



Immunohistochemistry using in detection of Frequency of P16INK4A tumor suppresser gene overexpression in woman infected with cervical carcinoma in mid Euphrates

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Abstract : This study was designed as a retrospective research. A total number of (56) formalin-fixed, paraffin embedded cervical tissues were included. 27 with malignant cervical carcinoma (CC) and 16 with benign cervical tumors, 13 apparently healthy cervical tissues were used as a control group. The age of these individuals (patients and control groups) ranged between 23 and 73 years. They were collected from the pathological archives of teaching laboratories at many different private histopathological laboratories in Babil, AL-Najaf, Kerbela, AL-Qadisiya, during the period from April 2015 to January 2016. After sectioning of these cervical biopsies and staining by hematoxyline and eosin, a final definitive histopathological diagnosis was done by a consultant histopathologist. The study was designed as Immunohistochemical study to demonstrate the expression state of tumor suppressor genes (P16) in those tissues with cervical carcinoma, benign tumors as well as apparently healthy cervical tissues. The obtained results are summarized as follows: the most affected age of the patients with cervical carcinoma (68-83 years) were represented by 100% while the most affected age of the benign tumors group and control was (20-35) were represented by 53%.40% respectively. The most common histopathological type among all studied archived cervical carcinoma was squamous cell carcinoma 66,6% followed by the adinocarcenoma 33.3%. Over expression of p16 was detected by IHC in 48.1% (13 out of 27) cervical cancer cases and in 43.7%(7 out of 16) benign cervical tumor group, while none of control group showed P16- over expression. A high percentage 46.2% (6 out of 13) in cervical cancer while 42.9% (3 out of 7) found in benign cervical tumor group has a moderate score (score II). In the present study the highest percentage of p16 expression showed within cervical cancer cases was 53.8%, and 42.9% within benign cervical tumor group that have moderate signal intensity. The present study showed the high percentage of over expression of p16 was 52% found within age group (36-51 years) followed by 36%, 34%, 25% in age group (52-67 years), (20-35 years), (68-83 years) respectively. The present study showed the high percentage 50% of p16 INK4A overexpression found within squamous cell carcinoma.

Introduction

The tumor suppressor gene p16INK4A belongs to a significant group of cyclin kinase inhibitor genes which negatively regulate the Rb protein and subsequently the G1 phase of cell cycle its located on chromosome 9p21¹(Brooks *et al.*, 2010). Inactivation of p16INK4A gene is understood to be an early genetic event in cervical tumorigenesis with later expansion of the cell cycle from G1 to S phase. The effect of loss of

p16INK4A gene expression appeared through allowing cell growth and transformation by inactivating (phosphorylating) Rb protein²(Clifford *et al.*, 2008).

The cancer is a second greatest common disease in females worldwide, it is the main cancer of women in most developing countries, wherever 80% of cases occur³ (Hesselink *et al.*, 2007). The risk of cervical cancer is more in women aging 40 years of age or older and those who smoke, take contraceptive drugs for more than 5 years, have the history of multiple sex partners or immunosuppression⁴ (Kufee *et al.*, 2003). However, infection by certain types of human Papilloma virus (HPV) has been considered as the most significant risk factor for the development of cervical cancer^{5,6}(Kjaer *et al.*, 1996; Kraus *et al.*, 2006). It appears that the incidence of most types of tumors is increased in Iraq at multifold key to transformation are the E6 and E7 oncoproteins, which work to disrupt cell-cycle regulation, inhibit apoptosis and stimulate cell-cycle progression by binding inhibiting the P53 and p16, RB p110 tumor suppressor genes, respectively¹ (Brooks *et al.*, 2010). Immunohistochemistry was performed for revealing of tumor suppressor gene p16, Objective: To determine the frequency of p16INK4a expression in uterine cervical biopsies with or without dysplasia. Therefore, p16INK4a Immunohistochemistry (IHC) provides valuable additional information in the interpretation of cervical histology with resultant improvement in definitive identification of dysplastic lesions and reduction of inter-observer disagreement in conventional histology.

Methods:

Fifty (56) formalin-fixed, paraffin-embedded uterine cervical tissue blocks from patients who had undergone hysterectomy or punch biopsy from the cervix, Among these 56 cervical biopsies (43) Malignant and benign blocks were collected from the archives of histopathology laboratories of different general hospital in Mid Euphrates as well as many private laboratories.

