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Research Article

THE SIMULTANEOUS EXISTENCE OF HPV-HIGH-RISK TYPES 45, 51, 52 AND LOW-RISK 42 -RELATED CERVICAL CANCER IN APATIENT; A CASE REPORT

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ABSTRACT **ARTICLE INFO** Cervical cancer is the second most common cancer in women worldwide and the third among the Article History: female population in Iran. HPV plays an important role in the development of cervical cancer, being Received 18th August, 2016 present in 95% of cases of cancer of the cervix. We report a case of Simultaneous Existence of HPV-Received in revised form High-risk types 45, 51, 52 and Low-risk 42 – Related Cervical Cancer in a Patient. We also discuss the 22nd September, 2016 clinical features of the disease, its Histopathological findings, and treatment and rigorous follow-up. Accepted 14th October, 2016 HPV was diagnosed after DNA extraction from paraffin blocks of DNA HPV by PCR with primers. Published online November, 30th 2016 HPV type 45, 51, 52, 42 was found in a patients. Results of the study confirm the previous reports concerning the relationship between HPV and cervix cancer. The case study showed that a patient Keywords: could at the same time there is HPV- High-risk types 45, 51, 52 and Low-risk 42 - Related Cervical Cancer.

Human Papillomavirus, CervicalCancer, Sexually Transmitted Diseases.

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INTRODUCTION

The human papillomavirus (HPV) is a member of the *Papillomavirus* genus of the family Papovaviridae (Reichman, 2001). To date HPV is the most frequent sexually transmitted infection. Its occurrence is associated with sexual activity, and in fact the prevalence of HPV peaks soon after initiation of sexual activity among young women (Lazacano-Ponc *et al.*, 2001). Certain types HPV called "high risk": 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 68, 73, and 82 are the principal cause of invasive cervical cancer (Muñoz *et al.*, 2003). In this casereport we describe the presence of HPV type 42, 45, 51 and 52 in a cervical cancer of a woman who denied havinghad sexual activity. HPV is one of the most common causes of sexually transmitted disease in both men and women worldwide. The incidence of new infections in the United

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States ranges from 1 million to 5,5 million per year, and the prevalence is estimated to be as high as 20 million (Cates, 1996). Of the many types of HPV, about 30 infect the genital tract through sexual contact. Genital HPV types infect primarily the cervix, vagina, vulva, penis and anus. These genital-type HPVs are further divided into high and low-risk types, according to the association with genital tract cancer. Low-risk HPV types include types 6, 11, 42, 43, and 44, and usually cause benign anogenital warts. High-risk HPV types include types 16, 18, 31, 33, 34, 35, 39, 45, 51, 52, 56, 58, 59, 66, 68 and 70, and cause anogenital cancer (Muñoz et al., 2003). Among the cancers attributable to high-risk HPV infection, cervical cancer has received the most attention. HPV-16, -18, - 31, -45 account for more than 90% of cervical carcinomas (Muñoz, 2003). Of these types, HPV-16 is the most often found, accounting for about half of the cervical cancer cases in the United States and Europe (Muñoz, 2003). In addition, high-risk HPV types have been related with other genital cancers, such as carcinoma of vagina, vulva, penis and anus, and their precancerous lesions (Anderson, 2002).

METHODS

This study was performed prospectively by obtaining cervical samples from patients attended at secondary public health services in shafagh lab. The cervical samples collected from 1096 patients were submitted to cytopathological analysis and molecular tests for HPV detection, searching for HPVs 16, 18, 31 and 58. Archive of 1093 samples in laboratories, 258 samples were positive for human papilloma virus genome that human papilloma virus genome search operation is polymerized chain reaction (PCR) based on the guidelines of the World Wide HPV - The World Health Organization has been leading the general primers and reverse sequence called PGMY was used (Anderson, 2002). 1200samples were paraffin samples from across the country to laboratories Shafagh (Tehran), 1093 samples were good. Blocks, the 2-1 micron sections 10 and poured in Ependroph tube and 1 ml of 60 ° C xvlol were added. Put it in the machine's Hot block for 20 minutes at 60 ° C and around 14,000 were centrifuged for 15 minutes and the same thing was repeated. After decanting xylol and 99% ethanol added to it similar to the pre-set at 60 ° C for 20 minutes and was repeated twice. The tubes were centrifuged and the supernatant drained and placed in the open air to be dry. Consequently, 300 µl of digestion buffer (pH 7.5 HCL-Tris 50Mm, 10Mm EDTA, 0.5% Sodium dodecyl sulfate, 50 Mm NaCl, and 1.5 mg / ml Proteinase K) products of Merck added and at 56 ° C for 24 hours were incubated with a protein that is available to be digested. After centrifugation, the supernatant was transferred to a new tube. Nucleic acid purification process to obtain DNA extraction, all samples were checked using PCR: PCR reaction mixture was prepared with a volume of 50 ml containing 35µl H₂O, 6µl 10 X Buffer, 2µl MgCl₂, 0.5µl dNTP, 0.5µl Primer F, 0.5 Primer R, Taq 0.5µl or 5µl of template DNA is prepared from Sinagen. After a PCR reaction on the Epondorph thermo cycler, the product is obtained. The hybridization buffer was prepared by mixing 20 mL of hybridization solution and 600 μ L of Cy5-HC-T1(60fmol/ μ L). By mixing the 220 µL of the hybridization buffer and 20 µL of the Cy5-labeled PCR product of the HPV genotypeOut of 240 μ L, 110 μ L of this hybridization mixture were loaded on the sample loading porton the HPV genotyping 9G membrane strip and allowed to hybridize for 20 min at 25 °C final 240 µL hybridization mixture was prepared. After hybridization, washing solution was loaded into the washing port and allowed to stand for 8 min. Then, the HPV genotyping 9G membranes were scanned by the BMT Membrane Readerto obtain final results. Each experiment was done more than three times. The flow diagram for thehybridization, washing and scanning for the HPV genotyping 9G membrane. The genotyping results can be obtained in 30 min by using HPV genotyping 9G membrane tests. Analysis of data using statistical software SPSS (version 22) was used.

