Absence of toll-like receptor 9 Pro99Leu polymorphism in cervical cancer [version 1; referees: 1 approved with reservations]

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Abstract

Background: Toll-like receptor 9 (TLR9) plays a key role in the elimination of viral pathogens by recognising their CpG DNA. Polymorphisms in the TLR9 gene may influence their recognition and subsequent elimination. Therefore, the present study was designed to elucidate the role of a rare unexplored TLR9 gene polymorphism C296T/ Pro99Leu (rs5743844) in cervical cancer susceptibility among Indian women.

Methods: The genotyping of TLR9 Pro99Leu polymorphism in 110 cervical cancer patients and 141 healthy controls was performed by polymerase chain reaction–restriction fragment length polymorphism (PCR-RFLP).

Results: The genotype frequency detected in both cervical cancer and control populations was 1.0 (CC), 0.0 (CT) and 0.0 (TT); while the allele frequency was found to be 1.0 (C) and 0.0 (T).

Conclusions: The present study results demonstrate no involvement of TLR9 C296T/ Pro99Leu polymorphism in cervical cancer susceptibility and supports worldwide minor allele frequency (MAF) (0.0002) status of the same as no nucleotide variation was detected in any of the study participants.

Keywords

Cervical cancer, TLR9, Polymorphism, Genotypic frequency, Susceptibility
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Author roles: Chauhan A: Formal Analysis, Investigation, Methodology, Visualization, Writing – Original Draft Preparation; Pandey N: Formal Analysis, Investigation, Writing – Review & Editing; Raithatha N: Investigation, Resources, Writing – Review & Editing; Patel P: Investigation, Resources, Writing – Review & Editing; Desai A: Investigation, Resources, Writing – Review & Editing; Jain N: Conceptualization, Funding Acquisition, Project Administration, Supervision, Validation, Writing – Review & Editing

Competing interests: No competing interests were disclosed.


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Grant information: The study was funded by Charotar University of Science and Technology (CHARUSAT).
The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Introduction
Cervical cancer is the fourth-most common cancer among women globally and second leading cause of cancer-related deaths in Indian women. Although persistent infection of high-risk human papillomavirus (hrHPV) is considered as the chief causative agent of cervical cancer, variations in host genetic make-up do influence the risk of acquiring HPV infection, and susceptibility to cervical carcinogenesis. In this context, variations in Toll-like receptors (TLRs), that play a crucial role in activating immune response by identifying pathogen-associated molecular patterns, have drawn significant attention, as single nucleotide polymorphisms (SNPs) in TLR genes have been shown to alter susceptibility to many infections and human diseases including cancer.

Ten functional TLR genes are known in humans, one of which, the TLR9 gene product, recognizes microbial DNA motifs. Frequently analysed TLR9 SNPs G2848A and −1486 T/C have been suggested to alter cervical cancer susceptibility, but no report is available elucidating the role of TLR9 Pro99Leu polymorphism in cancer. Although TLR9 Pro99Leu is a rare population SNP with a global minor allele frequency (MAF) of 0.0002 as reported in the single nucleotide polymorphism database (dbSNP), in-vitro analysis has revealed its significant role in DNA ligand hyporesponsiveness. Considering the fact that cervical cancer is largely caused by hrHPV infection and TLR9 has the ability to respond to viral DNA, the present study was designed to elucidate the association of the TLR9 Pro99Leu polymorphism with cervical cancer.

DNA isolation and genetic analysis
DNA was isolated from cervical cancer biopsies and cervical smears by standard phenol-chloroform extraction method. In the case of a low number of cervical cells, a spin-column based DNA isolation kit (Macherey-Nagel, Germany; Cat# 740952.50) was utilized as per manufacturer’s instructions. The quality and quantity of DNA was determined using ethidium bromide-stained 1% agarose gel on GelDoc system (BioRad, USA) as well as a NanoDrop 2000 (Thermofisher, USA). The TLR9 Pro99Leu polymorphism was detected using polymerase chain reaction –restriction fragment length polymorphism (PCR-RFLP) method as described by Kubarenko et al. Briefly, a 25µl PCR mix contained 0.1µM each of forward and reverse primer (Imperial Life Sciences, India), 0.1mM dNTP mix (Invitrogen, USA; Cat# 18427088), 2.5mM MgCl₂ (Vivantis, USA; Cat# RB0204), 1 unit Taq DNA polymerase (Kapabiosystems, USA; Cat# KK1015) and 100 to 150ng genomic DNA. The PCR was run on an MJ Mini thermal cycler (BioRad, USA).

