

Expression of IGF-IEc Isoform in Renal Cell Carcinoma Tissues

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Abstract. *Background/Aim:* Insulin-like growth factor-I (IGF-I) regulates various aspects of cancer biology. There is a growing body of evidence regarding the potential distinct role of IGF-I isoforms, particularly of IGF-IEc, in the pathophysiology of various human cancer types, however, there are no studies which examined the expression of the different IGF-I isoforms in renal cell carcinoma (RCC). This study aimed to characterize the expression of IGF-IEc in human RCC tissues and investigated whether its expression is associated with the histopathological type of RCC as well as with the overall survival of patients. *Materials and Methods:* Formalin-fixed paraffin-embedded renal tissue samples from 94 patients (58 males and 36 females) were assessed for IGF-IEc expression by immunohistochemistry. *Results:* RCC tissues showed mainly cytoplasmic IGF-IEc staining but immunoreactivity of IGF-IEc was also localized in the cell membrane. Significantly lower IGF-IEc expression was found in clear cell RCC vs. all other histological types ($p=0.010$), and this remained significant after adjusting for tumor size, grade, stage, and mitotic index ($p<0.05$). No association was found between IGF-IEc expression level and overall survival of patients with RCC. *Conclusion:* The differential expression of IGF-IEc isoform among the RCC histopathological types may indicate its histological type-specific regulation and possibly suggests a discrete biological role of this isoform in the pathophysiology of RCC.

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Renal cell carcinoma (RCC) is the most common kidney malignancy, affecting men more than women, and metastatic disease at presentation occurs in up to one-third of patients. The pathological stage (size of the tumor and the extent of invasion), grade, and histological cell type are widely used in clinical practice for the prognosis of RCC (1). In particular, clear cell is the most common histological type of RCC accounting for 60-70% of cases (2). It represents a genetically and histologically diverse group of cancers that includes chromophobe, papillary, unclassified RCC, and other rare subtypes such as renal medullary carcinoma (3-6).

Insulin-like growth factor-I (IGF-I) plays an important role in various aspects of cancer biology, such as cell growth, apoptosis resistance, cell differentiation and migration (7-10) and, thus, it has been implicated in the pathophysiology and prognosis of several human cancer types (11-14), including RCC (2, 15, 16). IGF-I is not only secreted by the liver, but is also produced by other organs such as skeletal muscle, kidney and brain (17-27). The *IGF1* gene consists of six exons and can produce multiple heterogeneous transcripts via alternative splicing during its transcription, namely IGF-IEa, IGF-IEb, and IGF-IEc, which encode the corresponding IGF-I protein isoforms (24, 26). Mature IGF-I peptide represents the common bioactive product of all IGF-I isoforms (24, 28) and numerous studies have shown that this peptide is involved in cell survival and protection from apoptosis, as well as in the process of uncontrolled cell division, which generally characterizes cancer development (10, 29, 30). Various types of human cancer cells, such as prostate, breast and osteosarcoma (8, 31-35), have been found to be affected by these IGF-I functions, while IGF-I has also been shown to contribute to cancer cell migration (36), tumor aggressiveness (37, 38) and neovascularization (39).

Interestingly, a new component of the IGF bioregulatory system has recently been studied for its potential role in carcinogenesis, specifically, IGF-I isoforms (precursors).

These undergo post-translational cleavage, generating the common mature IGF-I peptide but also different carboxyl-terminal extension (E-) peptides (24, 40) and there is a growing body of evidence regarding the potential role of IGF-I isoforms and their respective post-translational IGF-I products, other than mature peptide, in the pathophysiology of different cancer models both *in vitro* and *in vivo* (11, 13, 33, 34, 41-43). The differential regulation of the IGF-I isoforms in the pathophysiology of cancer (13, 33, 41) may imply their discrete biological roles, potentially *via* the putative Ea, Eb and Ec peptides (11, 18, 20, 33-35, 40, 44, 45). In particular, Ec peptide is a bioactive product of the IGF-IEc isoform and its action has been shown to be mediated *via* an IGF-I receptor-independent mechanism (11, 18-20, 33, 44) and has been postulated to be oncogenic (46).

However, to our knowledge, there are no studies examining the expression of the different IGF-I isoforms in RCC. Given the potentially distinct biological role, particularly of the IGF-IEc isoform and its post-translational product Ec peptide in different types of cancer (13, 33, 37, 38, 46), this study aimed to characterize the expression/localization of IGF-IEc in human renal cell carcinoma tissues and investigate whether its expression is associated with the histopathological type of RCC as well as with the overall survival of patients.

