Evaluating the Association between CCR5delta32 Polymorphism (rs333) and the Risk of Breast Cancer in a Cohort of Iranian Population

Amir TAJBAKHSH 1,2,3, Zahra FARJAMI 2,3, *Abolfazl NESAEI-BAJESTANI 4, Fahimeh AFZALJAVAN 2, Mahdi RIVANDI 2, Atfeh MOEZZI 2,3, Soheila ABEDINI 2, Mahla ASGHARI 2, Mohammad Mahdi KOOSHYAR 5, Fatemeh HOMAIE SHANDIZ 6, *Alireza PASDAR 2,7,8

1. Pharmaceutical Sciences Research Center, Shiraz University of Medical Sciences, Shiraz, Iran
2. Department of Medical Genetics & Molecular Medicine, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
3. Student Research Committee, Mashhad University of Medical Sciences, Mashhad, Iran
4. Department of Basic Sciences, Faculty of Medicine, Gonabad University of Medical Sciences, Gonabad, Iran
5. Department of Hematology-Onology, Imam Reza Hospital, Mashhad University of Medical Sciences, Mashhad, Iran
6. Cancer Research Center, Mashhad University of Medical Sciences, Mashhad, Iran
7. Division of Applied Medicine, Faculty of Medicine, University of Aberdeen, Foresterhill, Aberdeen, UK
8. Medical Genetics Research Center, Mashhad University of Medical Sciences, Mashhad, Iran

*Corresponding Authors: Emails: Abolfazlnesaei@gmail.com; PasdarA@mums.ac.ir

(Received 10 Feb 2020; accepted 15 May 2020)

Abstract

Background: CC chemokine receptor 5 (CCR5) is introduced as an immune response modulator. The activity of CCR5 influences breast tumour development in a p53-dependent manner. This study aimed to investigate the frequency of CCR5delta32 and its association with the risk of breast cancer in 1038 blood samples in North-East of Iran.

Methods: In this case-control study, we genotyped 570 control samples and 468 breast cancer patients by a gel electrophoresis-based gap-polymerase chain reaction (gap-PCR) method Mashhad, Iran. The data were analyzed using the SPSS software.

Results: Of 570 controls included, 542 (95.09%) had CCR5delta32 wild/wild (W/W) genotype, 28 samples (4.91%) had CCR5delta32 wild/deletion (W/D) genotype and none of them were CCR5delta32 deletion/deletion (D/D) genotype (0%). While 428 samples of patients (91.45%) had CCR5delta32 W/W genotype, 40 samples (8.55%) had CCR5delta32 W/D and CCR5delta32 D/D homozygous was nil (0%) amongst cases. All samples were in the Hardy–Weinberg equilibrium (\(P>0.05\)). According to the allele frequency, D allele, as a risky allele, in the cases was more than the control samples (0.0427 vs 0.0245, respectively) (\(P=0.0206\)). Hence, W/D genotype may confer a risk effect (OR=1.77, CI: 1.09-2.90; \(P=0.0206\)) compared with WW genotype between case and control groups.

Conclusion: There is a statistically significant association between CCR5W/D and breast cancer risk. CCR5 may be regarded as a target for the prevention of breast cancer in certain conditions such as interaction with p53 variants, which remains to be further investigated.

Keywords: CCR5D32; p53 pathway; Breast carcinoma; Immunogenetics; Metastasis
Introduction

One of the most prevalent cancers in women is breast cancer, which increases the mortality rate in women worldwide (1, 2). Breast cancer is introduced as the most frequent malignancy in Iranian women (3, 4). Based on the previous studies, genetic and environmental factors are complicated in the risk as well as the expansion of breast cancer (5-9). A functional correlation exists between cancer and inflammation receptors. The inflammatory responses to the breast cancer tumor site proliferation and development of cancer cells are also involved in metastatic breast cancer (10, 11). In addition, inflammatory factors such as chemokine-like chemokine receptor (CCR5), which affect the chemotactic factors for inflammatory cells, have important roles in leukocyte trafficking, chemotaxis, angiogenesis, lymphocyte development, inflammatory processes, tumor development and metastasis (12).

Chemokines are small soluble molecules secreted by cells, which are greatly well-known for their ability to influence cancer cell development via inflammation and to motivate cellular migration, mostly by leukocyte recruitment in inflammation (13, 14). Moreover, different types of tumour cells express chemokine and chemokine receptors (15). In addition, high levels of CCR5 are great co-receptors for infection of macrophages and T lymphocytes via the macrophage-tropic strains of HIV-1; which their expression has been identified in cancer tissues. The CCR5 may be notably involved in the metastasis and proliferation of various cancers like breast cancer (16, 17).

