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Research Article

ANALYSIS OF HUMAN PAPILLOMAVIRUS IN ARCHIVED CLINICAL SAMPLES OF BREAST CANCER PATIENTS Dr Shehroz Rana¹, Dr Shahid Iqbal¹, Dr Sundus Bukhari¹

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Abstract:

Introduction: Breast cancer is the most common cancer in women worldwide, and there were representing 22.9% of all new cancers in 2008 (an estimated 1.378 million new cases) and ranking second overall when both sexes are considered together. Aims and objectives: The basic aim of the study is to analyse the human papillomavirus in archived clinical samples of breast cancer patients. Material and methods: This descriptive study was conducted in health department of Puniab during October 2018 to March 2019. The data was collected from 50 patients of breast cancer. This study aimed to analyse the human papillomavirus in breast cancer patients. Genomic DNAs from tissue sections were prepared. For genotyping of HPV, the positive PCR products were analyzed by sequencing. The DNA sequence was determined with the Big-Dye terminator cycle sequence kit and an ABI 377A sequencer. Results: The data was collected from 50 patients. Statistical difference was observed in the HPV DNA status and HPV genotype between these two groups. HPV infection has increased the risk of breast cancer and had an OR of 13.953. The high-risk HPV types (HPV 16 and 18) were more prevalent than other HPV types in the cases. The HPV genotypes in samples of breast cancer patients were 26.67% for HPV-16 (4 isolates) and HPV-18 (4 isolates), 13.3% for HPV-23 (2 isolates) and HPV-6 (2 isolates), 6.67% for HPV-11 (1 isolate), HPV-15 (1 isolate), and HPV-124 (1 isolate), and one isolate could not be genotyped compared to HPV reference sequences while the sole detected HPV in control specimens was HPV-124. Conclusion: It is concluded that the presence of HPV genome in tumor tissues in women with breast cancer. HPV infection is associated with the development of breast cancer in women.

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INTRODUCTION:

Breast cancer is the most common cancer in women worldwide, and there were representing 22.9% of all new cancers in 2008 (an estimated 1.378 million new cases) and ranking second overall when both sexes are considered together. Despite of good prognosis of breast cancer, it was also the most common cause of death from cancer, with 13.7% of deaths the world total in woman. Mazandaran province is located in north of Iran and beneath the Caspian Sea. According to the annual report of Health Deputy of Ministry of Health and Medical Education in Iran, breast cancer in women was representing 23.38% of all new cancers in Mazandaran province in 2006-2007 and was the most frequent cancer of women [1].

The incidence of breast cancer is increasing almost everywhere, and this is due in part to increases in risk factors including decreased childbearing and breast feeding, increased exogenous hormone exposure, and harmful dietary and lifestyle changes [2]. On the other hand, breast cancer development might be a consequence of different environmental exposures, including viral infection [3]. Worldwide an estimated 12.1% of all human cancers (about 1.3 million cancer cases) were etiologically related to viral agents in 2002. Hence, the correlation of viral agents with breast cancer cannot be excluded.

During the last decades, a great interest was given to viral etiology of breast cancer [4]. Indeed, due to recent technical improvements and some encouraging new results, it has been a resurgence of interest in the possibility that a substantial proportion of human breast cancers may be caused by viral infections. High-risk genotypes of human papillomavirus (HPV) have been found in breast cancer cases [5].

There are controversial reports on the aetiology of HPV in breast cancer around the world. In the last two decades, considerable evidence has been found for a role for HPV in human breast cancer, but some studies suggested negative relationships. In vitro studies have shown that the main oncoproteins E6 and E7 from HPV16 are able to immortalize primary mammary epithelial cells and provided additional evidence for a possible role of this virus in breast carcinogenesis [6].

Aims and objectives

The basic aim of the study is to analyse the human papillomavirus in archived clinical samples of breast cancer patients.