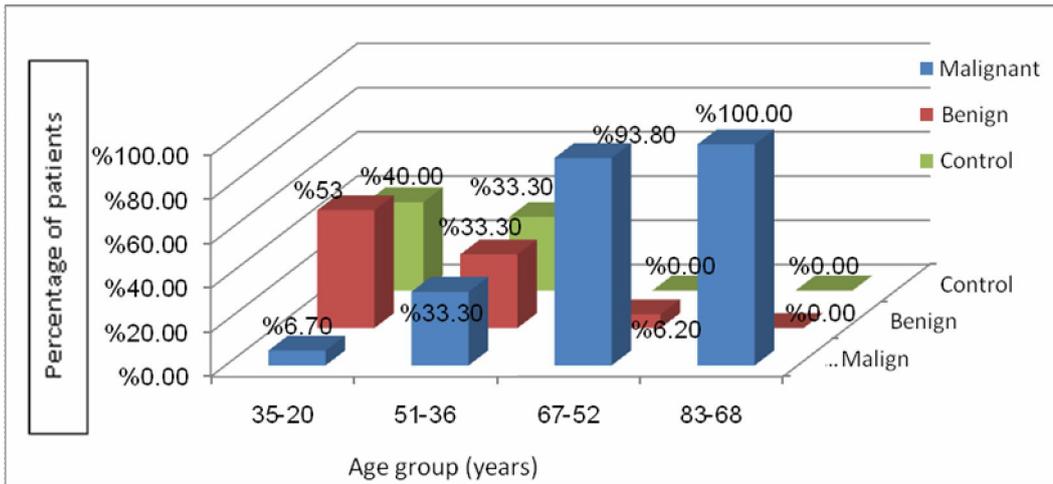
In addition thirteen cervical tissue blocks without any significant pathological changes have been obtained from patients sustained hysterectomies for uterine bleeding and were included as apparently healthy control group. Sections of 4- μ m thickness were cut from the paraffin blocks for hematoxylin-eosin staining and a detailed histopathological classification was assigned according to the criteria of the WHO (2011).

Immunohistochemistry.

Immunohistochemical staining was performed using the primary mouse monoclonal antibodies against p16INK4a, dilution 1:40 (clone E6H4, DakoCytomation), immunostaining for p16INK4a: After routine deparaffinization in xylene and rehydration through serial dilutions of alcohol the sections were subjected to heat-mediated antigen retrieval for 15 minutes in citrate buffer (pH 6.0). To minimize nonspecific binding, blocking was performed with 1% BSA at RT for 30 minutes. The primary antibodies were applied overnight at 4 °C followed by Envision visualization mouse system (DakoCytomation). 3,3'-diaminobenzidine (DAB) was used as the chromogen for 5 minutes and haematoxylin, as a counterstain. Stained sections were dehydrated and mounted in xylene. The percentage of immunopositive cells was evaluated (labeling index — LI). The immunoreactivity for all cell cycle regulatory proteins investigated in this study was evaluated as strong and weak according to the values of median. Statistical analysis was performed by SPSS statistical software package version 20, using the χ^2 test, t-test and ANOVA for comparing and finding any relations between HPV positivity and other variations. Statistical significance was assumed at the $P < 0.05$ level.

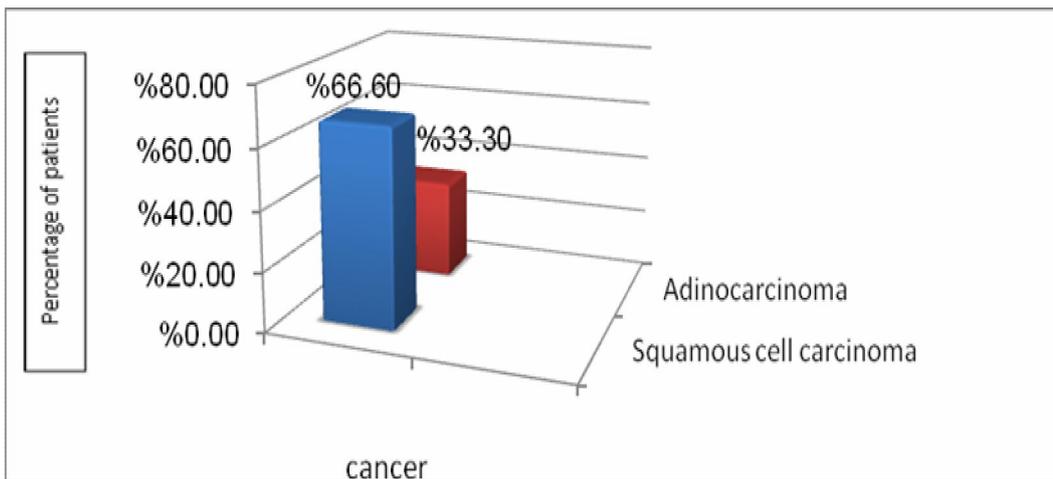
Results:

