

*Research Article***Immunohistochemical Expression of Survivin and B^V-H¹ in Renal Cell Carcinoma****Rabab A. Safwat, Nehad M. Abd El-Maqsoud, Dalia M. Abd El-Rehim, Heba M. Tawfik and Reda F. Abd El-meguid.**

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Abstract

Background: Kidney cancer is the ninth most common cancer in developed countries. According to last registries of Egyptian National Cancer Institute, renal cell carcinoma represents 9.7% of all malignant renal tumors. Survivin is a member of the inhibitor of apoptosis protein family that inhibits apoptosis and play a critical role in regulating mitosis and microtubule stability. B^V-H¹ (also known as PD-L¹) is a ligand that inhibits T cell – mediated immunity and has been implicated as a potent negative regulator of antitumor immunity.

Methods: The aim of the current study was to investigate the immunohistochemical expression and the relevant clinicopathological significance of survivin and B^V-H¹ and to study the relationship between the two markers in one hundred cases of RCC tumors including histologically confirmed 70 cases of clear renal cell carcinoma, 10 cases of chromophobe renal cell carcinoma, 10 cases of papillary renal cell carcinoma, 7 cases of mixed renal cell carcinoma, 3 cases of granular renal cell carcinoma and 0 cases of sarcomatoid renal cell carcinoma. **Results:** A significant association was found between nuclear survivin expression and different clinicopathological features including (primary tumor classification, regional lymph involvement, advanced tumor stage, perinephric fat invasion, lymphocytic infiltrate, SSIGN score, MR score ($p < 0.001$ for each), tumor size ($p = 0.001$), nuclear grading ($p = 0.002$) and coagulative tumor necrosis ($p = 0.002$). However, no significant association between cytoplasmic survivin expression and any of clinicopathological features. Regarding B^V-H¹ expression, the present study showed positive B^V-H¹ expression in 99% of RCC tumors. A significant association was found between B^V-H¹ expression and different clinicopathological features including, primary tumor classification, regional lymph involvement, advanced tumor stage, nuclear grading, coagulative tumor necrosis, perinephric fat invasion, lymphocytic infiltrate, SSIGN score, MR score ($p < 0.001$) and tumor size ($p = 0.001$). Combined expression patterns of both markers revealed 4 immunophenotypes, including 99 (99%) survivin^{Low}/B^V-H¹⁻ tumors, 14 (14%) survivin^{Hi}/B^V-H¹⁻ tumors, 9 (9%) survivin^{Low}/B^V-H¹⁺ tumors, and 70 (70%) survivin^{Hi}/B^V-H¹⁺ tumors. Among them, the survivin^{Hi}/B^V-H¹⁺ immunoprofile showed a strong significant association with the more aggressive clinicopathological features including advanced primary tumor classification, regional lymph involvement, advanced tumor stage, coagulative tumor necrosis, perinephric fat invasion, lymphocytic infiltrate, higher SSIGN score and MR score ($p < 0.001$) and higher nuclear grading ($p = 0.002$). On studying the differential expression of both markers in primary RCC tumors and their corresponding LN metastasis, no significant differences were noticed between primary tumors and their corresponding LN metastasis with high concordance rates were found between both locations. **Conclusion:** Taken together, it can be speculated that dual expression of survivin and B^V-H¹ can be used to predict RCC tumor aggressiveness.

Key words: Survivin- B^V-H¹ - RCC - Immunohistochemistry**Introduction**

Kidney cancer is the ninth most common cancer in developed countries⁽¹⁾. It consti-

tutes about 3% of all solid neoplasms and ranks 10th as the leading cause of cancer

mortality⁽⁷⁾. In Egypt, renal cell carcinoma represents nearly 1.7% of total adult malignancies and accounts for 0.7% of all malignant renal tumors⁽⁷⁾. Eighty percent of renal cell cancers are clear cell adenocarcinomas, the remainder being papillary (10%), chromophobe (0%), and collecting duct carcinomas (<1%)⁽¹⁾.

There are different factors influencing RCC prognosis which include anatomical, histological, prognostic nomograms and molecular factors^(8,9). Regarding the anatomical factors, they include tumor size, venous invasion, renal capsule invasion, adrenal involvement, lymph node, and distant metastasis. These factors are commonly gathered together in the universally used TNM staging classification system^(8,9,10), while the histological factors include Fuhrman grade, RCC subtype, sarcomatoid features and tumor necrosis and lymphocytic infiltrate^(8,9,10). Several clinic-pathologic scoring systems (also referred to as nomograms or algorithms) have been reported to predict outcomes for surgically treated RCC patients. Such algorithms include the 2002 American Joint Committee on Cancer (AJCC) TNM stage groupings, the (UCLA) University of California Los Angeles Integrated Scoring System (UISS), nomograms from Memorial Sloan-Kettering Cancer Center, and the Mayo Clinic stage, size, grade, and necrosis (SSIGN) score⁽¹¹⁾. These scoring systems alone do not fully account for the varied outcomes associated with RCC, and fail to reveal the molecular basis for RCC aggressiveness or rational targets for therapy⁽¹²⁾. As a result, there is considerable interest in the identification of tumor-associated biomarkers that might enhance RCC prognostication and guide development of new therapies⁽¹³⁾.

Survivin is a member of the inhibitors of apoptosis (IAP) family of antiapoptotic proteins⁽¹⁴⁾. Survivin has attracted attention as a unique member of the IAP gene family with a potential dual role in apoptosis inhibition and regulation of mitosis⁽¹⁵⁾. In fact, although survivin is undetectable in most adult tissues, it is demonstrated a strong survivin expression in most human solid tumor types as lung, colon, breast,

pancreas, liver cancer, as well as in hematologic malignancies. They also showed that high levels of the protein were predictive of tumor progression in terms of either disease-free or overall survival^(16,17,18,19,20). Several studies suggests that those RCC patients who present with tumors that express high levels of survivin are at increased risk of cancer progression and RCC death^(21,22,23,24,25).

BV homolog 1 (BV-H1) also known as Programmed cell death ligand 1 (PD-L1) or cluster of differentiation (CD274), is a protein is encoded by the CD274 gene in humans which belongs to group II BV family⁽²⁶⁾. BV-H1 on tumor cells promotes immune suppression by binding to PD-1 on activated T cells, thereby sustaining tumor growth inhibit tumor-specific T cell-mediated immunity, through binding to the T-cell PD-1 (or a putative non-PD-1) receptor, inducing T cell apoptosis, impairing cytokine production, and diminishing the cytotoxicity of activated T cells⁽²⁷⁾. Many studies revealed that BV-H1 is highly expressed in most human solid cancers including breast, colon, esophageal, gastric, head and neck squamous cell, kidney, liver, lung, ovarian, pancreatic, salivary and urothelial carcinomas, as well as in glioblastoma, wilms' tumor and melanoma^(28,29,30). In RCC many studies showed that RCC patients harboring tumors expressing BV-H1 are at significantly increased risk for progression and mortality^(31,32,33).

Both survivin and BV-H1 may promote RCC tumor progression: the former by promoting tumor cell immortalization and the latter through evasion of the immune system. Because both of these molecules act via very different mechanisms to preserve tumor cell viability, one might anticipate that RCC tumors expressing both of these molecules might behave significantly more aggressively than RCC tumors that express either marker alone. Alternatively, one might just as easily predict that these two molecules are randomly produced by increasingly dysplastic cells, overlapping as prognostic variables and acting as surrogate biomarkers for one another. Hence, we examined the clinical effect of combined

survivin and B ν -H ν expression in RCC tumors obtained from one hundreds surgically treated patients.

Material and Methods

Cases Selection: The present study comprised one hundred case randomly selected from formalin – fixed paraffin embedded cases of renal cell carcinomas which were chosen from the archive of histopathological laboratories of Minia University Hospital and National Cancer Institute (NCI) of Cairo (In the period between 2000 and 2011). The cases included; 50 case of clear renal cell carcinoma, 10 cases of chromophobe renal cell carcinoma, 10 cases of papillary renal cell carcinoma, 5 cases of mixed renal cell carcinoma, 5 cases of granular renal cell carcinoma and 5 cases of sarcomatoid renal cell carcinoma.

Clinical and pathological features: The available clinicopathological data were obtained from the pathology reports of the cases. This data includes patients' age and sex, tumor localization, tumor size, tumor necrosis, perinephric fat invasion, sarcomatoid differentiation, tumor type (tumor classification was performed according to the WHO criteria)⁽¹⁷⁾, nuclear grade was revised according to Fuhrman nuclear grading system and subdivided into 4 grades; 1, 2, 3 and 4 respectively⁽¹⁸⁾, tumor stage and lymph node metastasis was estimated according to TNM staging classification system⁽¹⁾. The key clinicopathological data of the patients are summarized in Table (1).

Regarding clear cell type, assessment of lymphocytic infiltrate was done. T lymphocytes cell infiltration is then categorized according to the density as: grade 0, absent; grade 1, focal infiltration (scattered lymphoid aggregates); grade 2, moderate infiltration; grade 3, marked infiltration⁽⁴⁾.

SSIGN score and Metastatic Risk score were also estimated according to the data obtained from the pathology reports in each case. All primary tumors and 11/22 (available blocks) of metastatic malignant

lymph nodes were prepared and stained with haematoxylin and eosin stain to revise the histological findings of all the cases.

