

## The Gene Expression of *ADAM9* in patients with gastric cancer in Iraq

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### Abstract

*ADAM9* disintegrin and metalloproteinase domain 9 gene, has been institute, and characterize overexpression, and dysregulation in a different of solid tumors. Objective: Evaluation the Gene Expression of *ADAM9* in gastric cancer patients in Iraq. Furthermore, found the correlation between *ADAM9* expression, and clinic-pathological parameters. 50 randomly patients FFPE blocks of stomach tissue (10 normal & 40 patients GC) were collected from the Gastroenterology and Hepatology Teaching Hospital. *ADAM9* Gene Expression has been achieved by using qPCR. Statistical analysis accomplished by SPSS system at ( $P < 0.05$ ). This study indicated that there were a significant differences between control and patients, also there was a significant correlation in invasion depth, lymph node involvement, and stages in patients, whereas there was non- significant association between the age, grade, gender, and histopathological type of patients in the expression of *ADAM9*. These results indicated that *ADAM9* could be a functional target for advanced gastric cancer therapeutic.

**Keywords:** *ADAM9*, Clinicopathological parameters, FFPE, Gastric cancer, Gene Expression.

### Introduction

Gastric carcinoma (GC) comprises a universal health issue. It is a disease with high aggressive and heterogeneous nature. It is one of the most prevalent reasons of cancer related death and takes advantage of an important encumbrance on international health sponsor [1]. In Iraq malignant neoplasm's represented the second leading cause of death. Gastric cancer trend demonstrated an instant rise after 2007; it is a fifth of eighteenth cancers in Iraq [2]. GC is the third main reason of cancer-related mortality in the world, leading round about 783,000 deaths in 2018, and over 1,000,000 new cases of gastric carcinoma per year [3]. The Lauren classification is the most communal classification of GC. It includes three main subtypes: intestinal, diffuse and mix [4], which they differ in many properties, such as: clinical characterize, genetics, morphology, epidemiology and development features [5]. *ADAM9* disintegrin and metalloproteinase domain 9, or meltrin- $\gamma$ , also known as metalloprotease/disintegrin/cysteine-rich protein 9 (MDC9), was first recognize in breast cancer in 1996 [6], has been institute, and characterize overexpression, and dysregulation in a different of solid tumors. It proposes that a main molecule includes in tumorigenesis in glioma, prostate, colon and breast cancer, which suggest *ADAM9* as an important molecule involved in tumorigenesis [7], [8]. Nevertheless, the role of gene in gastric cancer is remaining elusive, and merit to be explained [9]. It is greatly expressed in human tissues, and exhibits a plentiful rise in pathological cases [10]. Gene location in human: 8p 11.23, exon count: 22 and 4447BP full length [11]. It has several domains structures such as: The long *ADAM9*-L (110 and 84) KDa. The short *ADAM9*-S (55) KDa. *ADAM9*-S lacks exon 12 from the *ADAM9*-L genetic sequence [12]. Moreover, *ADAM9*, its N-terminus includes a signal sequence that controller the secretory pathway of it to passage to the cell surface, and the

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transmembrane domain that confirm it on the cell membrane [13]. ADAM proteins have been reported in many biological pathways such as: development, fertility, vascular endothelial cell function, inflammation, immunity, signaling transduction, neurodegenerative disease [14], [15], [16], [17]. Objective: To estimate *ADAM9* expression in patients with gastric cancer, and control. Furthermore, found the correlation between *ADAM9* expression, and clinicopathological parameters as: gender, age, invasion depth, histopathological type, involvement of lymph nodes, grade and stages of GC.

