



Detection of HPV16 viral load in L2 gene as a related predictor of cervical cancer among women in Dhi-Qar province by qRT-PCR

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Abstract

Background The most common infection among young women that increases the risk of developing cervical cancer (CC) is human papillomavirus (HPV). In this study, we are going to assess whether HPV16 DNA concentration helps indicate cervical cancer progression, as well as for age groups and their relationship to cervical cancer.

Methods Present study included 93 adult females suffering from cervical cancer during the period from 2017 to 2020. Molecular detection of HPV was done using amplification of the L2 gene (minor capsid protein).

Results Present results showed that 60 (65%) of the patients from 93 cervical cancer cases were infected by HPV16 while only 5 (8%) of healthy patients from the control group were positive for HPV16. So, the current study revealed high HPV16 load in cervical cancer ranged from 1.09×10^2 IU/ml to 5.07×10^3 IU/ml with a mean \pm SD of viral load was 1043.25 ± 8.50 IU/ml while in healthy individuals very low viral load ranging from 88 IU/ml to 101 IU/ml and mean \pm SD of viral load was 91.25 ± 2.90 IU/ml was reported.

Conclusion HPV16 viral load is significantly associated with cervical carcinoma among women in Dhi-Qar Province.

Keywords HPV16 · Viralload · Cervical cancer · qRT-PCR · L2 gene · hrHPV16

Introduction

Globally, cervical cancer is the second most common malignant condition found in women. For the development of cervical cancer, persistent oncogenic type Human papillomavirus HPV infection has been proved as a biological intermediate [1, 2]. There are 12 types of Human papillomavirus including 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, and 59 that has been considered to have oncogenic properties

[3]. A study conducted among women who are 16 years to 29 years of age has shown that yearly, 42% and 56% of the women are infected with HPV 16 and HPV 18 respectively [4]. In persistent infections, the viral load for HPV 16 and 18 remained higher and it was concluded that hrHPV viral load can be used as a marker for persisting infections. Probably it helps in differentiating between regressing intraepithelial neoplasia2 (CIN2) and CIN3 lesions [5]. This can also help in assessing the development of the same in cervical

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cancer [6] using serial High risk Human Papillomavirus viral load measurements. Previous studies have been able to diagnose the after effect of High risk Human Papillomavirus (hrHPV) infection. The degree of CIN based on 2–3 consecutive measurements also suggested the potential of using this parameter in HPV triage in women who are HPV positive [7]. The Increased HPV viral load has also been shown to be an alternative indicator for persistence. In predicting the risk of squamous intraepithelial lesions (SIL), the role of HPV viral load has also been reported [8, 9]. Besides, HPV 16 infections were revealed to last longer than other forms of oncogenic HPV. For measuring HPV viral load, there are many PCR assays. Recent studies use methods that target HPV16 E6 and L1 genes based on quantitative real-time PCR (qRT-PCR). In this study, we will concentrate on the genetics of the small capsid protein, L2, which plays a key role during the assembly of virions [10, 11]. L2, which is approximately 500 amino acids long have an estimated molecular mass of 55KDa [11]. Thus, the current study sought to determine whether hrHPV16 viral load can be used as a predictor of cervical cancer progression in Dhi-Qar Province via qRT-PCR amplification of minor capsid protein L2.

Materials and methods

Sample collection

Samples were collected from Al-Hussein Teaching Hospital in Dhi-Qar Province/Iraq in the Histopathology Laboratory, and 93 samples were taken from the cervical cancer tissue blocks they were stored in the period from 2017 to 2020. Samples were registered according to the name and age of the patient, histologically diagnosed, and divided according to the stage of cancer development. Another 60 healthy women were included in the control groups. The approval from the institutional ethics committee of Al-Hussein Teaching Hospital was taken, (Approval Number: 66 on 16.03.2020).

DNA extraction

The HPV16 DNA was extracted from formalin-fixed paraffin-embedded tissue blocks by using G-spin™ Total DNA Extraction Kit (Fixed tissues protocol) as per the company instruction. The viral DNA concentration and purification perform by using a Nanodrop spectrophotometer (THERMO. USA) by reading the absorbance at (260/280 nm).

Primer and qRT-PCR

Human papillomavirus qPCR primer for minor capsid protein L2 gene (F: TGAAAATCCCGCCTTTGAGC and R: TGTGCCTTCAGGT GTTTCAC) were designed in this study using NCBI-Genbank database sequence (MH777342.2). PCR master mix was done (RealMODTM Green SF 2 × qPCR mix) as per the company instructions. The PCR master mix component was then centrifuged using Exispin vortex centrifuge at 3000 rpm for 3 min. The threshold cycle number (CT value) was used for real-time data analysis.

