marker, it shows a significant increase in NPI in positive one than the negative ( $P= 0.02$ ) in ID genotype (Table 7). When different ACE I/D (rs1799752) genotypes were tested within different NPI groups MPI and PPI (Supplement Table 9), no significant differences were observed between different ACE I/D (rs1799752) genotypes in each NPI groups. For different hormonal markers, (Table 8) similarly, no significant differences in NPI when negative hormonal markers were compared to positive ones for ER and PR while Her2/neu expression marker show a significant increase in NPI in positive one than the negative ( $P= 0.05$ ).

### 3.5. Distribution of ACE I/D (rs1799752) GENOTYPE ACCORDING METASTASIS in BC Group

Metastasis the most worth complication in BC was detected in 24 patients, where 2 patients show ACE I/D (rs1799752) II genotype (bone metastasis), 20 patients show ID genotype and 2 patients show DD genotype (1 bone and 1 bone & lung metastasis). The most presented metastasis was in bone metastasis presented in 8 cases, bone and LN in 5 cases, lung in 5 cases, bone and liver in 3 cases, bone and lung in 2 cases and another case the metastasis goes to brain, bone and LN. Detailed presentation of different ACE I/D (rs1799752) genotype showing metastasis were presented in (Table 9).

## 4. DISCUSSION

Breast cancer is a complex and multifaceted disease, with the combination of environmental and genetic variables likely playing a role in the

disease's onset and progression. Breast cancer is now well recognised as the most often diagnosed cancer in women worldwide and a leading cause of cancer mortality in women [1]. BC is becoming more common in Egypt, and it remains a huge public health issue with no clear remedy. It accounts for 33% of all female cancer cases, with over 22,000 new cases identified each year [23]. Given the growing population, this is anticipated to increase enormously in the next years. According to the National Cancer Institute (NCI), Egypt [2] a three-fold rise is expected by 2050. RAS is represented by the system of enzymes and hormones which regulate arterial pressure, electrolytic and fluid balance. RAS activation directly or indirectly leads to activation of angiogenesis processes. As far as cancer development, progression and metastasis are associated with angiogenesis and proliferative processes, one may suppose that RAS could be related to cancer development. ACE is well known to be a key part of RAS, the polymorphisms especially I/D in ACE gene has been found to be associated with different diseases including cancer [24,25]. This study aimed to determine the association of the ACE I/D (rs1799752) gene polymorphism in breast cancer prediction risk in Egyptian population.

Analysis of ACE I/D (rs1799752) polymorphism on 163 Egyptian patients with BC, 79 BBD and 202 healthy controls from the same area, showed that the frequencies of different genotypes as well as different genetic models were revealed the same frequencies in different genotypes (II, ID and DD) within different studied groups (BC, BBD and C). the most present predominant genotype is ID where its frequencies was over 75% while the other two genotypes (II and DD) were shared the (20%) left frequency. This finding in concise with Sharma and coworker, [26], where they found that ID genotype was conferring approximately 2.5 folds risk for BBD and ACE polymorphism was projecting a protective role towards BC susceptibility.

The connection of the angiotensin converting enzyme insertion/deletion (ACE I/D) polymorphism with breast cancer has been studied in a number of meta-analysis studies. However, the outcomes are still up for debate. Some evidence suggests that the ACE I/D polymorphism is linked to an increased risk of breast cancer. ACE I/D has been linked to BC in general and by ethnicity [24,25], particularly among Asians and Caucasians [24,25]. To

further validate the apparent association, well-designed research with a bigger sample size and more ethnic groups are required. In agreement of the present results, a lack of association between ACE I/D (rs1799752) gene polymorphism and breast cancer risk was reported from different ethnic background like Ukraine [27], Pakistani [13], Indian [12,26] as well as Egyptians [11]. Although all these studies were in agree with the present results, all were lacking a good statistically participating numbers. In the present study, we correlate ACE I/D (rs1799752) gene polymorphism with different tumor characters, hormonal analysis and Predictive Index (NPI). DD genotype was found to be more present in the initially primitive cancer characters like cancer stage, grade and node status. Inversely it was more present in the worth hormonal receptor status. The present study observe that the ID genotype of ACE I/D (rs1799752) polymorphism

is the most predominant in different BC variant like grad and stage, while, the different ethnic Brazilian observes that DD genotype is the most predominant [28], this may be they did not perform the second PCR to differentiate the mistyping DD genotype.