## Materials and methods

### Samples collection

The current research is a retrospective study from January 2018 to December 2020. The total numbers of samples were 50 cases. 40 samples of gastric cancer patients formalin-fixed paraffin embedded blocks (FFPE) have been obtained randomly from surgically resected specimens in Gastroenterology and hepatology Teaching Hospital, Medical City/ Bagdad, with its reports (no chemotherapy received by these patients) after getting the official agreement from Iraq Ministry of Health, and Department of Medical City/ Baghdad. Each report contains clinic-pathological parameters (age, gender, histopathological type of tumor, grade of tumor, depth invasion of tumor, lymph nodes involvement, tumor stage/ TNM), which were diagnosis by pathological doctors of hospital. 10 samples of normal stomach tissue have been selected randomly from patients undergo (Sleeve gastrectomy) by private hospitals. These patients cases were classified depend on Lauren classification [4].

### Gene Expression study

#### Primers

Primers for Gene Expression have been listed depended on [18],[19] in (Table 1) as follows:

**Table (1): primers for Gene Expression**

Name of gene	Primer sequence	Reference
<i>ADAM9</i>	F- 5'-AGTGGCGGGAAAAGTTTCTT-3' R-5'-CCAGCGTCCACC-3'	[18]
<i>Beta-actin</i> (housekeeping gene)	F-5'-ATGATATCGCCGCGCTCGTC-3' R-5- CGCTCGGTGAGGATCTTCA-3,	[19]

The study of Gene Expression of *ADAM9* accomplished as follows:

#### RNA extraction

By using Qiagen RNeasy extraction kit (RNeasy Mini Kit (217504), Germany), total RNA was extracted from cancerous and non-cancer gastric tissues depended on manufacture protocol as follows: A scalpel used to trim excess paraffin off the sample block, which cut about (5–20)  $\mu\text{m}$  thick. It placed in a 1.5 ml microcentrifuge tube, 320  $\mu\text{l}$  of xylene was added, and vortex vigorously for (10 s). Tube incubated at 56°C for 3 min, and then allowed to cool at room temperature (15–25°C). 240  $\mu\text{l}$  of Buffer PKD was added and mixed by vortexing then it was centrifuged for 1 min at 11,000 x g. 10  $\mu\text{l}$  proteinase K was added to the lower, clear phase and mixed gently, incubated at 56°C for 15 min, and then at 80°C for 15 min. The lower, uncolored phase transferred into a new 2 ml microcentrifuge tube, which incubated on ice for 3 min. and

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then centrifuged for 15 min at 20,000 x g. The supernatant transferred to a new microcentrifuge tube. DNase Booster Buffer added approximately 25  $\mu$ l, and 10  $\mu$ l DNase I stock solution mixed by inverting the tube. Microcentrifuge tube incubated at room temperature for 15 min. 500  $\mu$ l Buffer RBC added to adjust binding conditions, and mixed the lysate thoroughly. 1200  $\mu$ l ethanol (100%) added to the sample, and mixed well. 700  $\mu$ l of the sample Transferred, including any precipitate that may have formed, to an RNeasy MinElute spin column placed in a 2 ml collection tube (supplied). The lid closed gently, and microcentrifuge tube centrifuged for 15 s at  $\geq 8000$  x g. 500  $\mu$ l Buffer RPE added to the RNeasy MinElute spin column, the lid closed gently, and centrifuged for 15 s at  $\geq 8000$  x g. The flow-through discarded. 500  $\mu$ l Buffer RPE added to the RNeasy MinElute spin column, the lid closed gently, and centrifuged for 2 min at  $\geq 8000$  x g. The collection tube discarded with the flow-through. The RNeasy MinElute spin column placed in a new 2 ml collection tube, the lid of the spin column opened, and centrifuged at full speed for 5 min, the collection discarded tube with the flow-through. The RNeasy MinElute spin column placed in a new 1.5 ml collection tube. 14–30  $\mu$ l RNase-free water added directly to the spin column membrane. The lid closed gently, and centrifuged for 1 min at full speed to elute the RNA.