Statistical analysis

The data thus obtained were analyzed statistically. A student's *t*-test was performed for independent variables. *U* Mann-Whitney test was done for dependent variables. STATISTICA 10 PL software and Statistical Package for Social Sciences version 20 was used for statistical analysis with Microsoft Excel 2010. Only results that had a *p*-value < 0.05 were considered statically significant [12–15].

Results

In the present study, The SYBR green qRT-PCR method was used for quantification of the HPV16 L2 gene (Fig. 1) and the results showed that among 93 women with cervical cancer there are 60 (65%) cases that are positive for hrHPV16 and only 5 (8%) were positive in the healthy control group (Fig. 2). Depending on the viral copy number, viral load was calculated and significant differences appeared between the case and the control in the level of viral load ($P = 0.001$). The present study revealed high hrHPV16 load in cervical cancer ranging from 1.09×10^2

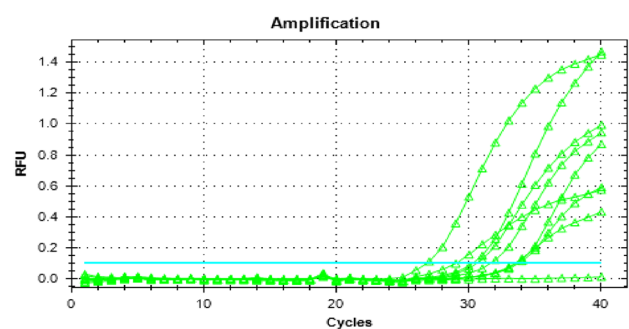


Fig. 1 Real-time PCR amplification plot of L2 gene for detection of HPV-16

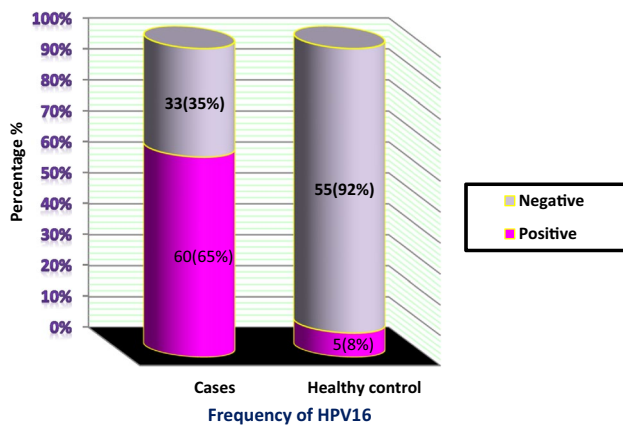


Fig. 2 Frequency of HPV16 in studied groups

Table 1 Frequency of HPV16 in studied groups

Viral load (IU/ml)	Case-control comparison		P-value
	Case	Control	
Range	$1.09 \times 10^2 - 5.07 \times 10^3$	88–101	
Mean \pm SD	1043.25 ± 8.50	91.25 ± 2.90	0.001*
SE	1.097	0.374	
N.	60	60	

*Significant correlation ($p < 0.05$)

IU/ml to 5.07×10^3 IU/ml with a mean \pm SD of viral load of 1043.25 ± 8.50 IU/ml while healthy individuals have very low viral load ranging from 88 IU/ml to 101 IU/ml and mean \pm SD of viral load of 91.25 ± 2.90 IU/ml was reported (Table 1).

Distribution of viral load according to patients' age groups in (Fig. 3) revealed that females with cervical cancer in the age group of 32–42 years and 43–52 years have the highest mean of hrHPV 16 loads but the mean of viral load was close in the age group 53–62 years and 63–78 years. However, these results showed statistically significant differences in the delivery of viral load according to patients' age groups ($P = 0.021$, $X^2 = 9.77$, $DF = 3$). Moreover, the Distribution of viral load according to cervical cancer stages also exposed statically significant differences ($P = 0.001$, $X^2 = 55.8$, $DF = 4$) when the highest mean (4022 IU/ml) of HPV16 load was detected in females who undergo from spread to distant cancer (stage III). The HPV16 load also showed an increase in patients in the cancer stages IV and II (3200 IU/ml and 3172 IU/ml respectively) whereas the lowest mean (987 IU/ml) of viral load appeared in stage I of cervical cancer as in (Fig. 4).