No association has been noted with ACE I/D (rs1799752) gene polymorphism in response to negative vs positive ER or PR hormonal status or metastasis, while the human epidermal growth factor receptor 2 (Her2) show a significant association to ACE I/D (rs1799752) genotype (P= 0.04, 0.03) in the co-dominant model as well as dominant model (II vs. ID and II versus ID+DD) respectively. This confirms the association of ID genotype with the aggressiveness type of BC. When analyzing different prognostic model a significant association in ACE I/D (rs1799752) genotype

**Table 1. Distribution of different genotype of ACE I/D (rs1799752) with risk estimate and allele frequencies in control, BC and BBD groups in different ACE genetic models**

ACE Genotype	Group's # (%)		
	Control (202)	BC (163)	BBD (79)
II	22 (10.9)	14 (8.6)	10 (12.6)
ID	158 (78.2)	129 (79.1)	62 (78.4)
DD	22 (10.9)	20 (12.3)	7 (9)
Allele			
I	202 (50)	157 (48.2)	82 (51.9)
D	202 (50)	169 (51.8)	76 (48.1)
Statistics	DD+ID vs II (Dominant)		BC vs BBD
OR	1.3	1.13	1.31
95% CI	(0.64- 2.63)	(0.65- 1.96)	(0.79- 2.2)
Sig. (P)	0.29	0.4	0.22
	DD vs II + ID (Recessive)		BC vs BBD
OR	0.87	1.26	1.38
95% CI	(0.46- 1.66)	(0.51- 3.07)	(0.55- 3.42)
Sig. (P)	0.4	0.4	0.32
	ID vs II + DD (Over-dominant)		BC vs BBD
OR	0.95	0.98	1.04
95% CI	(0.57- 1.58)	(0.52- 1.85)	(0.54- 2)
Sig. (P)	0.47	0.55	0.51
	D allele vs I allele		BC vs BBD
OR	1.07	1.05	1.11
95% CI	(0.8- 1.44)	(0.81- 1.38)	(0.85- 1.43)
Sig. (P)	0.34	0.38	0.25
	II vs ID (Co-dominant)		BC vs BBD
OR	1.28	0.86	1.28
95% CI	(0.63- 2.61)	(0.39- 1.93)	(0.76- 2.15)
Sig. (P)	0.3	0.43	0.25
	II vs DD		BC vs BBD
OR	1.43	1.29	1.6
95% CI	(0.58- 3.52)	(0.57- 2.95)	(0.73- 3.55)
Sig. (P)	0.29	0.37	0.18

**Table 2. Characteristic frequency of tumor characters in breast cancer patients (163 Patients, first column). Distribution of different genotype of ACE I/D (rs1799752) gene in different variables**