Immunohistochemistry for survivin and B ν -H ν

Immunohistochemistry was carried out using the avidinbiotin peroxidase complex method. Two, 3- μ m sections thickness from representative paraffin-embedded tissue blocks were sectioned for each case of the cohort and its available corresponding lymph node. One slide was stained with anti-survivin (Monoclonal mouse antibody, clone 12 C4, 0.2 ml concentrated, Dako; 1:100 dilution, incubated for one hour) using standard techniques. The second slide was stained with B ν -H ν , a mouse anti-human monoclonal antibody specific for B ν -H ν (Polyclonal rabbit antibody, 0.1 ml concentrated, US Biological; 1:100 dilution, incubated overnight).

Positive and negative control: One negative control tissue was processed for each run by omitting the specific primary antibody from the staining procedure and replaced with PBS. Regarding survivin, the positive control was sections of prostate adenocarcinoma, while sections of human tonsillar tissue were used as positive control for B ν -H ν expression.

Scoring system: To assess positive staining for survivin, the entire tissue section was screened for positive tumour cells, defined as cells with nuclear and /or cytoplasmic staining. Survivin nuclear and cytoplasmic staining was evaluated separately for each case.

- Nuclear survivin expression was evaluated as the percentage of tumor cells stained positive by counting numbers of survivin-positive (versus total) tumor cells in five representative high-powered fields (X 400 magnification). Cases were then stratified into low expression (Survivin^{low}) and high expression (Survivin^{hi}) corresponding to <10 positive cell per mm² and \geq 10 positive cells per mm² according to Parker et al.,⁽¹⁹⁾

- Cytoplasmic survivin expression was evaluated with each slide as the percentage of positively stained cells in five high power fields (X 400 magnification). Cases were

considered +ve when $\geq 10\%$ of tumor cells showed cytoplasmic survivin expression according to Byun et al.,⁽¹⁰⁾

Regarding B ν -H ν Expression, tissue section was screened for positive tumor cells, defined as cells with membranous and/or cytoplasmic staining. Cases were considered +ve when $\geq 10\%$ of tumor cells showed membranous and/or cytoplasmic B ν -H ν expression according to Thompson et al.,⁽¹¹⁾

Statistical analysis

All statistical analysis was done using statistical package of social science (SPSS® Release 16) (SPSS, Inc.) software. Association between immune reactivity and different clinicopathological data were done by Chi-square test. Spearman's rho coefficient was used for continuous variables to assess the correlation between the two markers. McNemer test was used to compare expression of survivin and B ν -H ν in primary tumors and their corresponding LN metastasis. Statistical significance was determined at p value of ≤ 0.05 .

Results

On studying the expression of survivin, we found that both nuclear and cytoplasmic survivin expressions were widely expressed in tumor cells. In contrast, it was undetectable in normal renal tubular cells.

For clear RCC cases, the association between lymphocytic infiltrate and SSIGN score was summarized in Table (1). A significant association was observed between lymphocytic infiltrate and SSIGN score ($p < 0.001$). The frequency of marked lymphocytic infiltrate was much higher in cases with high SSIGN score (45% of SR) reaching up to 90% compared to only one case with marked lymphocytic infiltrate was observed in whom with low SSIGN score (10% of SR).

The association between nuclear survivin expression and different clinicopathological features was summarized in table (2). A significant positive association was observed with different clinicopathological data including primary tumor classification,

regional lymph involvement, advanced tumor stage, perinephric fat invasion, lymphocytic infiltrate, SSIGN score, MR score ($p < 0.001$ for each), tumor size ($p = 0.001$), nuclear grading (fig. 1-A,B) ($p = 0.002$) and coagulative tumor necrosis ($p = 0.002$).

In the current study, we noticed that survivin was expressed in all histologic RCC types with a higher survivin immunostaining scores in SRCC type (fig. 1-C) and GRCC type as compared to clear cell type, papillary type and chromophobe type. Moreover, we demonstrated a significant association between survivin nuclear expression and lymphocytic infiltrate in ccRCC cases. On the other hand, no significant association was noticed between cytoplasmic survivin expression and any of clinicopathological features as shown in table (3).

Seventeen pairs of primary RCC and their corresponding LN metastasis were compared for nuclear and cytoplasmic survivin expression, which was summarized in table (4). Regarding both nuclear and cytoplasmic survivin, no significant difference were found between primary RCC and their corresponding LN metastasis ($p = 1.000$).

With respect to B ν -H ν expression, we reported a positive B ν -H ν expression in 29% of RCC tumors. The association between B ν -H ν expression and different clinicopathological features was summarized in table (5). A significant positive association was observed with different clinicopathological data including, primary tumor classification, regional lymph involvement, advanced tumor stage, nuclear grading, coagulative tumor necrosis, perinephric fat invasion, lymphocytic infiltrate, SSIGN score, MR score ($p < 0.001$ for each) and tumor size ($p = 0.001$).

Here in, we noticed that B ν -H ν expressed in all histologic RCC types (fig. 2-A,B,C). No significant difference was noticed among different histological subtypes of RCC, although a higher immunostaining scores were noticed more frequently in SRCC type and GRCC type as compared to other

histological subtypes. Our results showed a significant association between positive B^V-H¹ expression and lymphocytic infiltrate.

Primary RCC tumors and their corresponding LN metastasis were compared for B^V-H¹ expression, which was summarized in table (V). No significant difference between primary RCC and their corresponding LN metastasis (p=.720).

As the cytoplasmic expression of survivin showed no significant association with any of clinicopathological features as compared to its nuclear expression that showed a significant association with many of clinicopathological features, so we assessed the combined expression between B^V-H¹ and the nuclear type of survivin expression.

According to the combined expression patterns of both markers in patients with RCCs, 4 immunophenotypes were identified, including 04(04%) survivin^{Low}/B^V-H¹⁻ tumors, 14(14%) survivin^{Hi}/B^V-H¹⁻ tumors,

9(9%) survivin^{Low}/B^V-H¹⁺ tumors, and 20(20%) survivin^{Hi}/B^V-H¹⁺ tumors. The association of these immunoprofiles with different clinicopathological variables was shown in table (A).

In this study, our findings demonstrated a strong association of survivin^{Hi}/B^V-H¹⁺ immunoprofile and the more aggressive clinicopathological including advanced primary tumor classification, regional lymph involvement, advanced tumor stage, coagulative tumor necrosis, perinephric fat invasion, lymphocytic infiltrate, higher SSIGN score and MR score (p<.001 for each) and higher nuclear grading (p=.002). We also observed a high level of lymphocytic infiltrate within ccRCC cases with survivin^{Hi}/B^V-H¹⁺ expression. Finally, the present study identified a moderate positive significant correlation between nuclear survivin and B^V-H¹ expression levels (Sperman's rank correlation p<.001, r=.73) was identified (Fig. 1).

Table 1: Clinicopathological features for patients with RCC (n=100)

Clinicopathological features	No. (%)
Age at Surgery, y	
< 70	76 (76%)
≥ 70	24 (24%)
Sex	
Male	03 (03%)
Female	47 (47%)
Localization	
Right	00 (00%)
Left	00 (00%)
Histological subtypes	
Clear RCC	70 (70%)
Papillary RCC	10 (10%)
Chromophobe RCC	10 (10%)
Granular RCC	3 (3%)
Mixed RCC	2 (2%)
Sarcomatoid RCC	0 (0%)
Primary tumor classification	
T ¹ a	10 (10%)
T ¹ b	18 (18%)
T ² a	13 (13%)
T ² b	24 (24%)
T ³ a	20 (20%)
T ³ b	2 (2%)
T ⁴	3 (3%)
Regional lymph node involvement	
N ⁰	77 (77%)
N ¹	21 (21%)
N ²	2 (2%)

TNM stage groupings	
I	32 (32%)
II	33 (33%)
III	30 (30%)
IV	0 (0%)
Tumor size, cm	
<0	17 (17%)
0 to < 1	22 (22%)
1 to < 1.5	20 (20%)
≥ 1.5	41 (41%)
Nuclear grade	
1	19 (19%)
2	43 (43%)
3	28 (28%)
4	10 (10%)
Coagulative tumor necrosis	
-ve	48 (48%)
+ve	02 (02%)
Perinephric fat invasion	
-ve	73 (73%)
+ve	27 (27%)
Sarcomatoid differentiation	
-ve	92 (92%)
+ve	8 (8%)
Lymphocytic infiltrate*	
-ve	39 (00.7%)
Focal	14 (20%)
Moderate	11 (10.7%)
Marked	6 (8.6%)
SSIGN score*	
0y survival rate 100%	22 (31.4%)
0y survival rate 90%	17 (24.3%)
0y survival rate 74%	10 (21.4%)
0y survival rate 47%	13 (18.6%)
0y survival rate 0%	3 (4.3%)
MR score*	
Low risk	21 (30%)
Moderate risk	33 (47.1%)
High risk	16 (22.9%)

* Variable specific only for clear cell type group (n=70)

SSIGN: Mayo Clinic's Stage, Size, Grade and Necrosis scoring system

MR : Mayo scoring system for metastatic risk

Table (2): Association of lymphocytic infiltrate and SSIGN score for patients with clear RCC (n=70)

SSIGN	Total No. 70	Lymphocytic infiltration				P value
		Absent No. 39	Focal No. 14	Moderate No. 11	Marked No. 6	
0y. survival R. 100%	22	10(68.2%)	6(27.3%)	0(0%)	1(4.5%)	<0.001*
0y. survival R. 90%	17	13(76.5%)	3(17.6%)	1(5.9%)	0(0%)	
0y. survival R. 74%	10	8(80.0%)	2(20%)	0(0%)	0(0%)	
0y. survival R. 47%	13	2(15.4%)	2(15.4%)	6(46.2%)	3(23.1%)	
0y. survival R. 0%	3	1(33.3%)	0(0%)	0(0%)	2(66.7%)	