### RNA quantitation by Qubit 4.0

The Qubit® working solution was prepared by diluting the Qubit® RNA HS [Qubit™ RNA HS Assay Kit(Q32852), ThermoFisher(USA)] Reagent 1:200 in Qubit® RNA HS buffer. The volume 190  $\mu$ L from Qubit® working solution has been added to each tube designed to be as a standard, then 10  $\mu$ l from each provided standard solution has been added into same tubes, then vortexed. The Qubit® working solution as 197  $\mu$ L has been added to each tube prepared for sample and then 3  $\mu$ L of sample has been added individually. All composition has been vortexed and incubated at room temperature for 3 mins. Standards tubes have been inserted in Qubit instrument for creating concentration curve. Tubes for samples have been added one by one to read the concentration for miRNA in each sample.

### RT-qPCR protocol

This process divided into two phases, the first is done through synthesis of cDNA from RNA through specific primer for fas, fasl and beta actin transcripts, and protoscript cDNA synthesis kit [ProtoScript® First Strand cDNA Synthesis Kit(E6300S), NEB (UK)]. This procedure has performed through steps: 5  $\mu$ l from each extracted total RNA sample added into new PCR tube. Protoscript reaction mix that contains dNTPs, buffer and other essential components added as 10  $\mu$ l for each sample. MuLV Enzyme then added into reaction as 2  $\mu$ l per sample. 2  $\mu$ l of oligoT, and the volume completed up to 20  $\mu$ l by adding 1  $\mu$ l, and then this mixture was incubated for 60 min at 42 C° by using thermocycler as in (Table 2), and this followed by 80 C°.

**Table (2): Thermocycling protocol for cDNA synthesis**

Step	Temperature	Time
Primer annealing	30 C°	10 min
cDNA synthesis	42 C°	60 min
Heat inactivation	80 C°	5 min

The cDNA product quantification also done through Qubit 4.0. The second section of this protocol it's done by choosing the cDNA sample from patient, and control at the same run, for each sample there are three PCR tubes, one tube for each gene, fas, fasl and beta- actine which is consider as a house keeping

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gene in this study. The detection of quantity based on fluorescent power of SyberGreen. The reaction mix composed from component with their quantity as mentioned in (Table 3) below:

**Table (3): The reaction mix composed from component with their quantity**

Component	20ul Reaction
Luna Universal qPCR Master Mix [(M3003S), NEB (UK)]	10ul
Forward primer (10 µM)	1ul
Reverse primer (10 µM)	1ul
Template DNA	5ul
Nuclease-free Water	3ul

Quickly spin for PCR tubes to remove the bubbles, and collect the liquid (1 minute at 2000g), and then the program for Real-Time PCR was setup with indicated thermocycling protocol as shown in (Table 4).

**Table (4): Thermocycling protocol for Real-Time PCR**

Cycle Step	Temperature	Time	Cycles
Initial Denaturation	95 C°	60 seconds	1
Denaturation	95 C°	15 seconds	
Extension	60 C°	30 seconds (+plate read)	40-45
Melt Curve	60-95 C°	40 minutes	1

## Results calculation

The results were calculated, and analyzed by Livak formula:

Normalized Ct formula

$$\Delta Ct A = Ct_{GOI A} - Ct_{Ref A}$$

$$\Delta Ct B = Ct_{GOI B} - Ct_{Ref B}$$



$$\Delta \Delta Ct = \Delta Ct A - \Delta Ct B$$

normalized expression =

$$2^{-(\Delta \Delta Ct)}$$

**Ct** refer to stands for the cycle threshold of sample, it is the cycle number where the fluorescence generated.

$$\Delta Ct = Ct (\text{gene of interest}) - Ct (\text{housekeeping gene})$$

$$\Delta \Delta Ct = \Delta Ct (\text{sample}) - \Delta Ct (\text{control}) [20]$$

## Statistical analysis

Collected data analysis was accomplished by (statistical package for social science/ SPSS version- 24 software/IBM), Chi square ( $\chi^2$ ) used to estimate the correlation between clinic-pathological correlations, and (t-test, and ANOVA test) used for the data of Gene Expression, (P- values) valuable at the accepted level of significance in 0.05 ( $p < 0.05$  was considered significant) [21].