Variables	Patient number (percentage)		
	II	ID	DD
Genotype (163 Patients)	14 (8.6)	129 (79.1)	20 (12.3)
<b>Cancer stage</b>			
26 (15.9) T1	1 (3.8)	20 (76.9)	5 (19.3)
110 (67.5) T2	8 (7.3)	87 (79.1)	15 (13.6)
21 (12.9) T3	5 (23.8)	16 (76.2)	0 (0)
6 (3.7) T4	0 (0)	6 (100)	0 (0)
<b>Node Status</b>			
56 (34.4) N0	2 (3.6)	48 (85.7)	6 (10.7)
42 (25.7) N1	3 (7.1)	33 (78.6)	6 (14.3)
40 (24.5) N2	5 (12.5)	29 (72.5)	6 (15)
25 (15.4) N3	4 (16)	19 (76)	2 (8)
<b>Overall grade</b>			
3 (1.8) G1	0 (0)	2 (66.7)	1 (33.3)
116 (71.2) G2	9 (7.8)	92 (79.3)	15 (12.9)
44 (27) G3	5 (11.4)	35 (79.5)	4 (9.1)
<b>Tumor size</b>			
14 (8.6) <2cm	1 (7.1)	11 (78.6)	2 (14.3)
121 (74.2) 2- 5cm	10 (21.7)	95 (78.5)	16 (13.2)
28 (17.2) >5 cm	3 (10.7)	23 (82.1)	2 (7.2)
<b>NPI</b>			
9 (5.5) >2.4- 3.4	0 (0)	8 (88.9)	1 (11.1)
121 (74.2) >3.4- 5.4	9 (7.4)	95 (78.5)	17 (14.1)
33 (20.3) >5.4	5 (15.2)	26 (78.8)	2 (6)
<b>Estrogen receptor</b>			
33 (20.3) Negative	4 (12.1)	23 (69.7)	6 (18.2)
130 (79.7) Positive	10 (7.7)	106 (81.5)	14 (10.8)
<b>Progesterone receptor</b>			
39 (23.9) Negative	5 (12.8)	30 (76.9)	4 (10.3)
124 (76.1) Positive	9 (7.3)	99 (79.8)	16 (12.9)
<b>Her2/neu expression</b>			
89 (54.6) Negative	4 (4.5)	73 (82)	12 (13.5)
74 (45.4) Positive	10 (13.5)	56 (75.7)	8 (10.8)
<b>Metastasis</b>			
139 (85.3) Negative	12 (8.6)	109 (78.5)	18 (12.9)
24 (14.7) Positive	2 (8.3)	20 (83.4)	2 (8.3)
<b>Operation Site</b>			
100 (61.4) Lt MRM	5 (5)	80 (80)	15 (15)
63 (38.6) Rt MRM	9 (14.3)	49 (77.8)	5 (7.9)

**Table 3. Distribution of different genotype of ACE I/D (rs1799752) with risk estimate in response to Her2/neu expression marker in BC group**

Model	Genotype # (%) Her2/neu		OR (95% CI)	Sig. (P)
	Negative 89 (54.6)	Positive 74 (45.4)		
Co-dominant				
II	4 (4.5)	10 (13.5)	1	
ID	73 (82)	56 (75.7)	1.64 (1.12- 2.42)	0.04
DD	12 (13.5)	8 (10.8)	1.78 (0.95- 3.35)	0.07
Dominant	II vs ID+ DD		1.66 (1.14- 2.43)	0.03
Recessive	II+ ID vs DD		1.28 (0.49- 3.33)	0.39
Over-dominant	II+ DD vs ID		1.47 (0.69- 3.13)	0.21



**Table 4. Distribution of different genotype of ACE I/D (rs1799752) with risk estimate in response to Operation Site in BC group**

Model	Genotype # (%) Op. Site		OR (95% CI)	P
	Lt MRM 100 (61.4)	Rt MRM 63 (38.6)		
II	5 (5)	9 (14.3)	1	
ID	80 (80)	49 (77.8)	1.69 (1.08- 2.65)	0.05
DD	15 (15)	5 (7.9)	2.57 (1.09- 6.03)	0.02
Dominant	II vs ID+ DD		1.77 (1.13- 2.77)	0.04
Recessive	II+ ID vs DD		2.05 (0.71- 5.94)	0.13
Over-dominant	II+ DD vs ID		1.14 (0.53- 2.47)	0.44

**Table 5. Distribution of different genotype of ACE I/D (rs1799752) with risk estimate in poor prognostic hormonal status Her2 enriched model (ER<sup>-ve</sup> PR<sup>-ve</sup> Her2<sup>+ve</sup>) vs good prognostic hormonal status luminal A model, (ER<sup>+ve</sup> PR<sup>+ve</sup> Her2<sup>-ve</sup>) in BC group.**

Model	Genotype # (%)		OR (95% CI)	P
	ER <sup>+ve</sup> PR <sup>+ve</sup> Her2 <sup>-ve</sup> 64 cases	Her2 enriched 14 cases		
II	3 (4.7)	4 (28.6)	1	
ID	52 (81.2)	8 (57.1)	4.28 (1.72- 10.64)	0.01
DD	9 (14.1)	2 (14.3)	3.14 (0.77- 12.85)	0.11
Dominant	II vs ID+ DD		4.06 (1.71- 9.6)	0.01
Recessive	II+ ID vs DD		0.98 (0.18- 5.13)	0.63
Over-dominant	II+ DD vs ID		3.25 (0.95- 11.12)	0.06

**Table 6. Means and standard error of the mean of NPI for different genotype of ACE I/D (rs1799752) in BC group**

ACE genotype	N	Mean	Std. Error	Sig. <sup>a</sup>
II	14	5.05	0.204	
ID	129	4.68	0.072	0.10
DD	20	4.49	0.164	0.03 0.30 <sup>b</sup>

a= significance of II genotype vs other genotype, b= significance of ID genotype vs DD genotype.