Test of significance: Chi- square- test *P - value ≤ 0.05 are considered statistically significant

Low SSIGN: 0y. survival R. 100%, **Moderate SSIGN:** 0y. survival R. 74- 90%,

High SSIGN: 5y. survival R. 47%

Table (3): Association of nuclear survivin expression and clinicopathological features for patients with RCC (n=100)

Clinicopathological features	Total 100 (100%)	Nuclear survivin		P value
		<10 Low expression No. (%) 66(66%)	≥10 High expression No. (%) 34(34%)	
Age at Surgery, y				
<60	76(76%)	50(65.8%)	26(34.2%)	.9
≥60	24(24%)	16(66.7%)	8(33.3%)	
Sex				
Male	53(53%)	36(67.9%)	17(32.1%)	.6
Female	47(47%)	30(63.7%)	17(36.2%)	
Localization				
Right	50(50%)	33(66%)	17(34%)	1.0
Left	50(50%)	33(66%)	17(34%)	
Histological type				
Clear RCC	70(70%)	47(67.1%)	23(32.9%)	.2
Papillary RCC	10(10%)	7(70%)	3(30%)	
Chromophobe RCC	10(10%)	8(80%)	2(20%)	
Granular RCC	3(3%)	1(33.3%)	2(66.7%)	
Mixed RCC	2(2%)	0(0%)	2(100%)	
Sarcomatoid RCC	0(0%)	3(100%)	2(66.7%)	
Primary tumor classification				
T1a	10(10%)	10(100%)	0(0%)	<.001*
T1b	18(18%)	17(94.4%)	1(5.6%)	
T2a	13(13%)	13(100%)	0(0%)	
T2b	24(24%)	10(41.7%)	14(58.3%)	
T3a	20(20%)	4(20%)	16(80%)	
T3b	2(2%)	1(50%)	1(50%)	
T4	3(3%)	1(33.3%)	2(66.7%)	
Regional lymph node involvement				
N0	77(77%)	64(83.1%)	13(16.9%)	<.001*
N1	21(21%)	2(9.5%)	19(90.5%)	
N2	2(2%)	0(0%)	2(100%)	
TNM stage groupings				
I	32(32%)	32(100%)	0(0%)	<.001*
II	33(33%)	27(81.8%)	6(18.2%)	
III	30(30%)	6(20%)	24(80%)	
IV	5(5%)	1(20%)	4(80%)	
Tumor size, cm				
<0	17(17%)	16(94.1%)	1(5.9%)	<.001*
0 to < 7	22(22%)	18(81.8%)	4(18.2%)	
7 to < 10	20(20%)	10(50%)	10(50%)	
≥10	41(41%)	17(41.5%)	24(58.5%)	
Nuclear grade				
G1	19(19%)	17(89.5%)	2(10.5%)	.002*
G2	43(43%)	32(74.4%)	11(25.6%)	
G3	28(28%)	14(50%)	14(50%)	
G4	10(10%)	3(30%)	7(70%)	

Coagulative tumor necrosis				
-ve	48(48%)	42(87.0%)	6(12.0%)	<.001*
+ve	02(02%)	24(47.2%)	28(52.8%)	
Perinephric fat invasion				
-ve	73(73%)	61(83.6%)	12(16.4%)	<.001*
+ve	27(27%)	0(18.0%)	22(81.0%)	
Sarcomatoid differentiation				
-ve	92(92%)	63(68.0%)	29(31.0%)	.07
+ve	8(8%)	3(37.0%)	0(62.0%)	
Lymphocytic infiltrate*				
-ve	39(00.7%)	32(82.1%)	7(17.9%)	<.001*
Focal	14(2.0%)	11(78.6%)	3(21.4%)	
Moderate	11(10.7%)	2(18.2%)	9(81.8%)	
marked	7(8.7%)	2(33.3%)	4(66.7%)	
SSIGN score*				
0y SR 100%	22(31.4%)	22(100%)	0(0%)	<.001*
0y SR 90%	17(24.3%)	14(82.4%)	3(17.6%)	
0y SR 75%	10(21.4%)	10(76.7%)	0(33.3%)	
0y SR 50%	13(18.6%)	1(7.7%)	12(92.3%)	
0y SR 0%	3(4.3%)	0(0%)	3(100%)	
MR score*				
Low risk	21(30%)	21(100%)	0(0%)	<.001*
Moderate risk	33(47.1%)	20(70.8%)	8(29.2%)	
High risk	16(22.9%)	1(6.2%)	10(93.8%)	

Test of significance: Chi- square- test * P - value ≤ .05 are considered statistically significant
 * variable specific only for clear cell type group (n=70)

Table (4): Association of cytoplasmic survivin expression and clinicopathological features for patients with RCC (n=100)

Clinicopathological features	Total 100 (100%)	Cytoplasmic survivin		P value
		(-ve) <10 No. (%) 03(03%)	(+ve) ≥10 No. (%) 47(47%)	
Age at Surgery, y				
<70	76(76%)	42(00.3%)	34(44.7%)	.4
≥70	24(24%)	11(45.8%)	13(54.2%)	
Sex				
Male	03(03%)	32(70.4%)	21(39.6%)	.1
Female	47(47%)	21(44.7%)	26(55.3%)	
Localization				
Right	00(00%)	20(00%)	20(00%)	.0
Left	00(00%)	28(06%)	22(44%)	
Histological type				
Clear RCC	70(70%)	37(02.9%)	33(47.1%)	.9
Papillary RCC	10(10%)	0(00%)	0(00%)	
Chromophobe RCC	10(10%)	0(00%)	0(00%)	
Granular RCC	2(2%)	2(66.7%)	1(33.3%)	
Mixed RCC	2(2%)	1(00%)	1(00%)	
Sarcomatoid RCC	0(0%)	2(60%)	2(40%)	
Primary tumor classification				
T1a	10(10%)	0(33.3%)	10(66.7%)	.07
T1b	18(18%)	11(61.1%)	7(38.9%)	
T2a	12(12%)	10(76.9%)	3(23.1%)	

T ² b	24(24%)	16(66.7%)	8(33.3%)	
T ³ a	20(20%)	10(50%)	10(50%)	
T ³ b	2(2%)	1(50%)	1(50%)	
T ⁴	3(3%)	0(0%)	3(100%)	
Regional lymph node involvement				
N ⁰	77(77%)	41(53.2%)	36(46.8%)	0.9
N ¹	21(21%)	11(52.4%)	10(47.6%)	
N ²	2(2%)	1(50%)	1(50%)	
TNM stage groupings				
I	32(32%)	10(31.3%)	17(52.7%)	0.1
II	33(33%)	22(66.7%)	11(33.3%)	
III	30(30%)	10(33.3%)	10(33.3%)	
IV	0(0%)	1(33.3%)	0(0%)	
Tumor size, cm				
<0	17(17%)	7(41.2%)	10(58.8%)	0.0
0 to < 1	22(22%)	12(54.5%)	10(45.5%)	
1 to < 2	20(20%)	13(65%)	7(35%)	
≥ 2	41(41%)	21(51.2%)	20(48.8%)	
Nuclear grade				
G ¹	19(19%)	12(63.2%)	7(36.8%)	0.7
G ²	43(43%)	21(48.8%)	22(51.2%)	
G ³	28(28%)	14(50%)	14(50%)	
G ⁴	10(10%)	6(60%)	4(40%)	
Coagulative tumor necrosis				
-ve	48(48%)	27(56.2%)	21(43.8%)	0.0
+ve	52(52%)	27(52%)	25(48%)	
Perinephric fat invasion				
-ve	73(73%)	44(60.3%)	29(39.7%)	0.07
+ve	27(27%)	9(33.3%)	18(66.7%)	
Sarcomatoid differentiation				
-ve	92(92%)	49(53.3%)	43(46.7%)	0.8
+ve	8(8%)	4(50%)	4(50%)	
Lymphocytic infiltrate*				
-ve	39(100%)	21(53.8%)	18(46.2%)	0.3
Focal	14(36%)	6(42.9%)	8(57.1%)	
Moderate	11(28%)	0(0%)	11(100%)	
Marked	14(36%)	15(100%)	0(0%)	
SSIGN score*				
0y SR 100%	22(31.4%)	9(40.9%)	13(59.1%)	0.4
0y SR 90%	17(24.3%)	12(70.6%)	5(29.4%)	
0y SR 75%	10(14.3%)	7(70%)	3(30%)	
0y SR 50%	13(18.6%)	7(53.8%)	6(46.2%)	
0y SR 0%	3(4.3%)	2(66.7%)	1(33.3%)	
MR score*				
Low risk	21(30%)	9(42.9%)	12(57.1%)	0.0
Moderate risk	33(47.1%)	19(57.6%)	14(42.4%)	
High risk	16(22.9%)	9(56.2%)	7(43.8%)	

Test of significance: Chi- square- test P - value ≤ 0.05 are considered statistically significant

* variable specific only for clear cell type group (n=70)

Table (0): Comparison for nuclear and cytoplasmic survivin expression among 17 pairs of primary RCC and their corresponding LN metastasis.