Materials and Methods

Ethical approval. A retrospective selection of primary renal carcinoma tissue diagnostic biopsy samples was performed from the archives of the Pathology Department of a General Hospital and this research approach was approved by the Ethics Committee of the Medical School of the National and Kapodistrian University of Athens (approval number: 781/29-9-2009), while all experimental procedures conformed to the Declaration of Helsinki.

Patients. Formaldehyde-fixed and paraffin wax-embedded renal tissue samples, derived from 94 patients, 58 males and 36 females, who underwent radical nephrectomy for histologically proven renal carcinoma within the time period from 1986 to 1998 were retrospectively selected from the archives of the Pathology Department of the “Evangelismos” General Hospital of Athens. Based on the official pathology reports, detailed information was recorded and analyzed, while all tissue specimens were further re-evaluated and confirmed by another pathologist. The patients were between 36 and 82 years of age and divided into different subgroups based on their age, sex, tumor location, invasion and size, histological type, grade and stage according to the 2016 World Health Organization/International Society of Urologic Pathologists classification (47).

Immunohistochemical analysis. Paraffin wax-embedded renal tissue samples were processed for paraffin sections as described elsewhere (18) and a Bondmax automated system (Leica Microsystems, Newcastle upon Tyne, UK) was used for the immunohistochemical (IHC) staining of the sections. The sections were then incubated with specific anti-human IGF-IEc antibody (48) at a dilution of 1:1,000 in phosphate-buffered saline, as previously described (18).

Table I. Descriptive statistics of the patients' clinicopathological characteristics.

Characteristic		Value
Age (n=87), yrs	Mean±SD	63.0±9.9
IGF-IEc (n=89)	Mean±SD	171.7±55.9
Tumor size (n=94), cm	Mean±SD	8.0±3.5
Gender, n (%)	Female	36 (38.3%)
	Male	58 (61.7%)
Grade, n (%)	1	5 (5.3%)
	2	42 (44.7%)
	3	35 (37.2%)
	4	12 (12.8%)
Histological type, n (%)	Clear cell	65 (69.1%)
	Papillary type I	5 (5.3%)
	Papillary type II	5 (5.3%)
	Oncocytic	9 (9.6%)
	Chromophobe	5 (5.3%)
	Unclassifiable/sarcomatoid	5 (5.3%)
Mitotic index, n (%)	1	44 (46.8%)
	2	29 (30.9%)
	3	21 (22.3%)
Pathological stage, n (%)	T1A	10 (10.6%)
	T1B	25 (26.6%)
	T2	12 (12.8%)
	T3A	28 (29.8%)
	T3B	19 (20.2%)
Death, n (%)	No	52 (55.9%)
	Yes	35 (37.6%)
	Yes from other cause	6 (6.5%)

Secondary biotinylated goat anti-rabbit IgG antibody (Dako Real EnVision, Glostrup, Denmark) was used and tissue sections were visualized under light microscopy. Prostate cancer biopsy sections were used as positive control (33), while control for the specificity of the reactions obtained in immunohistochemical analysis was performed by substituting the primary IGF-IEc antibody with the antibody diluent (phosphate-buffered saline) only (negative control). One representative tumor section per case was evaluated independently by two blinded pathologists, using intermediate-power light microscopy. Expression/localization of IGF-IEc was assessed and categorized as either grade 1 (weak intensity), grade 2 (moderate intensity) or grade 3 (strong intensity) according to both the intensity and distribution of the staining, while absence of staining was categorized as grade 0 (IGF-Ec-negative). The percentage distribution of each grade was multiplied by the corresponding number (0, 1, 2, or 3) and the summation of those products comprised the total IGF-IEc expression score of the sample (range of expression level: 0-300).

Statistical analysis. Data analysis was performed using Stata 13 statistical software (StataCorp. LP, College Station, TX, USA). Comparison of IGF-IEc expression between groups was performed using *t*-test or Man-Whitney test. Kolmogorov-Smirnov or Shapiro-Wilk test was used to evaluate normality. Multiple linear regression was used to test differences of IGF-IEc expression between groups after controlling for potential confounders. Cox proportional hazards model was used to investigate association