The archival specimen collected in this study was related to cervical tumor patients whose ages were ranged from twenty three years to seventy three years. In malignant cervical tumors, the most commonly affected age stratum was (68-83) years which constituted 100%, while the age stratum (52-67 years) was constituted 93.8%, followed by 33.3%, 6.7% for age stratum (36-51 years) and (20 -30 years) respectively. In benign cervical tumors, the most affected age stratum (20 - 35 years) constituting 53% followed by 33.3% for age stratum (36 -51 years) and 0% in age stratum (52-67 years). In control cases the most affected age stratum (20 - 35 years) constituting 40% followed by 33.3% in age stratum (36-51), Statistical comparison of these age strata revealed significant differences ($p < 0.05$) between different groups according to age (fig1).



Fig(1) Distribution of studied groups among the age (years) strata.

Seventy-two cases of cervical cell carcinoma were included in this study. Clinicopathological assessment revealed that 66.6% (18 out of 27 cases) patients were with squamous cell carcinoma and 33.3% (9 out of 27 cases) were with adenocarcinoma, Statistical analyses revealed significant differences ($p < 0.05$) between malignant sample groups according to type of cancer (Fig. 2).



Fig(2) Histopathological types of the presented cervical carcinoma patients

Over expression of mutated P16 protein was detected as a brownish discoloration at nuclear localization (Figure 3). Over expression of p16 was detected in 48% (13 out of 27) cells with cervical cancers and in 43.7% (7 out of 16) cases with benign cervical tumor, while non-cases of control group showed P16- over expression. A highest percentage 46.2 % (6 out of 13 cases) was involving cases with malignant cervical tumor that have either strong score (score III) ,30.8%(4 out of 13) have low score (score I).While, in benign cervical tumor group, 42.9 % (3 out of 7) were found to have low score (score I) and none of control group showed positive signal. Statistically, significant differences ($p < 0.05$) were found on comparing the results (according to score) between cervical cancers, benign tumors and control group ,(Table 1).

Table (1): Distribution of immunohistochemistry of P16protein according to the signal scoring.

P16 over expression	Malignant cervicalcancers (n=27)		Benign cervical tumors (n=16)		Healthy cervical tissues (n=13)		P	
	N	%	N	%	N	%		
Negative	14/27	51.9	9/16	56.3	13/13	100	0.005*	
Positive	13/27	48.1*	7/16	43.7*	0/13	0.0		
Scoring	I	4/13	30.8	3/7	42.9	0/0		0.0
	II	3/13	23	2/7	28.6	0/0		0.0
III	6/13	46.2	2/7	28.6	0/0	0.0	0.236 N.S	