	Positive Expression Rate		Change in Expression Pattern			
	Primary (n=17)	Metastasis (n=17)	P = M	P > M	M > P	P value
Nuclear Survivin	10(58.8%)	14(82.4%)	14(82.4%)	2(11.8%)	1(5.9%)	1.000
Cytoplasmic Survivin	7(41.2%)	6(35.3%)	16(94.1%)	1(5.9%)	0(0%)	1.000

P: primary renal cell carcinoma tumor
 Test of significance: McNemar Test

M: metastatic malignant LN

Table (1): Association of BV-H¹ expression and clinicopathological features for patients with RCC (n=100)

Clinicopathological features	Total 100 (100%)	BV-H ¹ expression		P value
		-ve (<1+) No. (%) 71(71%)	+ve (≥1+) No. (%) 29(29%)	
Age at Surgery, y				
< 60	76(76%)	56(73.7%)	20(26.3%)	0.7
≥ 60	24(24%)	15(62.5%)	9(37.5%)	
Sex				
Male	53(53%)	37(69.8%)	16(30.2%)	0.4
Female	47(47%)	32(68.1%)	15(31.9%)	
Localization				
Right	50(50%)	30(60%)	20(40%)	0.8
Left	50(50%)	36(72%)	14(28%)	
Histological type				
Clear RCC	70(70%)	50(71.4%)	20(28.6%)	0.3
Papillary RCC	10(10%)	8(80%)	2(20%)	
Chromophobe RCC	10(10%)	8(80%)	2(20%)	
Granular RCC	3(3%)	2(66.7%)	1(33.3%)	
Mixed RCC	2(2%)	0(0%)	2(100%)	
Sarcomatoid RCC	0(0%)	3(60%)	2(40%)	
Primary tumor classification				
T1a	10(10%)	10(100%)	0(0%)	<0.001*
T1b	18(18%)	17(94.4%)	1(5.6%)	
T2a	13(13%)	12(92.3%)	1(7.7%)	
T2b	24(24%)	18(75%)	6(25%)	
T3a	20(20%)	9(45%)	11(55%)	
T3b	2(2%)	0(0%)	2(100%)	
T4	3(3%)	0(0%)	3(100%)	
Regional lymph node involvement				
N0	77(77%)	66(85.7%)	11(14.3%)	<0.001*
N1	21(21%)	0(0%)	21(100%)	
N2	2(2%)	0(0%)	2(100%)	
TNM stage groupings				
I	32(32%)	32(100%)	0(0%)	<0.001*
II	33(33%)	28(84.8%)	5(15.2%)	
III	30(30%)	11(36.7%)	19(63.3%)	
IV	5(5%)	0(0%)	5(100%)	

Tumor size, cm				
<0	17(17%)	10(11.2%)	2(11.8%)	.001*
0 to <1	22(22%)	20(22.9%)	2(9.1%)	
1 to <1.5	20(20%)	16(18.0%)	4(20%)	
≥1.5	41(41%)	20(22.8%)	21(51.2%)	
Nuclear grade				
G1	19(19%)	16(18.0%)	3(15.3%)	<.001*
G2	43(43%)	37(41.6%)	7(31.8%)	
G3	28(28%)	10(11.2%)	13(56.4%)	
G4	10(10%)	3(3.3%)	7(30.9%)	
Coagulative tumor necrosis				
-ve	48(48%)	43(47.6%)	0(0%)	<.001*
+ve	02(02%)	28(31.2%)	24(56.2%)	
Perinephric fat invasion				
-ve	73(73%)	63(69.3%)	10(43.5%)	<.001*
+ve	27(27%)	28(31.2%)	19(83.5%)	
Sarcomatoid differentiation				
-ve	92(92%)	67(73.8%)	20(87.3%)	.1
+ve	8(8%)	24(26.2%)	3(12.7%)	
Lymphocytic infiltrate*				
-ve	39(39%)	30(33.3%)	4(17.3%)	<.001*
Focal	14(14%)	11(12.2%)	3(13%)	
Moderate	11(11%)	2(2.2%)	9(39.1%)	
marked	7(7%)	2(2.2%)	4(17.3%)	
SSIGN score*				
0y SR 100%	22(31.4%)	22(100%)	0(0%)	<.001*
0y SR 90%	17(24.3%)	16(94.1%)	1(5.9%)	
0y SR 75%	10(14.3%)	9(60%)	1(6%)	
0y SR 50%	13(18.6%)	3(23.1%)	10(76.9%)	
0y SR 0%	3(4.3%)	0(0%)	3(100%)	
MR score*				
Low risk	21(30%)	21(100%)	0(0%)	<.001*
Moderate risk	33(47.1%)	26(78.8%)	7(21.2%)	
High risk	17(24.9%)	3(11.2%)	13(81.2%)	

Test of significance: Chi- square- test * P - value ≤ 0.05 are considered statistically significant.
 * Variables specific only for clear cell type group (n=70)

Table (V): Comparison for B^V-H¹ expression among 17 pairs of primary RCC and their corresponding LN metastasis.

	Positive Expression Rate		Change in Expression Pattern			
	Primary (n=17)	Metastasis (n=17)	P = M	P > M	M > P	P value
B ^V -H ¹ Expression	10(58.8%)	13(76.5%)	13(76.5%)	3(17.6%)	1(5.9%)	.120

P: primary renal cell carcinoma tumor

M: metastatic malignant LN

Test of significance: McNemar Test

Table (A): Association of combination of nuclear survivin expression & BV-H¹ expression and clinicopathological features for patients with RCC (n=100)

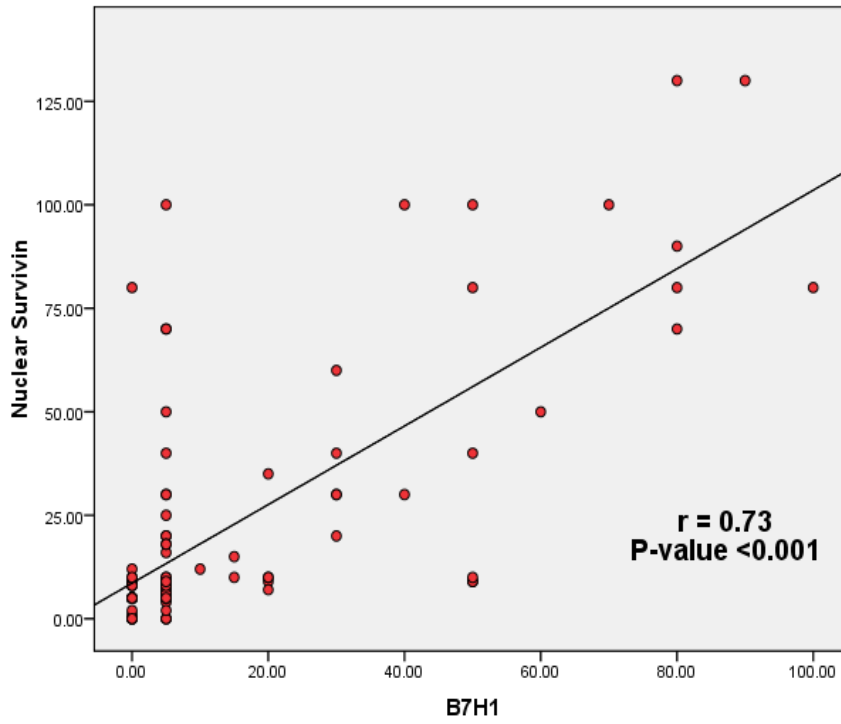
Clinicopathological features	Total 100(100%)	Combination of Nuclear survivin& BV-H ¹ expression				P value
		Low S/ -ve BV-H ¹ No. (%) 07(07%)	High S/ -ve BV-H ¹ No. (%) 14(14%)	Low S/ +ve BV-H ¹ No. (%) 9(9%)	High S/ +ve BV-H ¹ No. (%) 20(20%)	
Age at Surgery, y						
<70	76(76%)	07(09%)	10(13%)	7(9%)	4(18.4%)	0.6
≥70	24(24%)	13(05.2%)	2(8.3%)	3(12.0%)	7(20%)	
Sex						
Male	03(03%)	31(08.0%)	7(11.3%)	0(0.4%)	11(20.8%)	0.8
Female	47(47%)	27(05.3%)	8(11.7%)	4(8.0%)	9(19.1%)	
Localization						
Right	00(00%)	29(08.8%)	7(12%)	4(8%)	11(22%)	0.8
Left	00(00%)	28(07.6%)	8(11.6%)	0(1.0%)	9(18.8%)	
Histological type						
Clear RCC	70(70%)	40(057.1%)	14(20%)	7(10%)	13(18.6%)	0.0
Papillary RCC	10(10%)	7(70%)	1(10%)	0(0%)	2(20%)	
Chromophobe RCC	10(10%)	7(70%)	1(10%)	1(10%)	1(10%)	
Granular RCC	3(3%)	1(33.3%)	1(33.3%)	0(0%)	1(33.3%)	
Mixed RCC	2(2%)	0(0%)	0(0%)	0(0%)	1(50%)	
Sarcomatoid RCC	0(0%)	2(40%)	1(20%)	1(20%)	1(20%)	
Primary tumor classification						
T1a	10(10%)	10(100%)	0(0%)	0(0%)	0(0%)	<0.001*
T1b	18(18%)	17(94.4%)	0(0%)	0(0%)	1(5.6%)	
T2a	13(13%)	12(92.3%)	0(0%)	1(7.7%)	0(0%)	
T2b	24(24%)	12(50%)	7(29%)	3(12.5%)	3(12.5%)	
T3a	20(20%)	1(5%)	8(40%)	3(15%)	13(65%)	
T3b	2(2%)	0(0%)	0(0%)	1(50%)	1(50%)	
T4	3(3%)	0(0%)	0(0%)	1(33.3%)	2(66.7%)	
Regional lymph node involvement						
N0	77(77%)	00(0%)	11(14.3%)	9(11.7%)	2(2.6%)	<0.001*
N1	21(21%)	2(9.5%)	3(14.3%)	0(0%)	16(76.2%)	
N2	2(2%)	0(0%)	0(0%)	0(0%)	2(100%)	
TNM stage groupings						
I	32(32%)	32(100%)	0(0%)	0(0%)	0(0%)	<0.001*
II	33(33%)	23(69.7%)	0(0%)	4(12.1%)	1(3%)	
III	30(30%)	2(6.7%)	9(30%)	4(13.3%)	10(33.3%)	
IV	0(0%)	0(0%)	0(0%)	1(20%)	4(80%)	
Tumor size, cm						
<0	17(17%)	10(88.2%)	0(0%)	1(5.9%)	1(5.9%)	<0.001*
0 to <1	22(22%)	17(77.3%)	3(13.6%)	1(4.5%)	1(4.5%)	
1 to <2	20(20%)	12(60%)	4(20%)	3(15%)	1(5%)	
≥2	41(41%)	13(31.7%)	7(17.1%)	4(9.8%)	17(41.5%)	
Nuclear grade						
G1	19(19%)	10(78.9%)	1(5.3%)	2(10.0%)	1(5.3%)	0.002*
G2	43(43%)	30(69.8%)	7(16.3%)	2(4.7%)	4(9.3%)	
G3	28(28%)	10(35.7%)	0(0%)	4(14.3%)	9(32.1%)	
G4	10(10%)	2(20%)	1(10%)	1(10%)	7(70%)	