**Table 7. Means and standard error of the mean of NPI for different genotype of ACE I/D (rs1799752) in response to Her2/neu expression marker in BC group**

ACE	Her2/neu	N	Mean	Std. Error	Sig
II	Negative	4	5.22	0.17	
	Positive	10	4.99	0.28	0.49
ID	Negative	73	4.54	0.09	
	Positive	56	4.86	0.11	0.02
DD	Negative	12	4.59	0.23	
	Positive	8	4.35	0.22	0.46

**Table 8. Means and standard error of the mean of NPI for different hormonal marker status in BC group**

Hormonal Marker		N	Mean	Std. Error	Sig
ER	Negative	33	4.61	0.14	
	Positive	130	4.71	0.07	0.56
PR	Negative	39	4.77	0.14	
	Positive	124	4.66	0.07	0.47
Her2/neu	Negative	89	4.57	0.08	
	Positive	74	4.82	0.09	0.05

**Table 9. Distribution of different metastasis sites in different ACE I/D (rs1799752) genotype**

Site of Metastasis	II	ID	DD
Bone	2	5	1
Bone & LN	0	5	0
Bone & Liver	0	3	0
Bone & Lung	0	1	1
Bone & Brain & LN	0	1	0
Lung	0	5	0

( $P=0.01$ ) with the poor prognostic model of Her2 enriched model, ( $ER^{-ve} PR^{-ve} Her2^{+ve}$ ) for both the co-dominant model (II vs. ID) as well as dominant model (II versus ID+DD) when compared to the good prognostic hormonal status luminal A model, ( $ER^{+ve} PR^{+ve} Her2^{-ve}$ ). This again confirms the association of ID genotype with the aggressiveness type of BC. We found no studies concerning these different models to share their results with them.

The NPI frequency among different ACE I/D (rs1799752) genotype show no significant differences when different genotypes were tested within different NPI groups GPI, MPI and PPI. Significant differences were observed in NPI between II and DD genotype of ACE I/D (rs1799752) polymorphism where II shows the most worth NPI when compared to DD genotype. A significant difference in NPI was noted in response to Her2/neu expression marker in ID genotype of ACE I/D (rs1799752) polymorphism. When different markers have been analyzed in response to NPI only Her2/neu expression marker is show significant decrease NPI in negative expression individuals when compared to positive ones. These results can give us the chance to confirm the association between ACE I/D (rs1799752) ID genotype, NPI and Her2/neu expression marker. We found no studies concerning this association to share their results with them.

Metastasis is a complicated process in which a tumour spreads from its original location to other sections of the body. The actual mechanism of breast cancer metastatic beginning is uncertain. The most metastatic patients were observed in ID genotype of ACE I/D (rs1799752) polymorphism. We found no studies concerning these different models to share their results with them.

## 5. CONCLUSION

It seems that this is the first study that interested in correlate the most functional important gene

polymorphisms of ACE I/D (rs1799752) with different BC characteristic variants in Egyptian women. The study demonstrated no association in BC group in response to DD genotype or D allele of ACE I/D (rs1799752) polymorphism when compared to either BBD or control group. The ID genotype show the significantly correlated with the aggressive carcinogenesis of BC, suggesting its role in the pathogenesis of BC, this may explain the spread of this ethnic patients where ID genotype have the most frequency among different ACE I/D (rs1799752) polymorphism. This study confirm also that ID genotype have association with NPI, Her2/neu expression marker and metastatic distribution in BC patient. ACE I/D (rs1799752) polymorphism ID genotype have strong association to breast cancer carcinogenesis, poor prognosis and metastasis. It may be used as practical biomarker to guide the BC carcinogenesis and risk process. This may explain the high incidence of breast cancer in Egyptian population as it possesses the frequency for ACE I/D (rs1799752) genotype.