Inadequate and potent CCR5 expression is especially related to the non-metastatic progression of breast cancer. In addition, the local production of the Chemokine (C-C motif) ligand 5 (CCL5) is also significant in the development of breast tumour and associated with a poor prognosis of breast cancer (16, 17). CCR5 also results in the growth of breast cancer stem cells. Overexpression of the CCR5 cells indicates reduced p-γH2AX-Histone H2AX phosphorylation proteins, which alarms DNA damage and consequently leads to the enhancement of DNA repair (18). The deficiency of CCR5 affects the apoptotic cell death of melanoma via the prohibition of nuclear factor kappa light chain enhancer of activated B cells (NF-κB) and upregulation of IL-1Ra (19). Moreover, the CCR5 expression has an important role in the subpopulation of breast cancer cell lines and affects the functional response to CCL5.

Furthermore, oncogene transformation enforces the expression of CCR5, and the subpopulation of cells, which express functional CCR5 shows enhanced the invading characteristic of the cancer cells. The role of CCR5 in breast tumour cell growth (mostly in luminal breast cancer), suggests it affects the p53 of the MCF-7 cells. Moreover, CCR5 blockade increases the proliferation of MCF-7 cell line in the attendance of p53 but does not affect the proliferation in the xenografts carrying a p53 mutation (20). Additionally, Vicriviroc or Maraviroc, known as the CCR5 antagonists, block the function of CCR5 HIV coreceptor and reduce metastasis of basal breast tumour, but does not affect the cell viability/proliferation in vitro. Maraviroc decreases pulmonary expansion of breast cancer in vivo. Moreover, the antagonists of CCR5 can be used as an adjuvant combination therapy to decrease the possibility of metastatic breast cancer in patients with certain conditions (21). Therefore, prevention of CCR5 via an antagonist decreases the leukocyte influence and tumor growth and subsequently reduces the subcutaneous transfusion of the cells in vivo (22). In addition, a decrease in CCR5 acts as a suppressive receptor in cancer metastasis. The deficiency of CCR5 increases the delay of tumor growth, and the inhibitors of CCR5 prevent a rise in the cancer cells in cancers like breast cancer (23, 24). CCR5delta32 (CCR5D32) has been found in the CCR5 gene, located on chromosome 3p21.3. CCR5D32 induces a strong resistance in homozygote persons against the HIV-1 infection. Moreover, studies have been done on the distribution of CCR5D32 in various populations (25). The effect of CCR5D32 poly-
morphism is dependent on the type of cancer; although, other studies have not reported the same association (26, 27). This mutation was not present in Africans as well as most Asian people, but it was detectible in African-Americans, which the reason was explained as an ethnic combination (28, 29). The roles of the CCR5 receptor of chemokine CCL5 remain unclear in breast cancer progression and there is a controversy between articles. These variations might be due to the low statistical power, small sample size, clinical heterogeneity, ethnic difference, as well as the confounding effects that have not been taken into account. In our study, we removed these limitations and tried to investigate the relation between CCR5D32 and the risks of breast cancer with an appropriate sample size in an Iranian population.

Materials and Methods

Study population and blood collection
In this case–control study, 468 clinically confirmed sporadic breast cancer patients were recruited in Mashhad, Iran. After taking informed consent, 10 ml peripheral blood sample was collected from 1038 individuals (468 cases and the 570 controls).

The healthy female individuals were selected among women in the North East of Iran.

The genomic DNA extraction and genotyping
The pure genomic DNA was extracted from 1038 blood samples by the salting-out technique protocol (30, 31). The PCR was performed to identify the genotype of the cases and healthy controls by primers, which flank the 32- base pairs (bp) deletion. The reaction volume (10 μl) was composed of 5-10 ng of the genomic DNA template, 0.1 μM of each primer, 3 μl Master mix PCR mixture (2X) include 1.5 mM MgCl and 0.5 U of Taq polymerase in 2x reaction buffer (from 0.5U/μl) and 4 μl distilled water in the total reaction of 10 μl. The 5′ to 3′ sequence of common forward and reverse primers were as the following; forward primer sequence was 5′ AGG TCT TCA TTACAC CTG CAG C 3′, and reverse primer was 5′ CTT CTC ATT TCG ACACCG AAG C 3′ (Table 1) (32). Genotypes were detected according to the final size of PCR products, in which 169 bp and 137 bp products were related to wild-type and CCR5D32 genotypes, respectively (Fig. 1).