MATERIAL AND METHODS:

This descriptive study was conducted in health department of Punjab during October 2018 to March 2019. The data was collected from 50 patients of breast cancer. This study aimed to analyse the human papillomavirus in breast cancer patients. Genomic DNAs from tissue sections were prepared. For genotyping of HPV, the positive PCR products were analyzed by sequencing. The DNA sequence was determined with the Big-Dye terminator cycle sequence kit and an ABI 377A sequencer. The nucleotide sequences of HPV isolates that determined in this study have been deposited in GenBank data base.

Analysis

Data were processed by SPSS statistical software program version 16.0. The correlations were subjected to χ^2 (Pearson chi-square) and Fisher's exact test. Odds ratios and logistic regression were also calculated. Statistical significance was set as a – P-value less than 0.05.

RESULTS:

The data was collected from 50 patients. Statistical difference was observed in the HPV DNA status and HPV genotype between these two groups. HPV infection has increased the risk of breast cancer and had an OR of 13.953. The high-risk HPV types (HPV 16 and 18) were more prevalent than other HPV types in the cases. The HPV genotypes in samples of breast cancer patients were 26.67% for HPV-16 (4 isolates) and HPV-18 (4 isolates), 13.3% for HPV-23 (2 isolates) and HPV-6 (2 isolates), 6.67% for HPV-11 (1 isolate), HPV-15 (1 isolate), and HPV-124 (1 isolate), and one isolate could not be genotyped compared to HPV reference sequences while the sole detected HPV in control specimens was HPV-124.

Parameter	Cases ^a $(N = 50)$	Controls ^a $(N = 5.0)$	<i>P</i> -value	
HPV			0 0 0 2	
Positive	15 (25 9) ^b	1 (2.4)	0R13953	
Negative	43 (74 1)	40 (97 6)	(95% CI 1 762–110 526)	
	13 (71.1)	10 (97.0)	() 5 / 6 CI 1.702 110.520)	
HPV genotype (% within type)				
HPV-124	1 (6.25)	1 (100)		
HPV-23	2 (12.5)			
HPV-18	4 (25)			
HPV-16	4 (25)			
HPV-15	1 (6.25)			
HPV-11	1 (6.25)			
HPV-6	2 (12.5)			
Unknown	1 (6.25)			
	·		·	
HPV genotype (% within subjects)				
High-risk type	8 (14)	0	0.005	
Low-risk type	6 (10.5)	1 (2.4)		
Negative	43 (75.5)	40 (97.6)		
HPV genotype (% within subjects)				
Mucosal type	11 (19)	0	0.002	
EV-cutaneous type	4 (6.9)	1 (2.4)		
Negative	43 (74.1)	40 (97.6)		
Tumor type (% within tumor type)				
IDC	67 (84.8)			
ILC	8 (10.1)			
IDC-ILC mix	1 (1.3)			
MC	2 (2.5)			
DC	1 (1.3)			

 Table 1: The characteristics of study subjects and prevalence of HPV DNA status in breast cancer patients and non-cancer controls.

DISCUSSION:

HPVs belong to Papillomaviridae family, and epidemiological studies have shown that a persistent HPV infection is the most important risk factor for cervical cancer. HPVs are also considered to be one of the risk factors for human breast carcinogenesis. The concept of the relationship between HPV and breast cancer is based on the identification of HPV genome sequence in breast cancer tissues and immortalization of primary mammary epithelial cells by high-risk HPV [7]. However, involvement of HPV in breast cancer is controversial. Since 1992, a growing number of studies had identified HPVs in breast tumors by PCR around the world, with a positivity variation from 4% to 86% for suggesting negative [9] or positive relationships. These results reflect the controversy in the role of HPV in the pathogenesis of breast cancer. The controversy is influenced by the technical limitations and the epidemiology of HPV in different geographical area [10,11].

CONCLUSION:

It is concluded that the presence of HPV genome in tumor tissues in women with breast cancer. HPV infection is associated with the development of breast cancer in women.

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