*significant

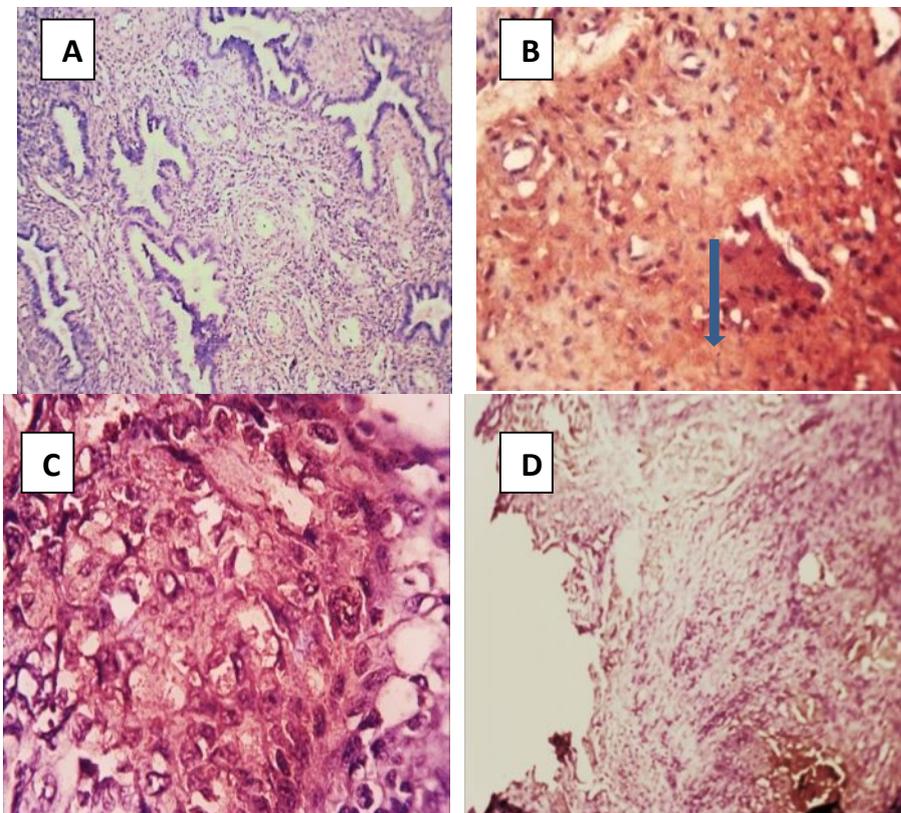


Fig (3) Immunohistochemical staining of P16 protein over expression using biotinylated -labeled anti-P16 protein antibody, stained by DAB-chromogen (Brown) and counter stained by mayer'shematoxyline (Blue). A. cervical cancer with negative P16 –ICH reactions(40X) B. Positive P16 –ICH reaction with strong score and high signal intensity (40X). C. Positive P16 –ICH reaction with moderate score and high signal intensity (40X). D. Positive P16 –ICH reaction with low score and high signal intensity (40X).

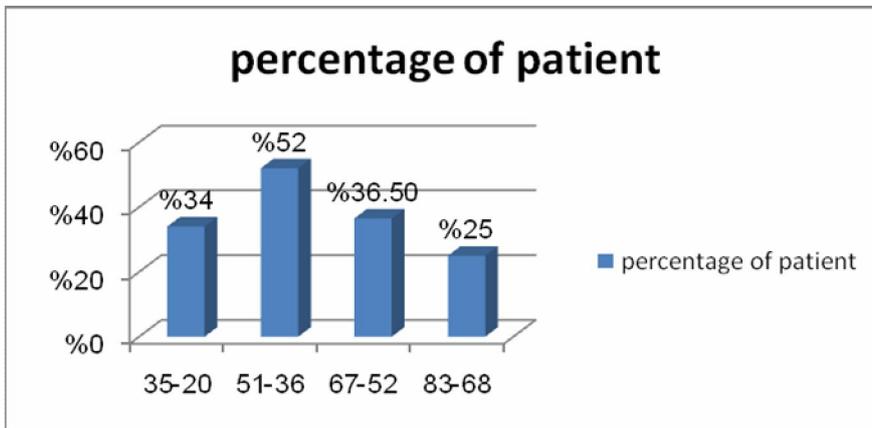
Twenty cases out of 56 (35.6 %) showed positive IHC- reactions of p16 over expression. None of healthy cervical tissues showed positive P16-IHC reaction. The highest positive P16-IHC reactions in those with malignant cervical cancer group were showed moderate signal intensity 53.8% (7 cases out of 13) while 30.8% (4 out of 13) found within strong signal intensity . In benign cervical tumor group, the percentage 42.9% (3 cases out of 7) have moderate and strong signal intensity. Statistically, non-significant differences ($p > 0.05$) were found on comparing each group of cervical cancers and benign cervical tumors to the control group (Table 2)

Table (2) : distribution of immunohistochemistry of P16 protein according to the signal intensity.

P16 over expression	Malignant cervical cancers (n=27)		Benign cervical tumors (n=16)		Healthy cervical tissues (n=13)		P
	N	%	N	%	N	%	
Negative	14/27	51.9	9/16	56.3	13/13	100	0.002*
Positive	13/27	48.1*	7/16	43.7*	0/13	0.0	
Scoring	Weak	2/13	15.4	1/7	14.2	0/0	0.148 N.S
	Moderate	7/13	53.8*	3/7	42.9*	0/0	
	High	4/13	30.8	3/7	42.9	0/0	

• **Significant P16 overexpression according to age groups**

The highest percentage of P16 overexpression found in age group(36-51years) was represented 52% ,followed by 36% ,34% ,25% showed within age group (52-67 years),(20-35years), (68-83years) respectively. Statistically theP16overexpression has no significant correlation to age. Table(3)



Fig(3): Occurrence of Immunohistochemistry for P16INK4A protein according to age groups

Over expressed-P16 protein in relation to cervical cancer types

The highest percentageof P16 – IHC reaction showed within squamous cell carcinoma were represented 50% (9 out of 18 cases) while adenocarcinoma was represented 44.4% (4 out of 9 cases), 75% (3 out of 4 cases) of adenocarcinoma that have high score (score III) while 44.4% (4 out of 9 cases), 33.4 % (3 out of 9 cases) in squamous cell carcinoma was showed within score (score III, II) respectively.Statistically, non – significant differences (p>0.05) was found between cervical cancer types and their P16-protein over expression.Table (4).