Coagulative tumor necrosis						
-ve	48(48%)	39(81.2%)	4(8.3%)	3(6.2%)	2(4.2%)	<.001*
+ve	52(52%)	18(38.6%)	10(19.2%)	7(11.0%)	18(35.6%)	
Perinephric fat invasion						
-ve	73(73%)	56(76.7%)	7(9.6%)	5(6.8%)	5(6.8%)	<.001*
+ve	27(27%)	13(17.7%)	7(20.9%)	4(11.8%)	10(30.6%)	
Sarcomatoid differentiation						
-ve	92(92%)	50(59.8%)	12(13%)	8(8.7%)	17(18.5%)	.2
+ve	8(8%)	34(40.2%)	77(87%)	81(91.3%)	73(79.5%)	
Lymphocytic infiltrate*						
-ve	39(50.7%)	30(76.9%)	5(12.8%)	2(5.1%)	2(5.1%)	<.001*
Focal	14(20%)	9(74.3%)	2(14.3%)	2(14.3%)	1(7.1%)	
Moderate	11(15.7%)	0(0%)	2(14.3%)	2(14.3%)	7(50.7%)	
marked	7(9.6%)	1(16.7%)	1(16.7%)	1(16.7%)	3(50%)	
SSIGN score*						
0y SR 100%	22(31.4%)	22(100%)	0(0%)	0(0%)	0(0%)	<.001*
0y SR 90%	17(24.3%)	13(76.5%)	3(17.6%)	1(5.3%)	0(0%)	
0y SR 74%	10(21.4%)	0(33.3%)	4(26.7%)	0(33.3%)	1(6.7%)	
0y SR 47%	13(18.6%)	0(0%)	3(23.1%)	1(7.7%)	9(69.2%)	
0y SR 0%	3(4.3%)	0(0%)	0(0%)	0(0%)	3(100%)	
MR score*						
Low risk	21(30%)	21(100%)	0(0%)	0(0%)	0(0%)	<.001*
Moderate risk	33(47.1%)	19(57.7%)	7(21.2%)	6(18.2%)	1(3%)	
High risk	16(22.9%)	0(0%)	3(18.8%)	1(6.2%)	12(75%)	

Test of significance: Chi- square- test *P - value $\leq .05$ are considered statistically significant

* variables specific only for clear cell type group

Figure (1): Correlation of nuclear survivin and B γ -H δ expression



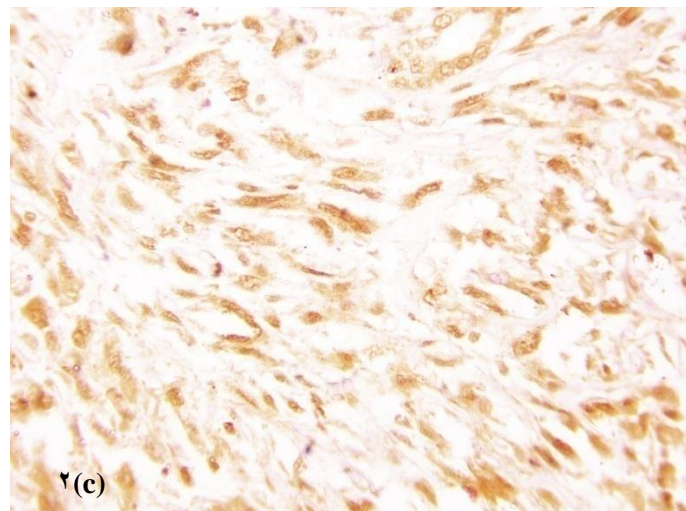
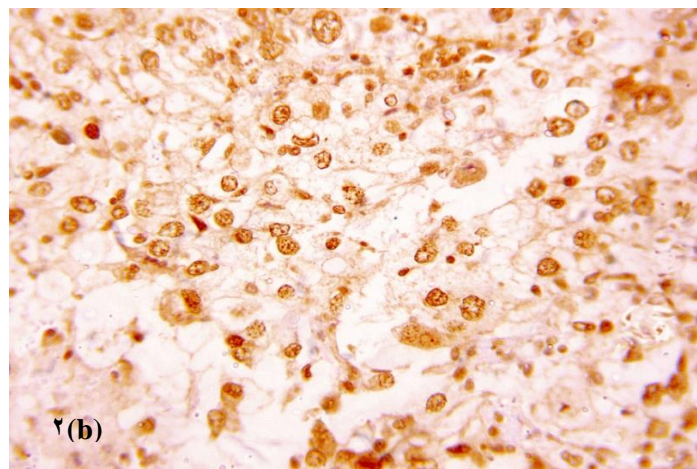
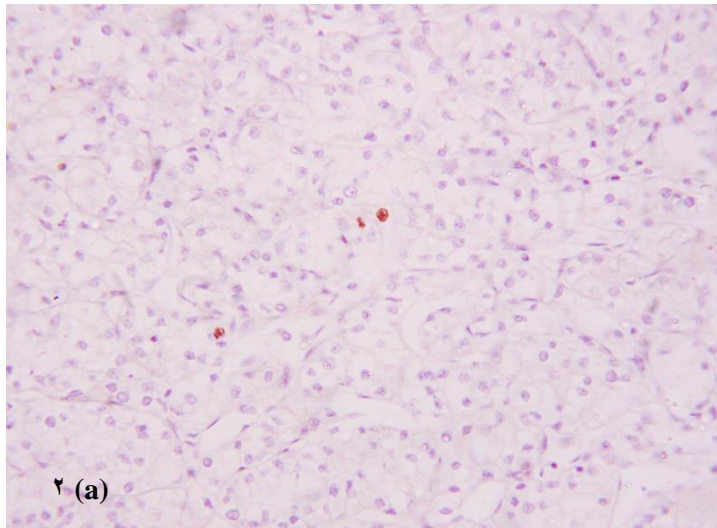


Fig. (1-A, B, C): Survivin immunostaining in representative sections of RCCs with (A) low nuclear survivin expression in grade 1 clear cell RCC, (B) high nuclear survivin expression in grade 2 clear cell RCC and (C) high nuclear and positive cytoplasmic survivin expression in sarcomatoid RCC (X400).