## Results

The results of 50 cases for this study referred that males total numbers in control group were 2 (20%) statuses, while females were 8 (80%) statuses, with male: female (M: F) ratio 1:4 (the majority of statuses from females). In patients with gastric cancer group, the number of males were 24 (60%) cases, while females number were 16 (40%) cases, and 3:2 in (M: F) ratio (the majority cases from males). Age divided into two age group equal or less than 50 years, and more than 50 years. Control group age ranged between (19-50) years for 10 (100%) statuses, which were within the age group equal or less than 50 years with mean age ( $33.9 \pm 10.027$ ), and the age of patients with gastric cancer which were ranged from (19-83) years with mean ( $55.325 \pm 15.423$ ). Patients number of equal or less than 50 years were 16 (40%) cases with mean ( $39.875 \pm 9.493$ ), and the number of patients in more than 50 years were 24 (60%) cases with mean age ( $65.625 \pm 8.234$ ). Histopathological subtype distributed in: intestinal type: patients numbers were recorded 23 (57.5%) cases. Diffuse type: 15 (37.5%) cases total number of patients, whereas mixed type: patients were registered 2 (5%) cases. The most cases for grade were moderately differentiated which were registered 25 (62.5%) cases, while poorly differentiated were 15 (37.5%) cases in total number of patients. Also, the current study was showed that gastric cancer invasion (subserosa) in about 15 (37.5%) cases. In invasion (serosa) total patients were 18 (45%) cases, while (muscularis propria) invasion were 7 (17.5%) cases in total patients. The total number of patients that diagnosed with lymph node involvement was about 32 (80%) cases, whereas patients without lymph node involvement total number were 8 (20%) cases. Invasive depth and lymph node metastasis (TNM) were used to distribute gastric cancer patients into advanced stages (III & IV), and early stage (II). Advanced stages (III & IV) total patient numbers were 27 (67.5%) cases. In (III) stage the total number of patients were about 12 (30%) cases, whereas IV stage total patient numbers were 15 (37.5%) cases. 13 (32.5%) cases were the total number of patients in early stage (II) as follow in (Table 5):

**Table (5): Study groups distribution depends on clinicopathological parameters**

Clinicopathological Parameters	Findings	Frequency (%)
<b>Gender</b>	Control	Male 2 (20%)
		Female 8 (80%)
	Patients	Male 24 (60%)
		Female 16 (40%)
<b>Age</b>	$\leq 50$	Control 10 (100%) with mean ( $33.9 \pm 10.027$ )
		Patients 16 (40%) with mean ( $39.875 \pm 9.493$ )
	$> 50$	Control -
		Patients 24 (60%) with mean ( $65.625 \pm 8.234$ )
<b>Histopathological types</b>	Patients	Intestinal 23 (57.5%)
		Diffuse 15 (37.5%)
		Mix 2 (5%)
<b>Grade of tumor</b>	Patients	Moderately 25 (62.5%)
		Poorly 15 (37.5%)
<b>Invasion depth of tumor</b>	Patients	pT2 7 (17.5%)
		pT3& pT4 33 (82.5%)
<b>Involvement of lymph node</b>	Patients	N0 8 (20%)
		N1,2&3 32 (80%)
<b>Stage of GC (TNM)</b>	Patients	II 13 (32.5%)
		III&IV 27 (67.5%)

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## The Gene Expression of *ADAM9*

The amplification of *ADAM9* by qPCR of some study group (control and patients) illustrated in fig. (1, A), which show Ct values of these groups. Furthermore, the fig. (1, B) show the different fold gene expression of *ADAM9* in control and patients.