## DISCLAIMER

The products used for this research are commonly and predominantly use products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge. Also, the research was not funded by the producing company rather it was funded by personal efforts of the authors.

## CONSENT AND ETHICAL APPROVAL

The patients were admitted to Mansoura University Oncology Center Hospitals, Mansoura, Egypt, over the years 2019 and 2020. The protocol approval was allowed by the Institutional Review Board (IRB) at Mansoura University before starting the study. All methods were performed in accordance to the guidelines and

regulations proposed in the 1975 Declaration of Helsinki. Informed consent letter was obtained from all the participants. All the patient related data including biological samples were anonymized to ensure confidentiality.

## COMPETING INTERESTS

Authors have declared that no competing interests exist.

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## APPENDIX

**S-Table 1. Distribution of different genotype of ACE (rs 1799752) with risk estimate in response to Estrogen receptor (ER) marker in BC group**

Model	Genotype # (%) ER		OR (95% CI)	Sig. (P)
<b>Co-dominant</b>	<b>Negative 33 (20.3)</b>	<b>Positive 130 (79.7)</b>		
II	4 (12.1)	10 (7.7)	1	
ID	23 (69.7)	106 (81.5)	1.84 (0.53- 6.39)	0.26
DD	6 (18.2)	14 (10.8)	0.93 (0.21- 4.19)	0.62
Dominant	II vs ID+ DD		1.65 (0.48- 5.65)	0.31
Recessive	II+ ID vs DD		1.84 (0.65- 5.23)	0.19
Over-dominant	II+ DD vs ID		1.16 (0.92- 1.47)	0.11

**S-Table 2. Distribution of different genotype of ACE (rs 1799752) with risk estimate in response to Progesterone receptor (PR) marker in BC group**

Model	Genotype # (%) PR		OR (95% CI)	Sig. (P)
<b>Co-dominant</b>	<b>Negative 39 (23.9)</b>	<b>Positive 124 (76.1)</b>		
II	5 (12.8)	9 (7.3)	1	
ID	30 (76.9)	99 (79.8)	1.83 (0.57- 5.89)	0.23
DD	4 (10.3)	16 (12.9)	2.22 (0.47- 10.45)	0.26
Dominant	II vs ID+ DD		2.04 (0.64- 6.49)	0.18
Recessive	II+ ID vs DD		0.77 (0.24- 2.46)	0.45
Over-dominant	II+ DD vs ID		0.84 (0.35- 2)	0.42

**S-Table 3. Distribution of different genotype of ACE (rs 1799752) with risk estimate in response to Metastasis status in BC group**

Model	Genotype # (%) Metast.		OR (95% CI)	Sig. (P)
<b>Co-dominant</b>	<b>Negative 139 (85.3)</b>	<b>Positive 24 (14.7)</b>		
II	12 (8.6)	2 (8.3)	1	
ID	109 (78.5)	20 (83.4)	1.1 (0.23- 5.3)	0.63
DD	18 (12.9)	2 (8.3)	1.43 (0.23- 8.97)	0.55
Dominant	II vs ID+ DD		1.04 (0.22- 4.96)	0.66
Recessive	II+ ID vs DD		1.63 (0.35- 7.55)	0.4
Over-dominant	II+ DD vs ID		1.32 (0.48- 3.6)	0.4

**S-Table 4. Distribution of different genotype of ACE (rs 1799752) with risk estimate in Triple – ve (very poor prognostic model) of hormonal status vs good prognostic hormonal status luminal A model, (ER<sup>+ve</sup> PR<sup>+ve</sup> Her2<sup>-ve</sup>) in BC group**

Model	Genotype # (%)		OR (95% CI)	Sig. (P)
<b>Co-dominant</b>	<b>ER<sup>+ve</sup> PR<sup>+ve</sup> Her2<sup>-ve</sup> 64 cases</b>	<b>Triple –ve 10 cases</b>		
II	3 (4.7)	0 (0)	1	
ID	52 (81.2)	8 (80)	1.15 (1.04- 1.27)	0.66
DD	9 (14.1)	2 (20)	1.22 (0.92- 1.61)	0.6
Dominant	II vs ID+ DD		1.16 (1.06- 1.28)	0.64
Recessive	II+ ID vs DD		1.43 (0.35- 5.87)	0.46
Over-dominant	II+ DD vs ID		1.08 (0.2- 5.76)	0.6