Table 1: Primer sequences that used in this study

<table>
<thead>
<tr>
<th>Primers</th>
<th>Sequence 5′-3′</th>
<th>Length</th>
<th>Products</th>
</tr>
</thead>
<tbody>
<tr>
<td>Forward</td>
<td>AGG TCT TCA TTACAC CTG CAG C</td>
<td>22 bp</td>
<td>CCR5W/W</td>
</tr>
<tr>
<td>Reverse</td>
<td>CTT CTC ATT TCG ACACCG AAG C</td>
<td>22 bp</td>
<td>CCR5D32</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>CCR5D/D</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>CCR5W/D</td>
</tr>
</tbody>
</table>

Wild: W; Deletion: D; Bp: basepairs.

Fig. 1: The gel electrophoresis of PCR amplified DNA. Lane 1: wild type (CCR5W/W); lanes 2 and 3: heterozygous genotype (CCR5W/D). P: Positive control sample; N: Negative control sample; L: 100 bp DNA size marker.
The reaction was performed in an Applied Biosystems PCR (Life Technologies). Under the following thermal conditions including first denaturation at 95 °C for 10 min; 33 cycles of 94 °C for 30 sec, 58 °C for 30 sec, and also 72 °C for 30 sec; and last elongation at 72 °C for 5 minutes. The electrophoresis of PCR products (5-7 μl) was done in 3% agarose gel (Invitrogen), staining with DNA Green Viewer (Pars Tous; Iran) (Consort, Germany), and then they were visualized under UV light using SYNGENE U: genius gel documentation system.

The collected information was analyzed using the SPSS statistics software ver. 12 (Chicago, IL, USA). In addition, differences in the allele and the genotype frequencies of CCR5D32 variant between cases and healthy samples were evaluated using gene count and also the χ² test. Moreover, Odd ratios (OR) with 95% confidence interval (CI) using logistic regression test was calculated. In this study, for all analyses, the cut-off values of P≤0.05 were considered to be significant.

**Ethical approval**

Our study was conducted in accordance with the Declaration of Helsinki after being permitted via the local ethics committee of Mashhad University of Medical Sciences, Iran (Ethical code: IR.MUMS.fm.REC.1394.399). In this line, written informed consent has been received from all cases and controls.

**Results**

Demographic data of the patients and controls including age, living place, habits and situation, family history of cancer and clinical information were collected in a questionnaire (Table 2). Of 570 controls included, 542 (95.09%) had CCR5D32 wild/wild (W/W) genotype, 28 samples (4.91%) had CCR5D32 wild/deletion (W/D) genotype and none of them were CCR5D32 deletion/deletion (D/D) genotype (0%). While 428 samples of patients (91.45%) had CCR5D32 W/W genotype, 40 samples (8.55%) had CCR5D32 W/D and CCR5D32 D/D homozygous was nil (0%) amongst cases. All samples were in the Hardy–Weinberg equilibrium. According to the allele frequency, the frequency of D allele, as a risky allele, in the cases was more than the control samples (0.0427 vs 0.0245, respectively) (P=0.0206). Hence, W/D genotype risk effect was calculated as (OR=1.77, CI: 1.09-2.90; P=0.0206) compared with WW genotype (Table 3).

**Table 2: Summary of clinic-pathological data and several demographic variables of the carcinoma patients and the control groups**