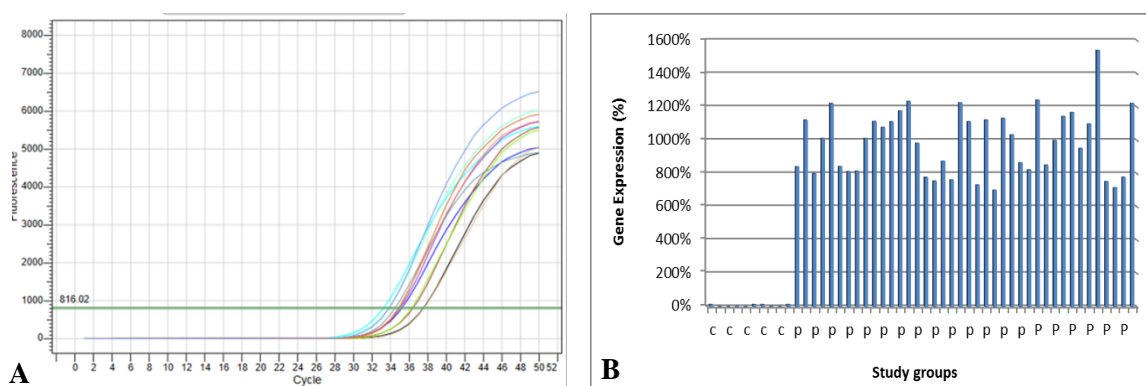


Figure (1): (A) *ADAM9* amplification by qPCR samples included some study groups. Ct values ranged from (32-36). The photograph was taken directly from mic- qPCR machine. (B) Illustrates the Gene Expression of *ADAM9* in control (c) and patients (p) with gastric cancer.

## The Gene Expression of a disintegrin and metalloproteinases (*ADAM9*) in control and patients with gastric cancer.

This study investigated the Gene Expression of *ADAM9* in study groups which contain (control and patients), the result indicated that this gene was not expressed in control group (n=10) with mean of fold Gene Expression ( $0.061 \pm 0.019$ ), and 6.0003 in variance, whereas it expressed in patients group (n=40) with mean ( $9.879 \pm 0.310$ ), and 188.028 in variance. Statistically, these differences made a significant association at  $P < 0.05$ ,  $P = 0.0001$  as showed in (Table 6), and fig. (2).

Table (6): The Gene Expression of *ADAM9* in control and patients with gastric cancer.

Group of study	Fold of Gene Expression		P-value
	Mean $\pm$ SE	Variance	
Control (n=10)	$0.061 \pm 0.019$	6.0003	$P = 0.0001^*$
Patients (n=40)	$9.879 \pm 0.310$	188.028	

\*t-test P-value is significant ( $P < 0.05$ )

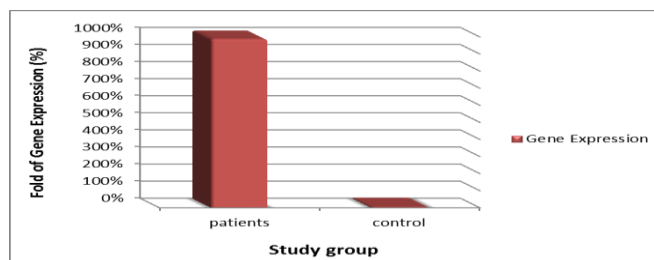


Figure (2): Graph illustrates the Gene Expression of *ADAM9* in control and patients with gastric cancer.

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### Patients samples distribution of fold Gene Expression of a disintegrin and metalloproteinases (*ADAM9*) depend on clinicopathological parameters