**S-Table 5. Distribution of different genotype of ACE- (rs 1799752) with risk estimate in the poor prognosis luminal B model (ER<sup>+</sup> PR<sup>+</sup> Her2<sup>+</sup>) of hormonal status vs good prognostic hormonal status luminal A model (ER<sup>+</sup> PR<sup>+</sup> Her2<sup>-</sup>) in BC group**

Model	Genotype # (%)		OR (95% CI)	Sig. (P)
Co-dominant	ER <sup>+</sup> PR <sup>+</sup> Her2 <sup>-</sup>	ER <sup>+</sup> PR <sup>+</sup> Her2 <sup>+</sup>		
	64 cases	55 cases		
II	3 (4.7)	6 (10.9)	1	
ID	52 (81.2)	44 (80)	1.45 (0.87- 2.42)	0.2
DD	9 (14.1)	5 (9.1)	1.86 (0.8- 4.33)	0.15
Dominant	II vs ID+ DD		1.49 (0.9- 2.48)	0.17
Recessive	II+ ID vs DD		1.63 (0.51- 5.21)	0.29
Over-dominant	II+ DD vs ID		1.08 (0.43- 2.69)	0.52

**S-Table 6. Distribution of different genotype of ACE (rs 1799752) with risk estimate in Triple – ve (very poor prognostic model) of hormonal status vs poor prognostic hormonal status Her2 enriched model (ER<sup>-</sup> PR<sup>-</sup> Her2<sup>+</sup>) in BC group.**

Model	Genotype # (%)		OR (95% CI)	Sig. (P)
Co-dominant	Triple –ve	Her2 enriched		
	10 cases	14 cases		
II	0 (0)	4 (28.6)	1	
ID	8 (80)	8 (57.1)	2.0 (1.22- 3.26)	0.1
DD	2 (20)	2 (14.3)	2.0 (0.75- 5.33)	0.21
Dominant	II vs ID+ DD		2.0 (1.29- 3.1)	0.09
Recessive	II+ ID vs DD		1.5 (0.17- 12.93)	0.56
Over-dominant	II+ DD vs ID		3.0 (0.46- 19.59)	0.23

**S-Table 7. Means and standard error of the mean of NPI for different genotype of ACE (rs 1799752) in response to Estrogen receptor (ER) expression marker in BC group**

ACE	ER	N	Mean	Std. Error	Sig
II	Negative	4	5.15	0.27	
	Positive	10	5.02	0.27	0.74
ID	Negative	23	4.58	0.17	
	Positive	106	4.70	0.07	0.53
DD	Negative	6	4.38	0.36	
	Positive	14	4.54	0.18	0.66

**S-Table 8. Means and standard error of the mean of NPI for different genotype of ACE (rs 1799752) in response to Progesterone receptor (PR) expression marker in BC group**

ACE	PR	N	Mean	Std. Error	Sig
II	Negative	5	5.24	0.23	
	Positive	9	4.95	0.29	0.46
ID	Negative	30	4.69	0.17	
	Positive	99	4.67	0.08	0.93
DD	Negative	4	4.77	0.37	
	Positive	16	4.42	0.18	0.41

**S-Table 9. Means and standard error of the mean of NPI for different genotype of ACE I/D (rs1799752) within different prognostic groups in BC group**

Group	ACE	N	Mean	Std. Error	Sig. <sup>a</sup>
MPI	II	9	4.64	0.20	
	ID	95	4.48	0.05	.369
	DD	17	4.39	0.13	.301 .521 <sup>b</sup>
PPI	II	5	5.80	0.12	
	ID	26	5.88	0.04	.512
	DD	2	4.70	0.13	.682 .883 <sup>b</sup>

*a= significance of II genotype vs other genotype, b= significance of ID genotype vs DD genotype. MPI= Moderate Prognosis. PPI= Poor Prognosis*

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