



## RESEARCH ARTICLE

# Evaluation of PD-1 Gene Susceptibility and Prognosis in Breast Cancer Patients in Iranian Population

Hosnie Hoseini<sup>1,\*</sup>, Azade Sarani<sup>2</sup><sup>1</sup>Department of Laboratory Sciences, Zahedan Branch, Islamic Azad University, Zahedan, Iran<sup>2</sup>Department of Midwifery, Faculty of Medical Science, Zahedan Branch, Islamic Azad University, Zahedan, Iran

## ARTICLE INFO

## Article history:

Received 24.06.2024

Accepted 02.08.2024

Published 14.10.2024

## \* Corresponding author.

Hosnie Hoseini

[hosniehoseini@gmail.com](mailto:hosniehoseini@gmail.com)<https://doi.org/>[10.18579/jopcr/v23.3.58](https://doi.org/10.18579/jopcr/v23.3.58)

## ABSTRACT

Programmed cell death-1 (PD1) protein has an inhibitory effect that reduces the activity of T cells. In this study, gene expression PD1 in patients with breast cancer compared to healthy subjects discussed. This study was performed on 25 patients with breast cancer as a case group and 25 healthy individuals as a control group. Real-time PCR method was used to evaluate gene expression. For the case group, the mean age was  $2.75 \pm 12.18$  and for the control group  $30.6 \pm 2.6$ . The results of our study showed that the expression of PD1 gene in the case group was higher than the control ( $p < 0.05$ ). As a result of our study show that expression of gene in the development of breast cancer, So PD1 can be used as prognostic gene in breast cancer study be considered.

**Keywords:** Breast cancer; Gene expression; Programmed cell death-1

## INTRODUCTION

One of the most common cancers in women, which is the second leading cause of death among women in the United States, is breast cancer<sup>1-3</sup>. Tumor and lymph node resection is a common treatment for breast cancer patients in the form of radiation therapy, hormone therapy or chemotherapy, and often carries many risks for patients with large tumors<sup>4,5</sup>. Most breast cancer patients are treated and survive with these treatments. Gene expression tests can be effective in diagnosing and treating breast cancer<sup>6-8</sup>. Programmed cell death protein is a protein from the family of immunoglobulins that has receptors PDL1 and PDL2 and is known as an inhibitory protein. PD1 is expressed on the surface of T cells and B lymphocytes and normal killer cells<sup>9-11</sup>. Although many studies have shown a link between gene expression and disease pathogenesis, little is known about the expression of PD1 gene and breast cancer<sup>12,13</sup>. Recent studies have shown that PD-1 gene expression is associated with BC pathogenesis, but studies indicate the importance of PD-1 gene in regulating T cell activity<sup>14</sup>. In this study, we investigated the expression of PD1 gene

in women with breast cancer in comparison with healthy individuals in Sistan and Baluchestan province, Zahedan.

## MATERIALS AND METHODS

*Patients and Samples*

Blood samples were taken from 25 patients with breast cancer as a case group and 25 healthy individuals as a control group. Patients' clinical information was obtained from their medical records. RNA was collected from all blood samples. The study protocol was also approved by the Medical Research Ethics Committee of Ali Ibn Abitaleb Hospital in Zahedan, Sistan and Baluchestan Province.

*PD-1 expression analysis*

Expression of PD-1 was analyzed via real time RT-PCR technique. Briefly, EDTA-treated blood sample were collected, and the total RNA was extracted using TRIZOL reagent (Invitrogen) according to manufacturer instruction. The extracted RNA then reversely transcribed into cDNA using Takara cDNA synthesis kit (Takara, Japan). Real time

**Table 1: Primer sets used for PD-1 expression analysis**

	Forward primer			Revers primer			Product Length
	Sequence (5'->3')	GC%	length	Sequence (5'->3')	GC%	length	
PD-1	CCGCACGAGGGACAATA	58.8	17	TCTCTCGCCACTGGAAATC	52.6	19	114

PCR was performed using a StepOnePlus real time PCR system (Applied Biosystems) using RealQ Plus 2x Master Mix (Ampliqon) and designed primer listed in Table 1. The  $\beta$ -actin primer was used as the housekeeping control gene.