<table>
<thead>
<tr>
<th>Characteristics</th>
<th>N</th>
<th>Cases</th>
<th>N</th>
<th>Controls</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age</td>
<td>359</td>
<td>51.6±11.6</td>
<td>536</td>
<td>42.5±12</td>
<td>P&lt;0.05*</td>
</tr>
<tr>
<td>BMI</td>
<td>320</td>
<td>27.4±5</td>
<td>513</td>
<td>25.3±4.4</td>
<td>P&lt;0.05*</td>
</tr>
<tr>
<td>Height</td>
<td>321</td>
<td>159.5±6.8</td>
<td>516</td>
<td>161.3±5.9</td>
<td>P&lt;0.05*</td>
</tr>
<tr>
<td>Weight</td>
<td>344</td>
<td>69.7±13.2</td>
<td>529</td>
<td>66.2±11.7</td>
<td>P&lt;0.05*</td>
</tr>
<tr>
<td>Marital status</td>
<td>897</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Married</td>
<td>331</td>
<td>(92.2%)</td>
<td>461</td>
<td>(85.7%)</td>
<td>P&lt;0.05*</td>
</tr>
<tr>
<td>Divorced</td>
<td>3</td>
<td>(0.8%)</td>
<td>1</td>
<td>(0.2%)</td>
<td></td>
</tr>
<tr>
<td>Widowed</td>
<td>6</td>
<td>(1.7%)</td>
<td>5</td>
<td>(0.9%)</td>
<td></td>
</tr>
<tr>
<td>Never-married</td>
<td>19</td>
<td>(5.3%)</td>
<td>71</td>
<td>(13.2%)</td>
<td></td>
</tr>
<tr>
<td>Abortion</td>
<td>642</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yes</td>
<td>117</td>
<td>(45.3%)</td>
<td>115</td>
<td>(29.9%)</td>
<td>P&lt;0.05*</td>
</tr>
<tr>
<td>No</td>
<td>141</td>
<td>(54.7%)</td>
<td>269</td>
<td>(70.1%)</td>
<td></td>
</tr>
<tr>
<td>The family history of cancer</td>
<td>870</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yes</td>
<td>192</td>
<td>(57.1%)</td>
<td>371</td>
<td>(69.5%)</td>
<td>P&lt;0.05*</td>
</tr>
<tr>
<td>No</td>
<td>144</td>
<td>(42.9%)</td>
<td>163</td>
<td>(30.5%)</td>
<td></td>
</tr>
<tr>
<td>History of cancer</td>
<td>847</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yes</td>
<td>23</td>
<td>(7.2%)</td>
<td>4</td>
<td>(0.8%)</td>
<td>P&lt;0.05*</td>
</tr>
<tr>
<td>No</td>
<td>298</td>
<td>(92.8%)</td>
<td>522</td>
<td>(99.2%)</td>
<td></td>
</tr>
</tbody>
</table>
Table 3: Distribution of the CCR5D32 genotypes and the allelic frequencies

<table>
<thead>
<tr>
<th>Genotypes/Models/Alleles</th>
<th>Breast carcinoma</th>
<th>Normal individuals</th>
<th>OR (CI 95%)</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genotypes</td>
<td>Number (%)</td>
<td>Number (%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CCR5&lt;sup&gt;W/W&lt;/sup&gt;</td>
<td>428 (91.45)</td>
<td>542 (95.09)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CCR5&lt;sup&gt;W/D&lt;/sup&gt;</td>
<td>40 (8.55)</td>
<td>28 (4.91)</td>
<td>1.77 (1.09-2.90)</td>
<td>0.0206</td>
</tr>
<tr>
<td>CCR5&lt;sup&gt;D/D&lt;/sup&gt;</td>
<td>0 (0)</td>
<td>0 (0)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Alleles</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>W</td>
<td>896 (95.72)</td>
<td>1112 (97.54)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>D</td>
<td>40 (4.28)</td>
<td>28 (2.46)</td>
<td>1.77 (1.09-2.90)</td>
<td>0.0206</td>
</tr>
</tbody>
</table>

Wild: W; Deletion: D.

Discussion

In our study, there was a significant association between heterozygous genotype (W/D) and breast cancer risk in Iranian breast cancer patients. Moreover, D allele, as a risky allele, in the cases was more than the control samples. The relation between genetic and environmental factors is widely investigated. In recent years, immunogenetics have an essential role in the pathogenesis of breast cancer. CCR5 is the receptor for chemotactic chemokines macrophage inflammatory protein-1 alpha (MIP1-α), MIP1β, and RANTES (CCL3, CCL4, CCL5). In addition, the CCR5D32 is located in the CCR5 promoter, which encodes a non-functional receptor (33, 34). Moreover, CCR5D32 allele has been shown to have a high frequency, among the different Caucasian populations (35, 36). A meta-analysis of an Indian population indicates that the CCR5D32 was associated with the risk of breast cancer (37). On the other hand, the CCR5D32 genotype has been correlated with better prognosis in patients of the Nijmegen discovery cohort with postmenopausal breast tumour (Nijmegen, Netherlands). The individuals, carrying the CCR5D32 genotype, demonstrate a longer metastasis-free survival (MFS) in this population (38).

In agreement with our investigation, in a meta-analysis study, the CCR5D32 was associated with the risk of breast cancer in the Indians (37). In the Netherlands population, the individuals carrying the CCR5D32, displayed a longer MFS in the postmenopausal subgroup of the initial cohort (38). In the Turkish population, the frequency of heterozygous genotypes was an independent risk factor for the breast cancer progression (39). In addition, another study reported a significant association between I/I and I/D alleles in the breast cancer patients with the CCR5D32 mutation; carried out with 500 breast cancer patient samples in a Pakistani population (40). Similar to our study, heterozygous genotype (W/D) in the breast patients was more than the control samples in a Pakistani population (41).