Upon confirmation of 337 bp PCR product on 2% ethidium bromide-stained agarose gel, 10µl PCR product was digested with BslI restriction enzyme (New England Biolabs, USA; Cat# R0555S) at 55°C overnight, separated on 12% polyacrylamide gel and analysed on a GelDoc system (BioRad, USA) for genotype identification. The details of PCR conditions and parameters for genotype consideration are mentioned in Table 1 and Table 2 respectively. To confirm the PCR-RFLP results, we performed Sanger sequencing of five randomly selected cervical cancer as well as control samples. All the sequencing reactions were performed on 3730xl DNA Analyzer (Applied Biosystems, USA) using BigDye™ Terminator v3.1 kit (Applied Biosystems, USA; Cat# 4337454) as per manufacturer’s instructions. The 10µl sequencing reaction was comprised of 7.0µl BigDye™ Terminator v3.1 Ready Reaction Mix, 10pmol forward primer, 2.5mM MgCl₂, 0.1mM dNTP mix and analysed on a GelDoc system (BioRad, USA) for genotype confirmation. The clinical staging of cervical cancer samples was done as per The International Federation of Gynecology and Obstetrics (FIGO) guidelines.

Biological specimens
Biopsies from 110 cervical cancer patients and cervical smears from 141 healthy volunteers were collected from Shree Krishna Hospital, Anand; Sir Sayajirao General Hospital, Vadodara; and GMERS Hospital, Ahmedabad, India. The samples were collected from 2012 to 2017. The cancer biopsies and healthy cervical smears were histopathologically and cytologically confirmed.

Methods

<table>
<thead>
<tr>
<th>Primer Sequence (5′ – 3′)</th>
<th>Thermal Profile</th>
<th>PCR Product</th>
<th>Visualized on</th>
</tr>
</thead>
<tbody>
<tr>
<td>FP: GGATGTGGATGTGGCTGAGG</td>
<td>(95°C – 5’) 1</td>
<td>337 bp</td>
<td>2% Agarose</td>
</tr>
<tr>
<td>RP: AACTGCAACTGGCTGTCC</td>
<td>(95°C – 45°, 66°C – 1°, 72°C – 30°) 35</td>
<td>337 bp</td>
<td>2% Agarose</td>
</tr>
<tr>
<td>(72°C – 10°) 1</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Abbreviations: TLR9, Toll-like receptor 9; FP, forward Primer; RP, Reverse Primer; PCR, Polymerase Chain Reaction; bp, base pairs

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>Digested Products (bp)</th>
<th>Genotype</th>
</tr>
</thead>
<tbody>
<tr>
<td>BslI</td>
<td>166 + 136 + 35</td>
<td>CC (Pro/Pro)</td>
</tr>
<tr>
<td></td>
<td>201 + 166 + 136 + 35</td>
<td>CT (Pro/Leu)</td>
</tr>
<tr>
<td></td>
<td>201 + 136</td>
<td>TT (Leu/Leu)</td>
</tr>
</tbody>
</table>
primer and 50ng PCR product. The sequencing results were analyzed on Sequencing Analysis Software version 5.3.1 (Applied Biosystems, USA).

Statistical analysis
Statistical analysis was performed on GraphPad Prism version 5.00 for Windows (GraphPad Software, USA). Age of patients and controls were compared using two-sided Student’s t-test. Due to the presence of single genotype across all the samples no additional statistical association was performed.

Results
Demographic and clinical characteristics
The average age of cervical cancer patients (52.43±11.78 years) and controls (51.8±11.35 years) was comparable without any statistically significant difference (p=0.668). Histopathologic analysis revealed all the cervical cancer cases to be of squamous cell carcinoma type. According to FIGO analysis, 9 (8.2%), 39 (35.5%), 55 (50%) and 7 (6.3%) patients belonged to Stage I, II, III and IV respectively.