### Statistical Analysis

The SPSS statistical software version 21 was used for all statistical analyses. Differences in characteristics among the genotypes and mRNA expression were compared using t-test for categorical data. Significant level was accepted at  $P \leq 0.05$ .

### RESULTS

A total of 50 patients were recruited in this study, 25 BC patients and 25 healthy controls. The mean age of BC patients and the healthy controls were  $2.75 \pm 12.18$  and  $30.6 \pm 2.6$  respectively. No significant difference was observed in age distribution between the BC patients and control group.

#### PD-1 mRNA expression analysis

In order to establish the relationship between BC prevalence and PD-1, the PD-1 expression level was determined by Real time PCR. The level analysis of PD-1 showed higher expression in BC patients compared to healthy controls (Table 2). The independent t-test showed that the increased level of PD-1 mRNA was significant ( $P < 0.05$ ).

**Table 2: PD-1 expression analysis**

Gene	Reaction efficiency	Expression	P-value
PD1	0.8	7.7	0.008

### DISCUSSION

After cancers such as lung, stomach and liver cancers, breast cancer is one of the most common cancers in the female population of the world, which can be the most common cause of death in women. programmed cell death is called apoptosis, which is clinically important because failure to control and regulate the mechanism of apoptosis leads to overexpression of certain genes and pathogenesis and plays an important role in the development of many cancers<sup>15</sup>. PD1 protein is a member of the CD28 family of immunoglobulins and has two receptors, PDL1 and PDL2. This protein has an inhibitory role. Inhibitory function and inhibitory signals of PD1 protein through its receptors lead to activation of T cell function, tolerance, and tissue damage

due to immunity<sup>16</sup>. There have also been many studies on PD1 gene polymorphisms and their role in breast cancer patients compared to healthy individuals, which have been introduced as prognosticators in the diagnosis and treatment of various cancers, including breast cancer. In addition, gene mutations have played a significant role in the development of breast cancer. Many studies have been conducted in this field. Eight studies (Chang, 2007,<sup>55</sup> Cobligh, 2005,<sup>47</sup> Esteva, 2005,<sup>48</sup> Gianni, 2005,<sup>49</sup> Cronin, 2004,<sup>44</sup> Habel, 2006,<sup>50</sup> Mina, 2006,<sup>51</sup> and Paik, 2004<sup>28</sup>) have examined the expression of different genes in breast cancer compared to healthy individuals using different methods such as real-time PCR or immunohistochemistry<sup>17-24</sup>. Cronin and colleagues showed that there is a significant relationship between PDL1 gene expression and the progression of breast cancer. The group and their colleagues studied the expression of five genes in breast cancer. In a clinical study, Oratz R and colleagues also investigated gene expression variation and their association with a variety of cancers, including breast cancer<sup>25</sup>. They showed that in patients with breast cancer, the expression of PD1 was significantly increased. According to these studies, the expression of PD1 gene can play an effective role in the development and progression of breast cancer. Zhou and colleagues also showed a link between PD1 gene expression and the incidence of breast cancer<sup>26</sup>. They showed that the expression level of PD1 was higher in patients with breast cancer than in the control group. Therefore, gene expression can serve as a prognostic marker in screening and immunotherapy in patients with breast cancer.

### CONCLUSION

The results of our study showed that the expression level of PD1 gene in patients with breast cancer was significantly higher compared to healthy individuals and it can be concluded that the expression of PD1 gene can be a prognostic factor in the early diagnosis of breast cancer. Therefore, it is suggested that more studies be performed on the relationship between the expression of more genes and breast cancer. In addition, according to the findings of the study have been obtained only from the people of Sistan-Baluchistan province, fertility studies in different ethnic groups are required.

#### Acknowledgments

The Evidence-based Practice Center thanks Dr Masoud Saravi and Dr Shirin Shahraki for their assistance with searching

and database management, and research organization and for her assistance with final preparations of the report.

### Conflict of Interests

The authors declare that there is no conflict of interests regarding the publication of this paper.