Furthermore, there was a strong association between the expressions CXCR5 in the breast cancer tissues from the German population (42). On the other hand, CCR5D32 was not connected to the risk of cancer (43). Moreover, in some studies, there was no significant correlation between this polymorphism and the risk of breast cancer such as in the North of India and Brazil (44-46).

CCR5 increases T cell responses to cancer cells via modulating the activation of helper-dependent CD8<sup>+</sup> T cell (47). Besides, CCR5 exerts main regulatory effects on the immunity mediated by CD4<sup>+</sup> and CD8<sup>+</sup> T cell. CCR5 has a particular, ligand-dependent role in improving anti-tumor responses. Efficient tumor rejection requires the expression of CCR5 via the CD4<sup>+</sup> and CD8<sup>+</sup> T cells (48). Furthermore, CCR5 was found to be mainly expressed in the CD8<sup>+</sup> T lymphocytes, and the frequency of CCR5<sup>+</sup>CD8<sup>+</sup> Cytotoxic T lymphocytes (CTLs) was higher in tumor-infiltrating lymphocytes (TIL), compared with the human peripheral blood mononuclear cells (PBMC) (48).

The activation of CCR5 in the CD4<sup>+</sup> cells contributed to increasing the expression of CD40 ligand, resulting in antigen-presenting cells (APCs) maturation and improved CD8<sup>+</sup> T-cell

Available at: http://ijph.tums.ac.ir

587
cross-priming as well as tumor infiltration. CCR5 leads to the reduction of chemical (3-
methylcholanthrene)-induced fibrosarcoma growth and incidence in mice (47). The
CCR5D32 has been associated with the lower expression of CCR5 and higher CC-chemokine
secretion levels of CD4+ cells (49). In this respect and from the results of our study, the reduction
in CCR5 leads to a decrease in the immune system defense against a tumor (especially a de-
crease in the T cell response).

Another explanation of our results may be related to the downstream pathways of the CCR5, as a
protective factor for breast cancer. The activity of CCR5 regulates breast cancer development in a
p53-dependent manner in MDA-MB-231 and MCF-7 cell lines (20). Mutation inactivates the
p53 tumor suppressor gene in approximately half of all human tumors (50). Prevention of CCR5
expression leads to increase the proliferation of tumor cells in wild-type p53 without affecting the
tumor cell proliferation in p53 mutation carriers in tumor xenograft models (20). In this line, the
data from a breast cancer clinical study (547 pa-
tients in a cohort study) displayed that disease-
free survival (DFS) was shorter in individuals car-
rying CCR5D32 allele and expressed wild-type
p53. The activity of CCR5 affects breast cancer
development in a p53-dependent manner. All
downstream pathways of CCR5D/D and
CCR5W/D are abolished or severely impaired in
patients with CCR5D32, respectively. Conse-
quently, activation of p53 mediated by CCR5 is
diminished. In this line, p53, as a tumor suppres-
sor, may be silenced in the CCR5D32 patients.
Furthermore, two p38-dependent pathways, Gi
and JAK2, help CCR5 to regulate p53 transcrip-
tional activity. These p38-dependent pathways
seem to be impaired/ silenced in the participants
with the CCR5D32 allele. Collectively, breast
cancers with normal p53, grow quicker and re-
lapse faster in the D32 carriers (20).

Conclusion

CCR5D32 may affect the risk of the breast cancer
in our population. The potential use of
CCL5/CCR5 may be a target for preventing
breast cancer metastasis. In addition, it can be
used as a marker of DNA damage/repair in the
tumor cells. Thus, further functional studies are
needed to investigate pathways related to the
CCR5, p53 and T cell response influencing the
risk of breast cancer.

Ethical considerations

Ethical issues (Including plagiarism, informed
consent, misconduct, data fabrication and/or fals-
sification, double publication and/or submission,
redundancy, etc.) have been completely observed
by the authors.

Acknowledgements

This manuscript was supported by the Student
Research Committee of Mashhad University of
science (Grant Numbers: 951734 & 961689).

Conflicts of interest

The authors report no conflicts of interest.

References

signaling system: a molecular target in breast
cancer therapy. Journal of Surgical Research,
(2005). Differentiation of tumours of ductal
and lobular origin: II. Genomics of invasive
ductal and lobular breast carcinomas. Biomed
Pap Med Fac Univ Palacky Olomouc Czech Repub,
Functional polymorphisms of FAS and FASL
gene and risk of breast cancer–pilot study of
134 cases. Plos One, 8 (1): e53075.
(2012). Bi-directional PCR allele-specific
amplification (bi-PASA) for detection of
caspase-8−652 6N ins/del promoter
polymorphism (rs3834129) in breast cancer.


Available at: http://ijph.tums.ac.ir