(Table 7) Show the fold of Gene Expression of *ADAM9* correlated with clinic-pathological parameters. This study donate that (60%) with mean ( $9.746 \pm 0.337$ ) of total numbers in gastric cancer patients were in males, which recorded in 24 cases, and (40%) 16 cases, with mean ( $9.211 \pm 0.70$ ) for female, statistically, no significant association between gender and the fold of Gene Expression, P- value were larger than 0.05 at ( $P < 0.05$ ). Patients age ranged from (19-83) years, patients from less or equal 50 years were recorded (40%), with mean ( $8.996 \pm 0.670$ ), and (60%), with mean ( $9.901 \pm 0.350$ ) in patients more than 50 years. P-value = 0.184 larger than 0.05 ( $P > 0.05$ ) so there was not a significant association between age and the expression of this marker. The current study showed that the total number of patients with intestinal type positive expressed were (57.5%), diffuse were (37.5%), and (5%) in mixed type, with mean ( $10.04 \pm 0.0092$ ,  $9.72 \pm 0.059$ ,  $8.69 \pm 0.012$ ) respectively. No significant association at ( $P < 0.05$ )  $P=0.151$ . There was about (62.5%) cases with gastric cancer at moderately differentiated grade with mean ( $9.975 \pm 0.387$ ), which were more than poorly differentiated grade, which recorded (37.5%), ( $8.794 \pm 0.622$ ) in mean, but there was not a significant correlation  $p=0.779$ . The fold of Gene Expression of *ADAM9* in invasion depth were recorded (20%), and ( $7.556 \pm 0.061$ ) mean in pT2, and (80%), and ( $20.671 \pm 0.060$ ) mean in p T (3 & 4), a significant association statistically at  $P < 0.05$ ,  $p=0.004$ . Also, this study indicated that there were (80%), ( $7.843 \pm 0.209$ ) of *ADAM9* fold of Gene Expression in patients involve lymph nodes (N1, N2&N3), whereas in patients without involvement of lymph nodes (N0) patients were (20%), ( $9.954 \pm 0.393$ ) mean. Statistically, these differences made a significant association between involvement of lymph nodes and the expression of this gene,  $p=0.012$ . The highest records of Gene Expression were in advanced stage (III&IV) of gastric cancer in (67.5%) with mean ( $20.432 \pm 0.738$ ), while it was (32.5%) with mean ( $7.800 \pm 0.129$ ) in early stage. Statistically, these differences made a significant association between stage of gastric cancer, and the expression of this gene at  $p < 0.05$ ,  $p= 0.0003$ .

**Table (7): The fold of Gene Expression of *ADAM9* correlated with clinicopathological parameters**

Clinicopathological parameters		Fold of Gene Expression of <i>ADAM9</i>			P-value
		Number (ratio)	Mean%	Mean $\pm$ SE	
Gender	Male	24 (60%)	975	$9.746 \pm 0.337$	$P=0.480^*$
	Female	16 (40%)	921	$9.211 \pm 0.70$	
Age	$\leq 50$	16 (40%)	899.6	$8.996 \pm 0.670$	$P= 0.184^*$
	$> 50$	24 (60%)	990.1	$9.901 \pm 0.350$	
Histopathological subtype	Intestinal	23 (57.5%)	1004	$10.04 \pm 0.0092$	$P= 0.151^{**}$
	Diffuse	15 (37.5%)	972	$9.72 \pm 0.059$	
	Mix	2 (5%)	869	$8.69 \pm 0.012$	
Grade of tumor	Moderately	25 (62.5%)	997.5	$9.975 \pm 0.387$	$P= 0.779^*$
	Poorly	15 (37.5%)	879.4	$8.794 \pm 0.622$	
Invasion depth of GC	pT 2	8 (20%)	755.6	$7.556 \pm 0.061$	$P= 0.004^*$
	pT3 & pT4	32 (80%)	206.7	$20.671 \pm 0.060$	
Involvement of lymph node	N0	8 (20%)	784.3	$7.843 \pm 0.209$	$P= 0.012^*$
	N1,2,&3	32 (80%)	995.4	$9.954 \pm 0.393$	
Stage of GC (TNM)	II	13 (32.5%)	780.0	$7.800 \pm 0.129$	$P= 0.0003^*$
	III&IV	27 (67.5%)	2043.2	$20.432 \pm 0.738$	

\*t-test, and \*\*ANOVA test, P-value is significant at ( $P < 0.05$ )