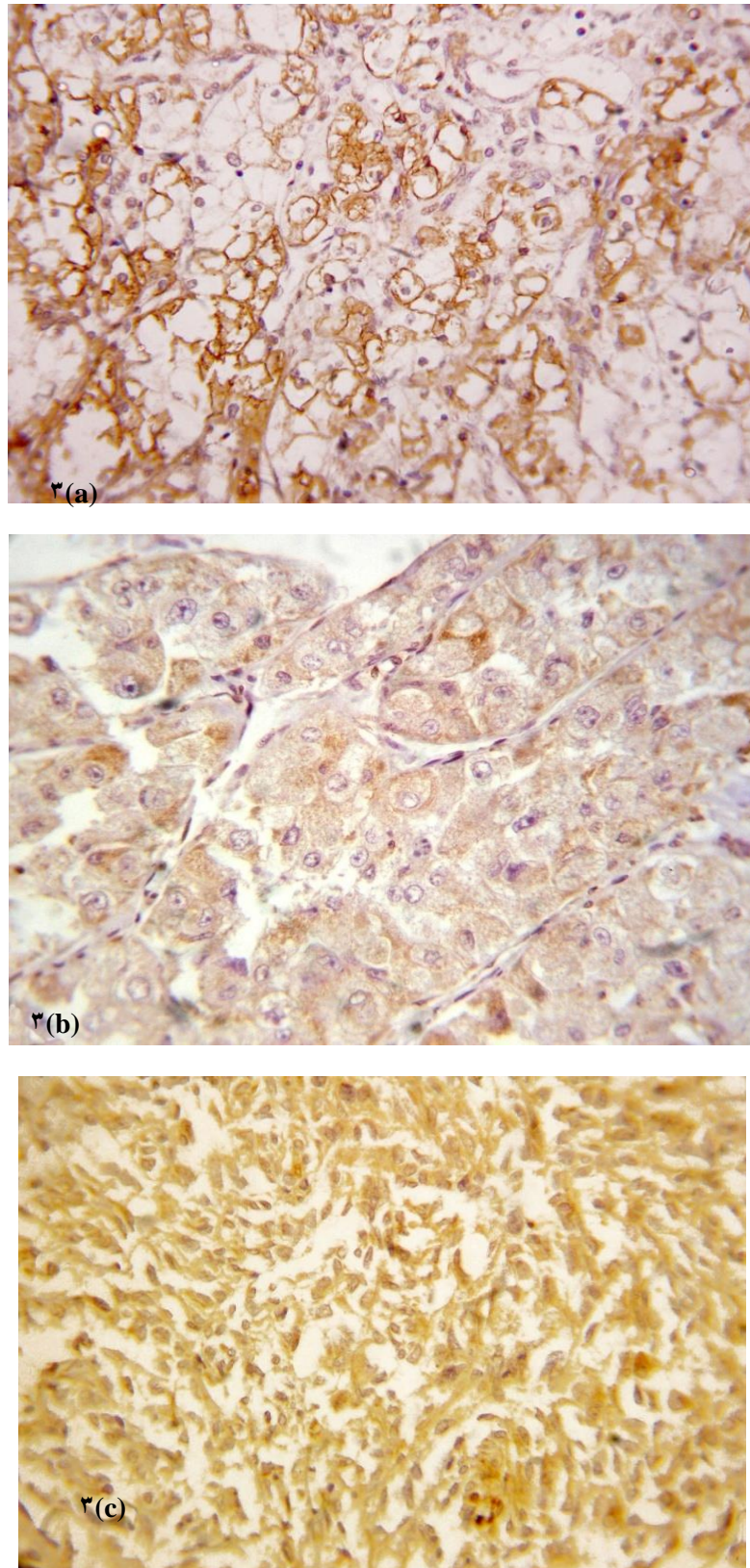


Fig. (3-A, B, C): Bcl-2 immunostaining in representative sections of RCCs with (A) positive membranous Bcl-2 expression in grade 1 clear cell RCC, (B) positive cytoplasmic Bcl-2 expression in grade 2 clear cell RCC and (C) positive cytoplasmic Bcl-2 expression in sarcomatoid RCC(X400).

Discussion

Renal cell carcinoma is recognized as a group of cancers that originate from the renal tubular epithelium and have distinct genetic and molecular backgrounds, unique morphological features and a characteristic clinical course⁽¹⁷⁾. The molecular mechanisms underlying the development of RCC are still poorly understood. Therefore, it is crucial to exploit markers that can accurately represent biological features of tumors and predict the outcome, which will help us to perform tailored therapy for individual cases.

The present work was conducted to study the immunohistochemical expression of survivin and B^V-H¹ in different types of RCC tumors, in order to evaluate their expression patterns and examine their association with various clinicopathological features and finally to investigate the presence of a possible relationship between both markers in RCC tumors.

In the current study, survivin expression was observed in both nuclei and cytoplasm of tumor cells, this was in line with Emaetig et al.,⁽¹⁸⁾ who reported both nuclear and cytoplasmic localization of survivin. Other studies reported survivin expression restricted to the nuclei of tumor cells^(1, 28, 29, 32), while others demonstrated its cytoplasmic expression^(20, 21, 33). These variations in survivin subcellular localization reported by different studies could be attributed to the different types of survivin antibody clones used which are specific for certain survivin localization. In contrast to RCC cells, survivin (nuclear and cytoplasmic) was undetectable in the adjacent normal renal tubular cell. Previous studies have shown the absence of survivin expression in normal renal tubular cells using immunohistochemical and reverse-transcription polymerase chain reaction assays^(20, 22, 33, 34). Therefore, one of the most significant features of survivin is its differential distribution in cancer compared with normal tissues. This sharp differential expression in cancer versus normal tissues is one the most intriguing features of survivin and sets it apart from other members of the IAP family; this can be

helpful particularly in therapeutic intervention⁽¹¹⁾.

The present study demonstrated a significant association between nuclear survivin expression and different clinicopathological features including primary tumor classification, regional lymph involvement, advanced tumor stage, perinephric fat invasion, lymphocytic infiltrate, SSIGN score, MR score, tumor size, nuclear grading and coagulative tumor necrosis.

In the current study, we noticed that survivin was expressed in all histologic RCC types with a higher surviving-immunostaining scores in SRCC type and GRCC type as compared to clear cell type, papillary type and chromopobe type, suggesting the expected role of survivin in more advanced renal cell carcinoma types. Moreover, we demonstrated a significant association between survivin nuclear expression and lymphocytic infiltrate in ccRCC cases. The CTL recognition of survivin possibly contributes to the significant increase in lymphocytic infiltration that is observed within survivin^{Hi} tumors, a hypothesis that enforce that ccRCCs is regarded as an immunogenic malignancy.

On studying the association between the SSIGN score and MR score with nuclear survivin expression, a significant association became evident between the nuclear survivin expression and SSIGN score and MR category. These results are in accordance with previous studies confirmed a significant association with death from RCC in cases with survivin^{Hi} expression after adjusting for the Mayo Clinic SSIGN score in relation to metastatic risk category^(1, 28, 29, 32). As regard the cytoplasmic expression of survivin, we noticed that the positive cytoplasmic survivin expression in 47% of RCC tumors. This was comparable with previous studies that reported expression rates ranged from 02.3% up to 79%^(20, 33). This wide difference in the expression rate could be related to biased case selection, different antibodies, scoring systems and different cutoff points for definition of positivity used by different

studies. Our results were similar to the findings that reported by Wang et al.,⁽¹¹⁾ who confirmed a higher cytoplasmic survivin immunostaining score in SRCC and GRCC but not in ccRCC, suggesting an important role of survivin in more aggressive subtypes of renal cell carcinoma. On studying the association of cytoplasmic survivin expression with different clinicopathological features, no significant association was observed between cytoplasmic survivin expression and any of clinicopathological features. Similarly, Wang et al.,⁽¹¹⁾ reported that the cytoplasmic immunostaining score of survivin in RCC tumors did not significantly correlate with clinicopathological features including nuclear grading and staging that explained by low expression rate. On the contrary, other studies reported that a high level of cytoplasmic survivin expression was significantly correlated with tumor pathological stage, grade, and lymph node metastasis^(12,13), but come in line with our results in the point of no significant association with other clinicopathological factors including age, sex, tumor size, histological type of RCC patients. The difference could be attributed to biased case selection, different scoring systems and different cutoff points for positivity used by different studies

On comparing the role of nuclear and cytoplasmic survivin expression in this cohort, nuclear survivin expression was significantly associated with aggressive tumor features, while no significant relations were noticed between cytoplasmic survivin expression and these features, although both nuclear and cytoplasmic survivin expression coexist in a considerable proportion of tumors.

Survivin seems to exist in γ subcellular pools (cytoplasmic and nuclear)⁽¹⁴⁾. This is consistent with its function in the regulation of both cell viability and cell division⁽¹⁵⁾. One possibility is that the nuclear pool of survivin is involved in promoting cell proliferation in most (if not all) cases, whereas the cytoplasmic pool of survivin may participate in controlling cell survival but not cell proliferation. Alternatively,

survivin has a number of splicing variants, which may differ in their subcellular localization and functions with respect to cell survival and cell division⁽¹⁶⁾. Survivin and survivin- γ B are predominantly cytoplasmic, whereas survivin- Δ Ex- γ is primarily nuclear. These different isoforms of survivin and their varied locations in the cell may represent a regulatory balance between apoptosis and inhibition of apoptosis⁽¹⁶⁾. As it is possible immunohistochemically to distinguish two intracellular pools of survivin, a nuclear and a cytosolic one, the prognostic significance of the protein has been analyzed in some studies as a function of its intracellular localization and inconsistent and sometimes contrasting results have been obtained regarding the prognostic value of nuclear vs. cytoplasmic survivin expression⁽¹⁷⁾. So the different prognostic value of survivin may reflect differential expression of survivin splice variants that exist.

In this study, a high concordance rate of survivin expression status was found between matched primary renal cell carcinoma and metastatic lymph node specimens. These results are in accordance with⁽¹⁸⁾ who reported survivin expression in both primary and metastatic lesions with no significant difference in between. These data along with our findings, suggest that survivin expression by tumor cells probably occurred before metastasis and that survivin bearing malignant cells have more ability to metastasize.

Our findings together with others suggests that nuclear survivin expression is an useful important biologic marker for aggressive RCCs, predicting prognosis in patients with RCC and for guiding the development of more effective methods for potential adjuvant therapy for high-risk patients.

Regarding B γ -H γ expression, in the current study we demonstrated a combined membranous and cytoplasmic expression. Some studies detected B γ -H γ cellular localization concentrated primarily within the cell membrane^(19,20,21), while others mentioned that equivalent staining was seen either in the cytoplasm or in the membrane

or even combined^(28,37,49). It is worthwhile to mention that there are different antibodies that can identify different cellular compartments including the cell surface and the cytoplasm. In our study, the antibody that used was known to identify both cellular compartments, membranous and cytoplasmic.

The current study demonstrated significant associations between B^V-H¹ expression and different clinicopathological features including, primary tumor classification, regional lymph involvement, advanced tumor stage, nuclear grading, coagulative tumor necrosis, perinephric fat invasion, lymphocytic infiltrate, SSIGN score, MR score and tumor size. Here in, we noticed that B^V-H¹ expressed in all histologic RCC types. No significant difference was noticed among different histological subtypes of RCC, although a higher immunostaining scores were noticed more frequently in SRCC type and GRCC type as compared to other histological subtypes, suggesting its role in these subtypes of renal cell carcinoma.