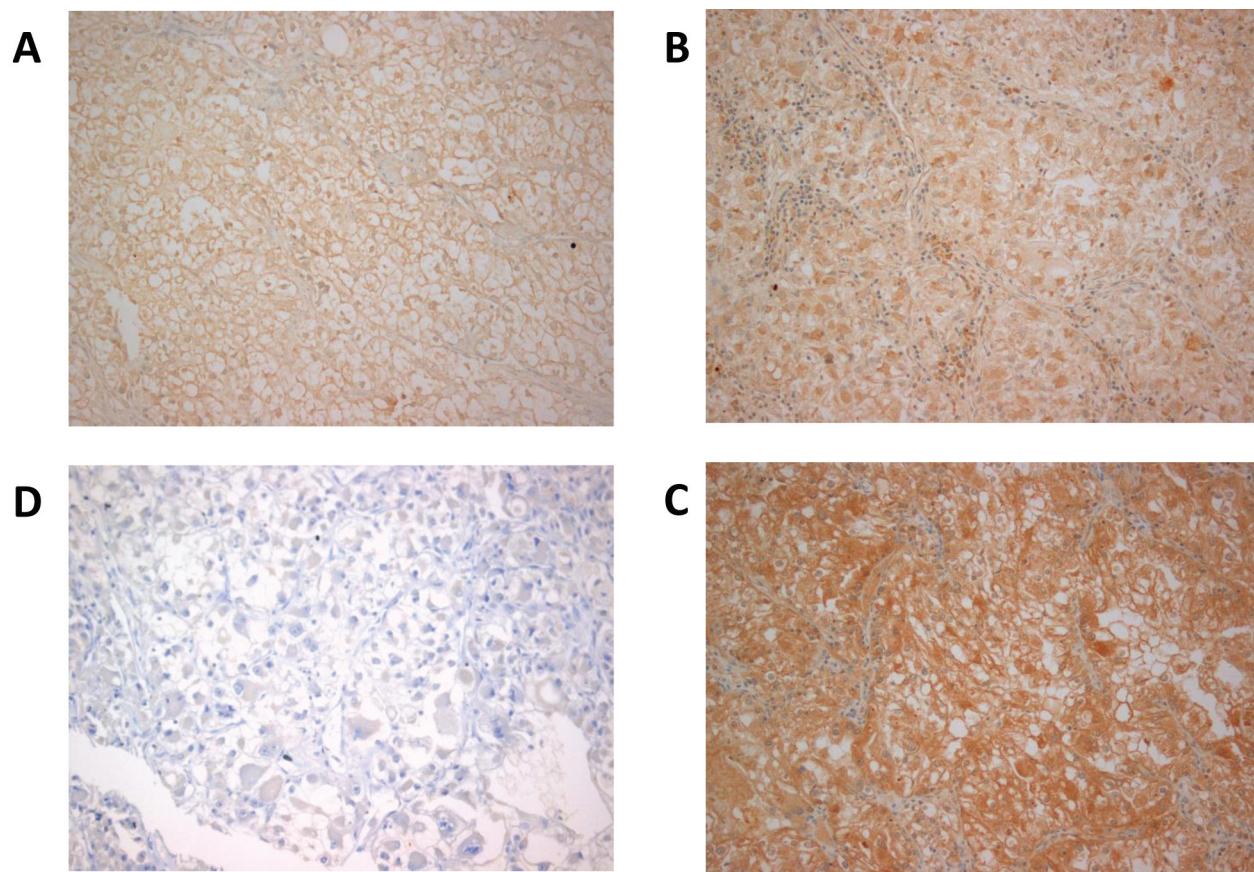


Figure 1. Representative images of weak (A), moderate (B) and strong (C) immunohistochemical staining of renal cell carcinoma tissue sections using the specific antibody to human insulin-like growth factor (IGF)-IEc. Note the positive (brown) staining with mainly cytoplasmic localization. Specificity of the immunohistochemical detection of IGF-IEc was confirmed by the absence of immunoreactivity in the control (D) (see text for details; magnification $\times 200$).

between IGF-IEc and risk of death from cancer. Fine and Grey competing risks model (49) was applied to assess confounding by other causes of death. The shape of the association between IGF-IEc and risk of death from cancer was evaluated using natural cubic splines with four knots. All analyses were performed at $\alpha=5\%$ level of statistical significance.

Results

Table I lists the clinicopathological characteristics of the patients included in the present study. Representative samples stained with the IGF-IEc specific antibody are shown in Figure 1. RCC tissues showed mainly cytoplasmic IGF-IEc staining but immunoreactivity of IGF-IEc was also localized in the cell membrane. The median IGF-IEc expression score overall was 184 (range=40-300; 25th and 75th percentile values of 125 and 215, respectively). Five out of 94 samples (~5%) were completely negative for IGF-IEc.

IGF-IEc expression in clear cell RCC *versus* all other histological types was significantly lower (Table II, $p=0.010$;

Table II. Comparison of insulin-like growth factor (IGF)-IEc expression score (mean \pm SD) by histological type.

Histological type		Other	<i>p</i> -Value
Clear cell (n=60)	161.1 \pm 57.3	193.5 \pm 46.7 (n=29)	0.010*
Sarcomatoid (n=5)	191.4 \pm 53.9	170.5 \pm 56.1 (n=84)	0.420

*After adjusting for size, grade, stage or mitotic index.