RESULTS

With surviving 258 existing human papilloma virus genome, determine the frequency of human papillomavirus genotypes were collected .with type-specific PCR results show a breakdown for each category. Among samples, 1096 of 258

(75%) were positive for a variety of oncogenes. Among 64 positive samples, the most common type in the type of 16 (46/63%). associated with the use of primers. View samples Other frequency types include types 18, 31 and 58 was 18/13%, 13/12 and 7/5% respectively. Multiple infections were observed in 12 samples (20%). Of the 15 samples, 14 samples had, samples with dual infection, there were 16 types. A trio of infection with the types of 16/18/31/58 was found.We report a case of Simultaneous Existence of HPV- High-risk types 45, 51, 52 and Low-risk 42 – Related Cervical Cancer in a Patient.

DISCUSSION

Human papillomavirus (HPV) is one of the most widely publicized and researched pathogenic DNA viruses. HPV detection rates depend on the population studied, the method of detection, the type of specimen and how it is obtained. Cervical cancer is closely related to persistent infection by highrisk Human Papillomaviruses (Tjalma et al., 2005). Scientific evidence gathered in the last five years strongly advocates the use of HPV NAT as a tool for primary screening for cervical cancer (Villa, 2008). In this study pathologic blocks were used for HPV testing by PCR methods. Today, the diagnosis of HPV infection is based on the detection of viral DNA (Grazyna et al., 2003). Cervical cancer world wide and the second most common cancer among womenisdeadly. The prevalence ofinfection indifferent communities. Young womenin Europeto 46% in the amount of pollution has been reported (Reitano, 1997; Motoyasusugase and Toshihiko, 1997). Over 100 genotype of the virus is known that at least 13 high-risk genotypes as typing sorted. Jenkinsand his colleagues based onthe most commonhigh-risk HPV types16 and 18 arein the world (Jenkins et al., 1996).

Comprehensivestatistics about the prevalence of the virus in relation to cervical cancer on cogene in there. High-risk HPV types have different geographical scope (Sasagawa et al., 2001). In a study conducted in Senegal of 16 and 58 were most associated with cervical cancer (Reitano, 1997). In a study in Japanof16, 51, 52 and 58 were in the cervix (Jenkins et al., 1996). Types 35 and 58 have beendominant in Mozambique (Motoyasusugase and Toshihiko, 1997). In Iran, several studies on the prevalence of HPV in women's. In this study Jabbarpoor et al (2008) on 72 samples of cervical cancer was performed in North West Iran, 42 (62%) for the presence of human papilloma virus genome, were positive. The most common types of HPV found in the samples, 16 with a frequency of 5/64 percent, followed by genotypes 31, 18 and 33 with a frequency of 22.6, 11.3 and 6.1 percent respectively in the next category respectively (15). HPV type 16 was the predominant infection (46/6%) in this study. in another study in Iran, the prevalence rate of HPV 16 was reported 6% (Sasagawa et al., 2001). The prevalence of HPV16 among Iranian patientswith cervical cancer is lower than those in Croatia (50%), Australia (53%), Thailand (41%), Colombia (69.9%), Spain (66.4%), Italy (32.6%), and China (48.8%) (Gree, 1997).

In this study, the frequency of patients with cervical cancer oncogene types in Table 1 that the rate of infection with the results of other studies of areas of Iran and other countries. The high prevalence of type 16 correspond with the results of international studies. The results of this study may be the first report on Iran in the prevalence of type 258 the infected samples to HPV type 16 is more. These results strengthen the hypothesis that the prevalence of type can in turn be a population different from other communities. Multiple infections also can be seen in Table 1 clearly. The single and multiple infections respectively 40 and 32 percent. This can result in the development of therapeutic strategies to target the virus to be used simultaneously with multiple special. Because of the sensitivity of the methods, samples containing very low levels of HPV DNA, are becoming viable HPV sample sources and in this study presence of HPV types 16,18 in samples (59.4%) were demonstrated. HPV type 16 was the predominant infection (44/64%) in this study. In another study in Iran, the prevalence rate of HPV 16 was reported 6.7% .We report a case of Simultaneous Existence of HPV- High-risk types 45, 51, 52 and Low-risk 42 – Related Cervical Cancer in a Patient.

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