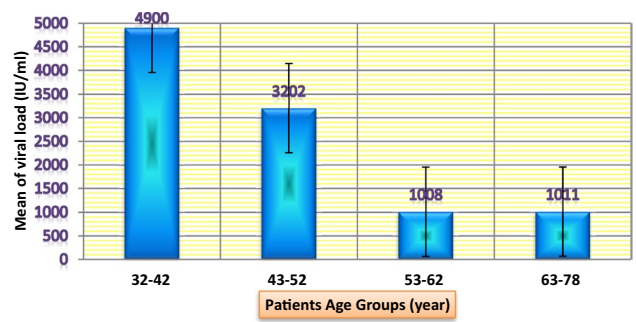


Fig. 3 Scattering viral load according to patients age groups ($P = 0.021$, $X^2 = 9.77$, $DF = 3$)

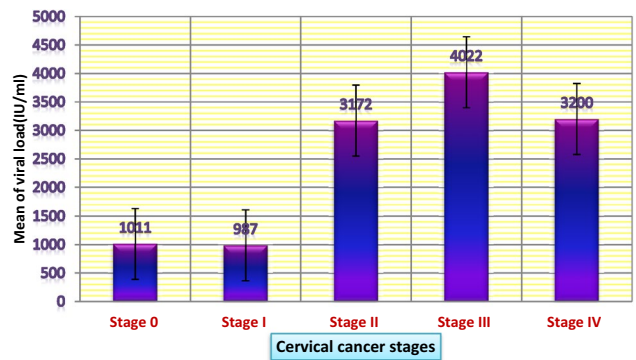


Fig. 4 Distribution viral load according to cervical cancerstages ($P = 0.001$, $X^2 = 55.8$, $DF = 4$).

Discussion

Epidemiological studies have shown that the first step in preventing cervical cancer and minimization of costs is the initiation of screening in the early stage [16–18]. The most prominent types of HPV are 18, 16, and 52 [19–28]. Following the previous study finding, the present study reported that 60 cases out of 93 cervical cancer are positive for hrHPV16. In a study conducted on a Mexican population, it was reported that geographical area also influences the frequency of viral genotypes. Reported in a study conducted in Jalisco, Aguascalientes, and Zacatecas showed that HPV 51 and 16 are the most prevalent ones [29–39]. In another study conducted in Tlaxcala, the highly prevalent genotype was HPV 16 and 18 [40]. In present data, females in the age group 32–42 years and 43–52 years have the highest hrHPV16 copy number, and that is consistent with another Iraqi study by Pity et al., (2019) who found the highest HPV positivity samples in the 30–49 years age group, An exceptionally high prevalence of cervical HPV was reported in Iraq due to the lack of a coordinated vaccine program in place [41]. Several studies have shown that

the measurement of viral load in cervical specimens for oncogenic HPV forms (including HPV16) is an appropriate predictor of recurrent infection and the risk of SIL and CC incidence [42–47]. However, the cervical cancer progression and its association with the HR-HPV viral load remains controversial. In the present study, the Distribution of viral load according to cervical cancer stages also exposed statically significant differences when the highest mean (4022 IU/ml) of HPV16 load detected in females who undergo spread to distant cancer (stage III) also showed an increase in patients in the cancer stages IV and II (3200 IU/ml and 3172 IU/ml respectively) whereas the lowest mean (987 IU/ml) of viral load appeared in stage I of cervical cancer. This finding was confirmed by past studies that have reported the association of high HPV load in cytological experiments with the increased risk of developing carcinoma in situ [48, 49]. Moreover, the current result agrees with Moberg et al. (2004), where it was reported that with an increase in the viral load in cervical smear the risk of future cancer development increases [50–55].

The hypothesis presented by Peitsaro et al. also supports the present study's finding [56]. Variations in sampling result in differing cell numbers in a sample and thus affect the viral load. This lack of a norm has established a major barrier to the use of viral load [57, 58]. Several studies have shown that increase in the viral load, and the risk and severity of the lesions increase [59, 60]. Shen et al. used micro-cutting technology in different grades of cervical cancer to gather viral load. This study reported that in high-grade disease viral load can be a crucial independent predictor [60, 61]. In some of the recent studies for HPV primary screening, the viral load was used either in combination or alone as a triage strategy [60, 62–64]. In a study by Duan et al. BioPerfectus Multiplex Real-Time PCR assay (BMRT) was used to quantitatively evaluate the number of single-copy genes. This assay is capable of detecting 14 subtypes of high-risk HPV and 7 subtypes of low and medium-risk strains and gives a viral load per unit cell [57]. However, the implementation of the qRT-PCR-based approach targeting the HPV16 L2 gene revealed consistency in the results for viral load and SIL and cancer grade [65–71]. To demonstrate this, a protocol based on PCR was used in this study to check if the viral load was an indicator of HPV 16 burden.

Conclusion

To conclude, hrHPV16's viral load is associated with the severity of cervical lesions. In primary screening, qRT-PCR can be used for HPV-positive females. To determine their relative importance for cervical cancer growth, larger cohort studies are warranted.

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Declarations

Conflict of interest None, has no conflict of interest.

Ethical approval All procedures performed in studies involving human participants were following the ethical standards of the institutional and/or national research committee and with the 1964 Helsinki declaration and its later amendments or comparable ethical standards.

Informed Consent Written informed consent was given by the patients and the control subjects for their tissue samples to be included in this study.

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