### REFERENCES

- Jemal A, Siegel R, Ward E, Murray T, Xu J, Thun MJ. Cancer Statistics, 2007. *CA: A Cancer Journal for Clinicians*. 2007;57(1):43–66. Available from: <https://doi.org/10.3322/canjclin.57.1.43>.
- Kanduc D, Mittelman A, Serpico R, Sinigaglia E, Sinha AA, Natale C, et al. Cell death: apoptosis versus necrosis (review. *International Journal of Oncology*. 2002;21(1):165–170. Available from: <https://pubmed.ncbi.nlm.nih.gov/12063564/>.
- Kam PC, Ferch NI. Apoptosis: mechanisms and clinical implications. *Anaesthesia*. 2000;55(11):1081–1093. Available from: <https://doi.org/10.1046/j.1365-2044.2000.01554.x>.
- Daniail NN. BCL-2 family proteins: critical checkpoints of apoptotic cell death. *Clinical Cancer Research*. 2007;13(24):7254–7263. Available from: <https://doi.org/10.1158/1078-0432.ccr-07-1598>.
- Miller SA, Dykes DD, Polesky HF. A simple salting out procedure for extracting DNA from human nucleated cells. *Nucleic Acids Research*. 1988;16(3):1215. Available from: <https://doi.org/10.1093/nar/16.3.1215>.
- Xie T, Ho SL, Ma OC. High resolution single strand conformation polymorphism analysis using formamide and ethidium bromide staining. *Journal of Molecular Pathology*. 1997;50(5):276–278. Available from: <https://doi.org/10.1136/mp.50.5.276>.
- Koda M, Kanczuga-Koda L, Reszec J, Sulkowska M, Famulski W, Baltaziak M, et al. Expression of the apoptotic markers in normal breast epithelium, benign mammary dysplasia and in breast cancer. *Folia Morphologica*. 2004;63(3):337–341. Available from: <https://pubmed.ncbi.nlm.nih.gov/15478112/>.
- Ghayad SE, Vendrell JA, Bleche I, Spyrtos F, Dumontet C, Treilleux I, et al. Identification of TACC1, NOV, and PTTG1 as new candidate genes associated with endocrine therapy resistance in breast cancer. *Journal of Molecular Endocrinology*. 2009;42(2):87–103. Available from: <https://doi.org/10.1677/JME-08-0076>.
- Sorbello V, Fuso L, Sfiligoi C, Ponzzone R, Biglia N, Weisz A, et al. Quantitative real-time RTPCR analysis of eight novel estrogen-regulated genes in breast cancer. *International Journal of Biological Markers*. 2003;18(2):123–129. Available from: <https://doi.org/10.1177/172460080301800205>.
- Blencowe BJ. Alternative splicing: new insights from global analyses. *Cell*. 2006;126(1):37–47. Available from: <https://doi.org/10.1016/j.cell.2006.06.023>.
- Schena M, Shalon D, Davis RW, Brown PO. Quantitative monitoring of gene expression patterns with a complementary DNA microarray. *Science*. 1995;270(5235):467–470. Available from: <https://doi.org/10.1126/science.270.5235.467>.
- Baldwin D, Crane V, Rice D. A comparison of gel-based, nylon filter and microarray techniques to detect differential RNA expression in plants. *Current Opinion in Plant Biology*. 1999;2(2):96–103. Available from: [https://doi.org/10.1016/S1369-5266\(99\)80020-X](https://doi.org/10.1016/S1369-5266(99)80020-X).
- Watson A, Mazumder A, Stewart M, Balasubramanian S. Technology for microarray analysis of gene expression. *Current Opinion in Biotechnology*. 1998;9(6):609–614. Available from: [https://doi.org/10.1016/S0958-1669\(98\)80138-9](https://doi.org/10.1016/S0958-1669(98)80138-9).
- Schena M, Heller RA, Thieriault TP, Konrad K, Lachenmeier E, Davis RW. Microarrays: biotechnology's discovery platform for functional genomics. *Trends in Biotechnology*. 1998;16(7):301–306. Available from: [https://doi.org/10.1016/S0167-7799\(98\)01219-0](https://doi.org/10.1016/S0167-7799(98)01219-0).