Our results showed a significant association between positive B^V-H¹ expression and lymphocytic infiltrate. This may be attributed to the fact that the positive B^V-H¹ tumor cells might inhibit the function of tumor infiltrating T cells, either through the induction of apoptosis or anergy and contributes to the profile of immunosuppression observed in RCC patients that is responsible for immune-mediated tumor destruction for this treatment-refractory malignancy.

In this series, the expression rate of B^V-H¹ was much higher in cases with high SSIGN score compared to those with moderate SSIGN score. Keeping up with our findings, similar results were demonstrated by previous studies that confirmed a significant association with death from RCC in cases with positive B^V-H¹ expression after adjusting for the Mayo Clinic SSIGN score in relation to metastatic risk category^(28,37). Our results showed a significant association between positive B^V-H¹ expression and lymphocytic infiltrate. A

similar result was reported by other studies^(21,28,37). These results are supported by hypothesis that tumor express B^V-H¹, might further inhibit the function of tumor infiltrating T cells, either through the induction of apoptosis or anergy. This contributes to the profile of immunosuppression observed in RCC patients. As such, blockade of B^V-H¹ may theoretically permit immune-mediated tumor destruction for this treatment-refractory malignancy.

Based on its recognized ability to impair the function and survival of activated tumor-specific T cells, we infer that B^V-H¹ expressed by RCC tumor cells and associated increased infiltrating lymphocytes, may contribute to the profile of immunosuppression that is observed in patients with RCC, so we further speculate that intratumoral B^V-H¹ functions as a critical host determinant of treatment responses in patients who receive immunotherapy for management of advanced RCC (i.e., IL-2, IFN vaccination, or T cell adoptive therapy).

Taken together, our previous findings suggest that positive B^V-H¹ expression is a useful important biologic marker for aggressive RCCs, predicting prognosis in patients with RCC.

In the current study a high concordance rate of B^V-H¹ expression status between matched primary renal cell carcinoma and metastatic lymph node specimens was found. This can be explained by the fact of positivity of tumor cells for B^V-H¹ occurs early in the process of tumorigenesis that can later on metastasize.

One of the new modalities in immunotherapy is the use of cell surface signaling molecules (CSSMs) which make ideal targets for mAb immunotherapy. Antagonist mAbs targeting inhibitory CSSMs such as PD-1 and B^V-H¹ promote immune activation against cancer may results in the generation of immune memory and, consequently, a durable response against cancer, which is of critical importance in immunotherapeutics⁽⁶¹⁾.

Herein, studying the combined expression patterns of survivin and B ν -H \backslash revealed a strong association of survivin^{Hi}/B ν -H \backslash ⁺ immunoprofile and the more aggressive clinicopathological features. The frequency of survivin^{Hi}/B ν -H \backslash ⁺ expression was higher in cases with T ξ and T γ than those with both T ν and T \backslash and in cases positive for lymph node metastases than those negative for lymph node metastases.

Our results also demonstrated that the highest incidences of grade ξ and γ tumors were more frequently noticed in survivin^{Hi}/B ν -H \backslash ⁺ cases and the rate of survivin^{Hi}/B ν -H \backslash ⁺ expression in cases with perinephric fat invasion and coagulative tumor necrosis were much higher compared to those without perinephric fat invasion and coagulative tumor necrosis. Conversely, the survivin^{low}/B ν -H \backslash ⁻ phenotype was more frequently seen among stage I and stage II tumors with the highest incidences in grade \backslash and γ tumors as well as small sized tumors. All these findings were agree with that reported by Krambeck et al.,^(7A) who demonstrated that a combination of survivin^{Hi}/B ν -H \backslash ⁺ expression was significantly associated with several adverse clinicopathological features and form the most aggressive phenotype.

Furthermore, the current work demonstrated a highly significant association between SSIGN score and MR score with the combined survivin/B ν -H \backslash immunoprofile. The rate of survivin^{Hi}/B ν -H \backslash ⁺ expression was higher in ccRCC cases with high SSIGN score compared to those with moderate SSIGN Score. None of tumors had low SSIGN score showed survivin^{Hi}/B ν -H \backslash ⁺ expression. Also a significant positive association was evident in relation to immunoprofile with MR score in which the rate of survivin^{Hi}/B ν -H \backslash ⁺ expression was higher in cases with high risk category (50%) compared to those with intermediate (30%) and low risk category risk categories (20%).

Our findings showed that a combined survivin/B ν -H \backslash expression can provide a more significant degree of further stratify-

cation among each category of ccRCC risk patients based upon SSIGN score. So this further stratification within the same risk category can help to provide additional prognostic information that contributes in the therapeutic interventions. This was in line with a similar study was conducted by Parker et al.,^(7B) Owing to applicability of patient's follow up data records in their center, survival analysis could be conducted, so they could demonstrated that patients within the same risk category with combined expression are associated with poorer cancer-specific survival and the use of this combined expression can provide additional information to further stratify among patients initially predicted to be at intermediate risk and high risk by the SSIGN score with limited ability to be applied to low risk patients.

In our study, we observed high levels of lymphocytic infiltrate within survivin^{Hi}/B ν -H \backslash ⁺ tumors relative to the survivin^{Low}/B ν -H \backslash ⁻ tumors. So the combined effect of survivin^{Hi}/B ν -H \backslash ⁺ on ccRCC tumor aggressiveness occurs at the cellular level could be explained as the tumor cell survivin can be recognized by CTLs that lead to significant increase in lymphocytic infiltration, this significant increase in lymphocytic infiltration produce IFN- α , which cause tumor cell B ν -H \backslash expression to be up-regulated. This up regulation inhibits the function of tumor-infiltrating T cells, either through the induction of apoptosis or anergy⁽⁸⁾.

The current study demonstrated a moderate positive correlation between nuclear survivin and B ν -H \backslash expression. Also there was a distinctively positive correlation between combined nuclear survivin and B ν -H \backslash and clinicopathological features related to tumor progression indicating that these two markers may act in concert to mediate a more aggressive tumor behavior and poor outcome. Given that both survivin and B ν -H \backslash are widely expressed within human malignancies including RCC, we anticipate these observations will have broad implications for improving prognostication and treatment of RCC and other malignancies.

Conclusion and Recommendations

Our results can confirm that RCC patients whose tumors exhibit high levels of nuclear survivin expression based on immunohistochemical (IHC) analysis are at markedly increased risk of cancer progression and poor prognosis from RCC relative to patients whose tumors express low levels of survivin suggesting that this biomarker lends meaningful prognostic information beyond standard clinical and pathologic indices. Our findings suggest that positive B^V-H¹ expression is a useful important biologic marker for aggressive RCCs, predicting prognosis in patients with RCC, the basis for these associations may relate to the recognized ability of B^V-H¹ to inhibit antitumor T-cell-mediated immunity. As such, B^V-H¹ may represent a target for RCC immunotherapy and a potential biomarker to facilitate patient assignment to treatment, as well as aid in the determination of prognosis both before and after therapy.

References

1. Lipworth L, Tarone RE, Lund L and McLaughlin KJ. Clin Epidemiologic characteristics and risk factors for renal cell cancer. *Epidemiol.*, 2009; 1: 33-43.
2. Jemal A, Siegel R and Ward E. Cancer statistics. *Ca Cancer J Clin.*, 2012; 62: 5-26.
3. Mokhtar N, Adel I and Gouda I. Cancer Pathology Registry 2003-2008 And Time Trend Analysis: Malignant urinary system tumors, 1st Ed. National Cancer Institute, Egypt. 2007.
4. Delahunt B. Advances and controversies in grading and staging of renal cell carcinoma. *Modern Pathology*, 2009; 22: 24-36.
5. Ljungberg B, Cowan N, Hanbury DC, Hora M, Kuczyk MA, Merseburger AS, Mulders PF, et al., Guidelines on Renal Cell Carcinoma European Association of Urology. 2012.
6. Sobin LH, Gospodarowicz MK and Wittekind C. TNM classification of malignant tumors. UICC International Union Against Cancer. Chichester, Wiley- Blackwell (ed), 7th edition. 2009; 200-207.
7. Wagner B, Patard JJ and Mejean A. Prognostic value of renal vein and inferior vena cava involvement in renal cell carcinoma. *Eur Urol.* Feb 2009; 55(2): 402-409.
8. Webster WS, Lohse CM, Thompson RH, Dong H, Frigola X, Dicks DL, Sengupta S, et al., Mononuclear cell infiltration in clear-cell renal cell carcinoma independently predicts patient survival. *Cancer*, 2007; 107: 47-53.
9. Sengupta S, Lohse CM and Leibovich BC. Histologic coagulative tumor necrosis as a prognostic indicator of renal cell carcinoma aggressiveness. *Cancer*, 2005; 104(3): 511-520.
10. Volpe A and Patard JJ. Prognostic factors in renal cell carcinoma. *World J Urol.*, 2010; 28(3): 319-327.
11. Ficarra V, Galfano A and Mancini M. TNM staging system for renal cell carcinoma: current status and future perspective. *Lancet Oncol.*, 2007; 8: 504-508.
12. Sorbellini M, Kattan MW and Snyder ME. A postoperative prognostic nomogram predicting recurrence for patients with conventional clear cell renal cell carcinoma. *J Urol.*, 2005; 173: 48-51.
13. Ficarra V, Martignoni G and Lohse C. External validation of the Mayo Clinic stage, size, grade and necrosis (SSIGN) score to predict cancer specific survival using a European series of conventional clear cell renal cell carcinoma. *J Urol.*, 2007; 176: 1230-1239.
14. Caldas H, Jiang Y, Holloway MP, Fangusaro J, Mahotka C, Conway EM and Altura RA. Survivin splice variants regulate the balance between proliferation and cell death. *Oncogene*, 2005; 24(12): 1994-2007.
15. Altieri DC. Validating survivin as a cancer therapeutic target. *Nat Rev Cancer*, 2003; 3: 47-54.
16. Zhu H, Chen XP and Zhang WG. Expression and significance of new inhibitor of apoptosis protein survivin