TLR9 Pro99Leu polymorphism
PCR amplification revealed the presence of a single intact band of 337 bp (Figure 1; Dataset 1). A single genotype CC (Pro/Pro) was detected across all the sample types (Table 3; Dataset 2) which was evident by the presence of 166 bp, 136 bp and 35 bp DNA bands after RFLP assay (Figure 2; Dataset 3). Sanger sequencing of the randomly selected PCR products corroborated with RFLP results (Figure 3; Dataset 4).

Dataset 1. Raw, unedited agarose gel images of PCR amplification of TLR9 gene segment for C296T/ Pro99Leu polymorphism from 50 samples consisting of 26 controls and 24 cervical cancer cases
http://dx.doi.org/10.5256/f1000research.14840.d20340

Figure 1 is a representative picture of the same.

Dataset 2. Age, clinical stage and TLR9 genotype status among cervical cancer patients as well as age and TLR9 genotype status among controls
http://dx.doi.org/10.5256/f1000research.14840.d203406

Figure 1. Representative PCR picture showing amplification of TLR9 gene segment for C296T/ Pro99Leu gene polymorphism on ethidium bromide-stained 2% agarose gel. Lane M is 100 bp molecular marker (Takara, Japan; Cat# RR820A), Lane 1 is negative control and Lanes 2–7 are tumor DNA showing PCR products of 337 bp. (Abbreviations: PCR, Polymerase Chain Reaction; TLR9, Toll-like receptor 9; bp, base pair).

Table 3. Genotype and allele frequencies of TLR9 C296T/ Pro99Leu polymorphism in cervical cancer patients and healthy controls.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Cervical Cancer n (%)</th>
<th>Controls n (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CC</td>
<td>110 (100.0)</td>
<td>141 (100.0)</td>
</tr>
<tr>
<td>CT</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
</tr>
<tr>
<td>TT</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
</tr>
<tr>
<td>Allele</td>
<td></td>
<td></td>
</tr>
<tr>
<td>C</td>
<td>220 (100.0)</td>
<td>282 (100.0)</td>
</tr>
<tr>
<td>T</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
</tr>
</tbody>
</table>
Figure 2. Representative PAGE picture of RFLP results for TLR9 C296T/ Pro99Leu polymorphism on 12% polyacrylamide gel. Lane M is 100 bp molecular marker, Lane 1 is undigested PCR product and Lanes 2 to 6 are showing digested PCR products of 166 bp and 136 bp (35 bp band is not visible) by BsaI enzyme representing CC genotype. (Abbreviations: PAGE, Polyacrylamide Gel Electrophoresis; RFLP, Restriction Fragment Length Polymorphism).

Figure 3. Sanger sequence electropherogram of (A) a healthy individual and (B) patient showing single peak (highlighted) of C allele of TLR9 C296T/ Pro99Leu SNP representing CC genotype. (Abbreviations: SNP, Single Nucleotide Polymorphism).
Discussion

Although hrHPV infection is the primary etiological agent of cervical carcinogenesis, the role of host genetic factors, especially those associated with body immunity such as TLRs, cannot be ignored. TLR9 SNPs −1486 T/C and G2848A have been found to be contradictorily associated with cervical cancer risk. In Polish and Mexican populations both TLR9 −1486 T/C and G2848A polymorphisms were suggested to be risk factors for cervical carcinogenesis. In two independent studies on Chinese population, a positive association with TLR9 G2848A SNP was detected but no involvement of TLR9 −1486 T/C was found, however, the other study suggested −1486 T/C was not a contributory factor to cervical carcinogenesis. From India, a single report on North Indian patients revealed a marginal role of TLR9 G2848A polymorphism with cervical cancer risk.