- The TAILORx Breast Cancer Trial. 2018. Available from: <https://www.cancer.gov/types/breast/research/tailorx>.
- McShane LM, Altman DG, Sauerbrei W, Taube SE, Gion M, Clark GM. Reporting recommendations for tumour MARKer prognostic studies (REMARK). *British Journal of Cancer*. 2005;93(4):387–391. Available from: <https://doi.org/10.1038/sj.bjc.6602678>.
- Chang M, Pho M, Dutta D, Stephans JC, Shak S, Kiefer MC, et al. Measurement of gene expression in archival paraffin-embedded tissues: development and performance of a 92-gene reverse transcriptase-polymerase chain reaction assay. *American Journal of Pathology*. 2004;164(1):35–42. Available from: [https://doi.org/10.1016/s0002-9440\(10\)63093-3](https://doi.org/10.1016/s0002-9440(10)63093-3).
- Cronin M, Sangli C, Liu ML, Pho M, Dutta D, Nguyen A, et al. Analytical Validation of the Oncotype DX Genomic Diagnostic Test for Recurrence Prognosis and Therapeutic Response Prediction in Node-Negative, Estrogen Receptor-Positive Breast Cancer. *Clinical Chemistry*. 2007;53(6):1084–1091. Available from: <https://doi.org/10.1373/clinchem.2006.076497>.
- Cobleigh MA, Tabesh B, Bitterman P, Baker J, Cronin M, Liu ML, et al. Tumor gene expression and prognosis in breast cancer patients with 10 or more positive lymph nodes. *Clinical Cancer Research*. 2005;11(24 Pt 1):8623–8631. Available from: <https://doi.org/10.1158/1078-0432.ccr-05-0735>.
- Esteva FJ, Sahin AA, Cristofanilli M, Coombes K, Lee SJ, Baker J. Prognostic role of a multigene reverse transcriptasePCR assay in patients with node-negative breast cancer not receiving adjuvant systemic therapy. *Clinical Cancer Research*. 2005;11(9):3315–3319. Available from: <https://doi.org/10.1158/1078-0432.ccr-04-1707>.
- Habel LA, Shak S, Jacobs MK, Capra A, Alexander C, Pho M, et al. A population based study of tumor gene expression and risk of breast cancer death among lymph node-negative patients. *Breast Cancer Research*. 2006;8(3):1–15. Available from: <https://doi.org/10.1186/bcr1412>.
- Mina L, Soule SE, Badve S, Baehner FL, Baker J, Cronin M, et al. Predicting response to primary chemotherapy: gene expression profiling of paraffin-embedded core biopsy tissue. *Breast Cancer Research and Treatment*. 2007;103(2):197–208. Available from: <https://dx.doi.org/10.1007/s10549-006-9366-x>.
- Paik S, Tang G, Shak S, Kim C, Baker J, Kim W, et al. Gene Expression and Benefit of Chemotherapy in Women With Node-Negative, Estrogen Receptor-Positive Breast Cancer. *Journal of Clinical Oncology*. 2023;41(20):3565–3575. Available from: <https://dx.doi.org/10.1200/jco.22.02570>.
- Sorlie T, Tibshirani R, Parker J, et al. Repeated observation of breast tumor subtypes in independent gene expression data sets. *PNAS*. 2003;100(4):8418–8423. Available from: <https://doi.org/10.1073/pnas.0932692100>.
- Oratz R, Paul D, Cohn AL, Sedlacek SM. Impact of a Commercial Reference Laboratory Test Recurrence Score on Decision Making in Early-Stage Breast Cancer. *JCO Oncology Practice*. 2007;3(4):182–186. Available from: <https://doi.org/10.1200/JOP.0742001>.
- Zhou AM, Floore A, Delahaye LJM, Witteveen AT, Pover RCF, Bakx N, et al. Converting a breast cancer microarray signature into a highthroughput diagnostic test. *BMC Genomics*. 2006;7:1–10. Available from: <https://doi.org/10.1186/1471-2164-7-278>.