Table (4): The Relation of P16 – overexpression with cervicalcancertyping

P16 over expression	Squamous cell carcinoma (n=18/27)		Edenocarcinoma (n=9/27)		P	
	N	%	N	%		
Negative	9/18	50	5/9	55.5	0.245 N.S	
Positive	9/18	50	4/9	44.5		
Scoring	I	2/9	22.2	0/4		0.0
	II	3/9	33.4	1/4		25
	III	4/9	44.4	3/4		75

Discussion:

The pathological and clinical data of Cervical Cancer were measured to explore this challenging group of malignancies in relative to their existing information. Look over the 56 cases which were included in this study, it was established the age of the patients with cervical tumor and apparently healthy control was ranging between 23-73 years (Fig. 1). The current results are reliable with those reported world-wide where these cervical cancer commonly affecting females over forty years of age⁷ (Goodman, 2002). Moreover, it was observed that the percentages of cervical cancer cases are improved with the proceeding of age of patients. These results could reflect that age is a significant risk factor in cancer changes affecting cervical epithelial tissues lesions. In present study the results could have their significance when identifying that the age of the cervical cancer patients is a strong factor both for the incidence and management of the disease⁸ (American Cancer Society, 2009).

Overall, aging increases the incidence of the malignant changes in cervical epithelial tissues^{9,10} (Grey and Lila, 1994; Koyama *et al.*, 2007). In current study, the peak age frequency was 68-83, 52-67 years which constituted 100%, 93.8, respectively (Figure 1). A similar peak frequency was recorded in other reports from other countries that older women have increased rates of cervical cancer⁶ (Krauset *al.*, 2006). This is similar to another study by Aslaniet *al.*, where patients' age ranged from 20 to 80 years¹¹ (Hong *et al.*, 2010).

The recent numbers that show younger women being affected more by the disease has led many professionals to modify ages to include older and younger women, the most recommended ages for screening are between 20-70 years of age even though some researchers suggest that screening under the age of 25 is poor use of resources (Paul *et al.*, 1991). The current findings of high percentage of cervical cancer with the increasing of the patients' age could be correlated by many other factors which improve the appearance of malignant cervical tumor in old age group through the proceeding of age such as genetic predisposition, hormonal factors and changes in life style which characterized by a highly caloric diet rich in fat, and refined carbohydrate which in turn are reinforced by many previous studies done by¹³

Squamous cell carcinoma is the cervical cancer with the most incidences; while the incidence of adenocarcinoma of the cervix has been increasing in recent decades¹⁴. (Kumar, 2007). In the present study, squamous cell carcinoma was found to be the most common type (66.6%) among the group of cervical cancer patients. This result means that the woman is likely to have an invasive cancer, in contrast the type of glandular cell abnormalities adenocarcinoma constituted 33.3%. Cancers of the glandular cells are called *adenocarcinomas*, in some cases, the pathologist examining the cells can tell whether the adenocarcinoma started in the endocervix, in the uterus (endometrium), or elsewhere in the body⁸ (American Cancer Society, 2009).

Occurrence of p16 INK4A among cervical tissues tested:

One of the most significant themes still unresolved in the cure and management of Cervical Cancer is our inability to define earliest changes that lead to the disease and target it for treatment. Thus, the documentation of reliable biomarkers such as p16 tumor suppressor gene, treatment represents a crucial requirement not only for translational academic but also for clinical oncologists¹⁵ (Buchynska *et al.*, 2007). The p16 INK4A gene is exclusively the cell cycle regulating genes and encodes a nuclear protein p16, that phosphorylate the retinoblastoma gene product (pRb), thus blocking G1-S cycle progression. This gene when inactivation stimulates cell proliferation, therefore is found in many diverse types of carcinomas such as gastric carcinoma, bladder tumor, glioma, breast cancer, cervical cancer and head and neck tumors¹⁶ (Chen, *et al.*, 2004).