- in hepatocellular carcinoma. *World J Gastroenterol.*, 2005; 11:3800-3809.
17. Invernizzi R, Travaglini E and Benatti C. Survivin expression, apoptosis and proliferation in chronic myelomonocytic leukemia. *Eur J Haematol.*, 2006; 76:494-501.
18. Bhanot U, Hevdrich R and Moller P. Survivin expression in pancreatic intra-epithelial neoplasia (PanIN): steady increase along the developmental stages of pancreatic ductal adenocarcinoma. *Am J Surg Pathol.*, 2006; 30:704-709.
19. Hinnis AR, Luckett JC and Walker RA. Survivin is an independent predictor of short-term survival in poor prognostic breast cancer patients. *Br J Cancer.*, 2007; 96:739-45.
20. Wu YK, Chen KT and Kuo YB. Quantitative detection of survivin in malignant pleural effusion for the diagnosis and prognosis of lung cancer. *Cancer Lett.*, 2009; 273(2):231-235.
21. Li F, Yang J, Ramnath N, Javle MM and Tan D. Nuclear or cytoplasmic expression of survivin: What is the significance? *International Journal of Cancer.* April, 2005; 114, (4): 509-512.
22. Zamparese R, Pannone G, Santoro A, Muzio L, Corsi F, Pedicillo MC, Scillitani EL, et al. Survivin expression in renal cell carcinoma. *Cancer Invest.*, 2008; 26: 929-935.
23. Parker A S, Leibovich BC, Lohse CM, Sheinin Y, Kuntz SM, Eckel-Passow J E, Blute ML, et al., Development and evaluation of bioscore, A Biomarker panel to enhance prognostic algorithms for clear cell renal cell carcinoma. *Cancer.* May 2009; 110(10):2092-2103.
24. Emaetig F, El-Gehani K, El-nahwie H, El-Hasadi I, Sassi S, Al-Ammari S, Buhmeida A, et al. Survivin expression in renal cell carcinoma and its correlation with clinicopathological parameters. *J Interdiscipl Histopathol.*, 2013; 2147-4362.
25. Carreno BM and Collins M. The B γ family of ligands and its receptors: new pathways for co-stimulation and inhibition of immune responses. *Annu Rev Immunol.*, 2002; 20:29-53.
26. Seliger B, Marincola F M, Ferrone S and Abken H. The complex role of B γ molecules in tumor immunology *Trends. Mol Med.* December 2008; 14 (12): 500-509.
27. Tsushima F, Tanak N and Otsuki P. Predominant expression of B γ -H γ and its immunoregulatory roles in oral squamous cell carcinoma. *Oral Oncol.*, 2006; 42: 268-274.
28. Inman BA, Sebo TJ, Frigola X, Dong H, Bergstralh EJ, Frank I, Fradet Y, et al., PD-L γ (B γ -H γ) expression by urothelial carcinoma of the bladder and BCG-induced granulomata: associations with localized stage progression. *Cancer*, 2007; 109:1499-1505.
29. Geng L, Huang D, Liu J, Qian Y, Deng J, Li D, Hu Z, Zhang J, et al., B γ -H γ up-regulated expression in human pancreatic carcinoma tissue associates with tumor progression. *J Cancer Res Clin Oncol.*, 2008; 134: 1021-1027.
30. Routh JC, Ashley RA, Sebo TJ, Lohse CM, Husmann DA, Kramer SA and Kwon ED. B γ -H γ expression in wilms tumor: correlation with tumor biology and disease recurrence. *J Urol.*, 2008; 9: 312-322.
31. Thompson RH, Gillett MD and Cheville JC. Co-stimulatory B γ -H γ in renal cell carcinoma patients: indicator of tumor aggressiveness and potential therapeutic target. *Proc. Natl Acad. Sci.*, 2004; 101:171-177.
32. Thompson RH, Kuntz SM and Leibovich BC. Tumor B γ -H γ is associated with poor prognosis in renal cell carcinoma patients with long-term follow-up. *Cancer Res.*, 2006; 66: 3381-3385.
33. Eble JN, Sauter G and Epstein JI. Pathology and genetics of tumors of the Urinary System and Male Genital Organs. World Health Organization Classification of Tumors, IARC, France. 2004.
34. Sun M, Lughezzani G and Jeldres C. A proposal for reclassification of the Fuhrman grading system in patients

- with clear cell renal cell carcinoma. *Eur Urol.* 2009; Nov., 06(0):770-81.
30. Byun SS, Yeo WG, Lee SE and Lee E. Expression of Survivin in Renal Cell Carcinomas: Association with Pathologic Features and Clinical Outcome. *Urology*, 2007; 69(1):34-37.
31. Thompson RH, Dong H and Kwon ED. Implications of B γ -H γ expression in clear cell carcinoma of the kidney for prognostication and therapy. *Clin Cancer Res.*, 2007; 13:709-710.
32. Lei Y, Geng Z, Guo-Jun W, He W and Jian-Lin Y. Prognostic significance of survivin expression in renal cell cancer and its correlation with radioresistance. *Mol Cell Biochem.*, 2010; 324: 23-31.
33. Krambeck AE, Dong H and Thompson RH. Survivin and B γ -H γ are collaborative predictors of survival with renal cell carcinoma and represent potential therapeutic targets for patients. *Clin Cancer Res.*, 2007; 13:1749-1756.
34. Parker AS, Lohse CM, Leibovich BC, Chevillet JC, Sheinin YM and Kwon E. Comparison of digital image analysis versus visual assessment to assess survivin expression as an independent predictor of survival for patients with clear cell renal cell carcinoma. *HumPathol.* August 2008; 39(8): 1176-1184.
35. Wang GC, Hsieh P, Hsu H, Sun G, Nieh S, Yu C and Jin J. Expression of cortactin and survivin in renal cell carcinoma associated with tumor aggressiveness. *World J Urol.*, 2009; 27:507-513.
36. Parker AS, Kosari F, Lohse CM, Thompson RH, Kwon ED, Murphy L, Riehle DL, et al., High expression levels of survivin protein independently predict a poor outcome for patients who undergo surgery for clear cell renal cell carcinoma. *Cancer*, 2006; 107:37-40.
37. Fortugno P, Wall NR, Giodini A, O'Connor DS, Plescia J, Padgett KM, Tognin S, et al., Survivin exists in immunochemically distinct subcellular pools and is involved in spindle microtubule function. *J Cell Sci.*, 2002; 115: 070-80.
38. Li F. Survivin study: what is the next wave? *J Cell Physiol.*, 2003; 197: 8-29.
39. Badran A, Yoshida A, Ishikawa K, Goi T, Yamaguchi A, Ueda T and Inuzuka M. Identification of a novel splice variant of the human anti-apoptosis gene survivin. *BiochemBiophys Res Commun.*, 2004; 314: 92-7.
40. Noton EA, Colnaghi, R, Tate S, Starck C, Carvalho A and Ko FP. Molecular analysis of survivin isoforms: evidence that alternatively spliced variants do not play a role in mitosis. *J. Biol. Chem.*, 2006; 281:1287-1290.
41. Shariat SF., Ashfaq R, Karakiewicz PI, Saeedi O, Sagalowsky AI and Lotan Y. Survivin expression is associated with bladder cancer presence, stage, progression, and mortality. *Cancer.* March 2007; 109(6):117-1113.
42. Taube JM, Anders RA, Young GD, Xu H, Sharma R, McMiller TL, Chen S, et al., Co-localization of Inflammatory Response with B γ -H γ Expression in Human Melanocytic Lesions Supports an Adaptive Resistance Mechanism of Immune Escape. *SciTransl Med.* March 2012; 4(127): 127-137.
43. Ghebeh H, Ayel -Mohammedy S, Al-Omair A, Tanz A, Lehe C, Al-Qudaihi G, Elkum N, et al., The B γ -H γ (PD-L γ) T lymphocyte -inhibitory molecule is expressed in breast cancer patients with infiltrating ductal carcinoma: correlation with important high-risk prognostic factors. *Neoplasia.* March 2006; 8(3):190-198.
44. Loos M, Langer R, Schuster T, Gertler R, Walch A, Rauser S, Surg AT, et al., Clinical significance of the costimulatory molecule B γ -H γ in barrett carcinoma. *Ann Thorac Surg.*, 2011; 91:1020-1031.
45. Weber J. Immune checkpoint proteins: A new therapeutic paradigm for cancer-preclinical background: CTLA-4 and PD-1 blockade. *Semin Oncol.*, 2010; 37(0):430-439.

51. Andersen MH, Pedersen LO, Capeller B, Brocker EB, Becker JC and Straten P. Spontaneous cytotoxic T-cell responses against survivin-derived MHC class I-restricted T-cell epitopes in situ as well as ex vivo in cancer patients. *Cancer Res.*, 2001; 61:5964-5968.