## Discussion

In Iraq malignant neoplasm's represented the second leading cause of death. Gastric cancer trend demonstrated an instant rise after 2007; it is a fifth of eighteenth cancers in Iraq [2]. GC comprises a universal health issue. It is a malignancy disease with high aggressive nature. It is one of the most prevalent reasons of cancer related death and takes advantage of an important encumbrance on international health sponsor [1]. Gastric cancer treatment is restricted because of its heterogeneity and genetic complicated [22] so find of special biomarkers is important for management the development of gastric cancer, and identified the effective treatments for patients [23]. The current study indicated that the total number of male more than female, and the number of older patients (more than 50 years) more than younger (equal or less than 50 years), as in the study of Lou *et al.* [24] which is show that men is higher incidence than women. Furthermore, there is a maximal sex differences in older age. Moreover, as in the Globocan 2012 report, standardized rates of age of gastric cancer was twice more in men than in women [25]. The study of Radkiewicz *et al.* [26] is demonstrated that rise of risk for gastric cancer is associated with male sex, the portion of cancer explicated by factors correlated to male sex is huge, and males suffer poorer survival in most cancer sites. A probable exposition is either the preventative impact of estrogen in women, or other effects as diversity in diet and occupational exposure may participate to rise gastric cancer incidence in males [27],[28]. Many studies mention that the intestinal type is the general type with rising the risk of adenocarcinoma, in age range (55-80) years, commonly appear in male more than female in ratio (2:1) [29],[30]. Also, in [31] author reminded that (54%) of cases were intestinal subtype, which located in distal stomach (non- cardia). All these results are corresponded with this study, which intestinal type was the highest ratio compare with diffuse and mix type. The study recorded that moderately differentiated was the high ration than poorly, which is similarity in [32], in contrast the study of Zhang *et al.* [33] which found that poorly differentiated was the domain differentiated. Advanced stage (III&IV) depend on TNM staging was the highest ratio than early stage (II) this result agree with Chen *et al.* and Lee *et al.*[34],[35].ADAM9 is a one of ADAM family anchored to the membrane member's. Many reports have mentioned that there are high expressions of ADAM9 in GC. It associated with cancer proliferation and invasion [36], [37]. It was a significant upregulated in patients with gastric cancer compared with normal tissue on mRNA and protein level as show in (Table 6). As in (Table 7) this study declared that there was not a significant association between age and the expression of the gene which is match with Grutzmann *et al.*[38]. In the study of Wang *et al.* [39] demonstrated that there were a significant correlated in invasion depth of tumor, involvement of lymph nodes and stages of GC, and no significant association in age, gender, and grade of GC and the fold of Gene Expression of this gene, these results matched with current study as in (Table 7).ADAM9 have an essential in some signaling pathway roles, in which transportation of acquaintance could prompt several exacerbations of inconvertible in disease [40]. There are many constructions about ADAM9 role in cancer advancement. It intermediates the secretion of growth factor ligands, which regulate the signaling of EGFR. In the gastric, the EGFR trans-activation accomplish by peptides as: (gastrin, angiotensin II, bradykinin, bombesin, or substance P) that intermediated by EGFR-ligand shedding by ADAMs [41]. Furthermore, it trans-membrane protein-derived ligands releases as: (heparin-binding-EGF, amphiregulin, TGF $\alpha$ , and TNF $\alpha$ ) [42]. In the study of Kim *et al.* [18] found that knock-down of ADAM9 blocks EGFR phosphorylation, and down-stream ERK activation that RAV-18 inhibited tumor growth, in line with EGFR, and ERK phosphorylation in vivo. So, suppression of EGFR ligand shedding by ADAM9 with following reduced the activity of EGFR, and down-stream signaling might be a technique against the anti-tumor activity of RAV-18.

**Conclusion:** ADAM9 could be speculating as a prospect target for GC prohibition, therapeutic treatment, and diagnosis.



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