Immunohistological expression of p16^{INK4a} was seen only in dysplastic/neoplastic cells, and was never observed in normal cervical epithelium. Thus, p16^{INK4a} expression appears to be a strong, specific and subtle biomarker of cervical neoplasia, confirming the results of previous smaller series^{17,18} (Klaes *et al.* 2001, Dray *et al.*, 2005). Although other pathways cannot be ruled out, increased expression of p16^{INK4a} in the setting of CC probably occurs mainly as a result of inactivation of RB by high-risk HPVs. Incidental support for this evidence comes from the observation that increasingly high p16^{INK4a} expression scores were seen in cervical specimens showing invasive carcinoma, lesions known to be closely associated with high-risk HPV infection¹⁹ (Ostor, 1993).

In current study, we found the positive signals of P16-IHC in malignant cervical tumor were 48.1 %, followed by 43.7% in benign cervical tumor, and 0.0% in healthy cervical tissues (table 1). Among the 27 cervical cancer cases in this study, 14 (51.9%) were negative for p16 protein immune-expression. These findings are in agreement with reports published by Lana Lesnikova *et al*, 2009²⁰ who demonstrated that p16 overexpression in CC cases have 98.5% the differences in p16 expressing between this finding and our finding may be due false positive or false negative result or due to poorly preservative of formalin fixed paraffin embedded tissue. The non-expression rate of p16 protein also correlated with the presence of metastatic disease at diagnosis and development of distant recurrence disease. The concordance between the P16 protein expression and high grade cervical abnormality is documented by¹⁷ Klaes *et al*, (2001) who demonstrated that most if not all HSILs were P16 INK4A positive, which is in agreement with results reported by Nicolet *et al.*, (2012)²¹ where P16 expression was observed in 19/35 (54.3%). In present study P16 INK4a positivity in cervical cancer was relatively agreement to the findings of between 50% and 60% in the studies reported by Agoffet *et al* and Klaes *et al* (Agoffet *et al*, 2003; Klaes *et al*, 2001)^{17,24}.

In the current study, p16 immunoreactivity was calculated depending on the scoring. That is used by several studies²² (Tam SW, 1994). In the present study, the highest percentage of P16-IHC score signal found in high score (III) was (46.2%) were found within cervical cancer and in low score (I) 42.9% within benign tumor. This result was agreement with study of Maxwell *et al.*, (2010)²³ that found the high percent in strong scoring (III). According to the intensity signals, it was detected the highest percent of p16-INK4A in the moderate intensity (53.8%) for malignant cervical tumor, followed by 30.9% in the strong intensity. while In the benign cervical tumor it was found the highest percent of p16 INK4A in the moderate and strong intensity in (42.9%). while none detected any signals in control group (Figure: 4-3).

The score as 1, 2, or 3 was considered as p16 -positive in order to show the differentially expressed levels of p16 INK4A between neoplastic spindle cells and non-spindled cells. In the present study, the score of p16 INK4A expression was determined based on both the intensity and the percentage of positive tumor cells. According to the intensity, staining in the nuclei of cancer cells was determined as the positive hybridization signal²⁴. (Agoffet *et al*, 2003).

In present study found the high percentage of p16 INK4A over expression found within age group 36--51 years was 52% followed by 36% in age group (52-67 years) Zhang, (2009) found the high percentage in median of age as 59.6% (range, 20–89 years). years this result is consistent with our result where the high percentage of P16 ranging between age group (36-51 years) and age group (52-67) years (Figure 3). This result explained by (Hend, *et al.*, 2006)²⁵ as high expression of P16 was more frequently detected in adult CC patients form than in young age. The present study showed the high percentage of p16 INK4A over expression found within squamous cell carcinoma were represented as 50% while in adenocarcinoma the p16 INK4A expression have 44.4% By analogy, these observations are supported by the findings of Reed, *et al.*, (1996)²⁶ where they found that 70% of poorly differentiated squamous cell carcinoma carcinoma have abnormalities in the expression of P16.²⁷⁻⁵¹

Conclusion:

We establish that highest age – specific frequency was noticed in elderly aged- patients with cervical malignant age group of (52–67 years), (67-83 years) and in benign cervical tumors in age group (20 – 35 years). Also majority cervical carcinomas are pronounced by strong expression of p16 INK4a proteins, although in need of corroboration on a larger pool of cases, show that p16 INK4a may represent promising tool toward the identification of patients with poorer prognosis who may benefit from more aggressive therapy and HPV screening.

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