To date, no report is available on the rare TLR9 Pro99Leu polymorphism in cancer, which has been shown to be associated with DNA ligand hyporesponsiveness in HeLa cell lines. Considering the fact that cervical cancer is majorly caused by hrHPV infection and the TLR9 Pro99Leu polymorphism is associated with DNA ligand hyporesponsiveness, the present study investigated, for the first time, the role of the TLR9 Pro99Leu polymorphism in cervical cancer susceptibility. This is also the first report to study this polymorphism in any of the cancer types globally. Our results revealed the presence of a single genotype CC (Pro/Pro) among cases and controls, demonstrating no significance of the Pro99Leu polymorphism to cervical cancer susceptibility. A complete absence of Pro99Leu in our study population corroborates with the report of Lee and group (2006) where neither controls nor lung tuberculosis and sarcoidosis patients had the TLR9 Pro99Leu polymorphism. Similarly, the Pro99Leu polymorphism was not detected among healthy Caucasians as well as pneumococcal disease, bacteraemia, and leprosy patients. Moreover, according to dbSNP, the global MAF of this polymorphism is 0.0002, and our results, albeit on a smaller cohort, do solicit its rare polymorphism status. Therefore, a direct role of this SNP in cancer, as well as other diseases, seems a remote possibility. Nonetheless, a comprehensive analysis of a larger cohort covering a varied ethnic population globally is suggested to comprehend its role in microbial infection and/or disease susceptibility including cancer.

Conclusion

The preliminary data obtained from the present study does not suggest a role for the TLR9 Pro99Leu polymorphism in cervical cancer susceptibility. However, analysis on a larger cohort worldwide may provide more insights into the frequency distribution of Pro99Leu polymorphism and reveal its influential role in various human diseases including cancer.

Data availability

Dataset 1. Raw, unedited agarose gel images of PCR amplification of TLR9 gene segment for C296T single nucleotide polymorphism, obtained after performing Sanger sequencing on five samples each of cervical cancer and healthy controls.

Dataset 2. Age, clinical stage and TLR9 genotype status among cervical cancer patients as well as age and TLR9 genotype status among controls.

Dataset 3. Raw, unedited polyacrylamide gel electrophoresis images of 27 controls and 24 cervical cancer PCR amplified products that underwent restriction fragment length polymorphism (RFLP) analysis.

Dataset 4. Nucleotide sequences spanning TLR9 gene segment for C296T single nucleotide polymorphism, obtained after performing Sanger sequencing on five samples each of cervical cancer and healthy controls.

Ethical considerations

The research was carried out following due approval from ethics committee of all the participating institutes. Participants were verbally informed and explained about the study, and were provided with an information sheet. Written informed consent was obtained from the participants who agreed to enrol in the present study. Personal information of all the study subjects was kept confidential.

Competing interests

No competing interests were disclosed.

Grant information

The study was funded by Charotar University of Science and Technology (CHARUSAT).

The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Acknowledgement

Authors thank Dr. Anjana Chauhan, Gynec Cancer Surgeon, Ex Associate Professor, Gujarat Cancer and Research Institute, Ahmedabad, India for stimulating discussions.
References


With the global minor allele frequency of 0.0002, the studied sample size is too small. It is interesting to observe that there is only one genotype (homozygous wild type) present in the studied cohort. The power of the study should be mentioned by the authors. The conclusion drawn from the limited data set may not reflect the real situation. I suggest the authors to first calculate the number of samples required for the study on the basis of the frequency of minor/major alleles to achieve about 80% power of study and increase the sample size accordingly.

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Partly

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Yes

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Partly

**Competing Interests:** No competing interests were disclosed.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.
Dear Dr. Gopeshwar Narayan,

We thank you for approving our manuscript and appreciate your valuable suggestions. Please find below the response towards your reservations:

**Reservation:** With the global minor allele frequency of 0.0002, the studied sample size is too small. It is interesting to observe that there is only one genotype (homozygous wild type) present in the studied cohort. The power of the study should be mentioned by the authors. The conclusion drawn from the limited data set may not reflect the real situation. I suggest the authors first to calculate the number of samples required for the study on the basis of the frequency of minor/major alleles to achieve about 80% power of study and increase the sample size accordingly.

**Response:** Due to the complete absence of minor allele, the power of present study cannot be calculated. However, considering the global minor allele frequency of 0.0002 of the SNP, we calculated the power of study using [Online Sample Size Estimator](https://www.smppowercalculator.com/) which was found to be 3.6%. To achieve 80% power of study approximately 40000 cases and controls are required. It is presently not possible for us to collect and analyze such a larger sample size. Studies on Pro99Leu polymorphism with similar sample size and results have also been reported by Kubarenko et al., 2010 and Lee et al., 2006, which have been cited in the article.

**Competing Interests:** No competing interests were disclosed.