Figure 2). This finding remained significant after adjusting for tumor size, grade, stage, and mitotic index ($p<0.05$). Higher IGF-IEc levels were found in sarcomatoid (five cases) compared to other cell types although not a statistically significant finding ($p=0.420$) (Table II).

The Cox proportional hazards as well as Fine and Grey competing risks models did not suggest a clinically meaningful association between IGF-IEc level and risk of death from cancer [hazard ratio (95% confidence interval) of

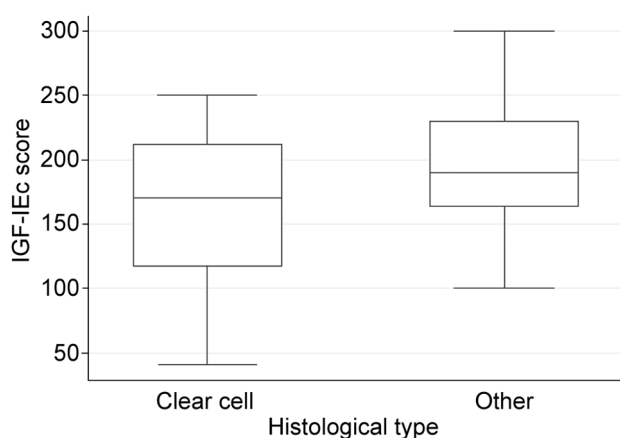


Figure 2. Box plots representing the distribution of insulin-like growth factor (IGF)-IEc expression values by cell type. The line within each box is the median value, upper and lower whiskers represent the minimum and the maximum values, and the box shows the interquartile range.

1.001 (0.994-1.007) and 1.000 (0.994-1.007), respectively] under assumption of a linear association. When the linear association assumption was relaxed, a non-linear, non-significant ($p=0.470$) association was identified between IGF-IEc level and overall survival, the shape of which was polynomial as depicted in Figure 3.

Discussion

The present study investigated the IHC expression/localization of the IGF-IEc isoform in different histological types of RCC tissues, revealing significant differences in the IGF-IEc levels between clear cell RCC and all other histological types and these differences remained significant after adjusting for tumor size, grade, stage or mitotic index, alternatively. To our best knowledge, this is the first study investigating the expression pattern of IGF-IEc isoform in different types of renal cancer, showing an association between low expression of IGF-IEc and specific RCC pathology. Moreover, it was demonstrated that its expression/localization in RCC tissues was mainly cytoplasmic, while no significant association was found between IGF-IEc level and overall survival of patients with RCC.

IGF-I has been shown to play an important role in cell proliferation and protection from apoptosis in a wide variety of cancer types such as of the prostate, breast, lung, colon, stomach, esophagus, sarcoma, leukemia, liver, pancreas, thyroid, brain, ovary and uterus (cervix and endometrium) (50-53). In particular, studies that have addressed the role of IGF-I or its receptor (IGF-IR) in RCC (2, 15, 16, 54-56) implicated the IGF-I system in the development and progression of RCC, specifically reporting IGF-IR

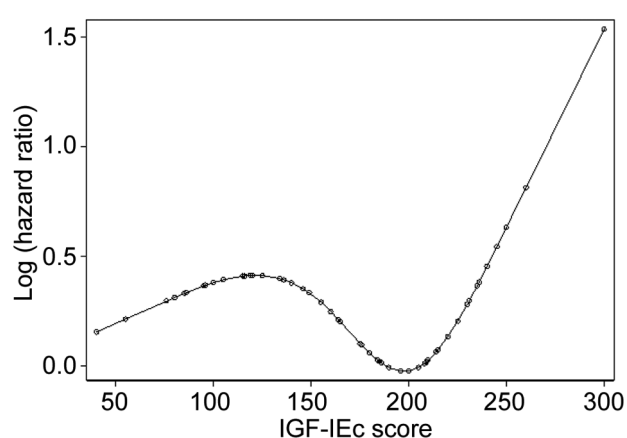


Figure 3. The polynomial shape of the association revealed between score for insulin-like growth factor (IGF)-IEc isoform expression and risk of cancer death in patients with renal cell carcinoma.

expression to be increased in RCC, which in its turn was associated with poorer cancer-specific survival and increased risk of death compared to patients who had tumors with low IGF-IR expression (2, 15).

Interestingly, there has been a growing interest in the investigation of the expression pattern of the IGF-I isoforms in cancer, as well as in other conditions and pathologies (13, 18-20, 25, 33, 57, 58), since a differential regulation of the IGF-I isoforms in such pathologies may indicate a distinct biological role for the different IGF-I precursor polypeptides or their extension peptides (*i.e.* Ea, Eb and Ec). The role of the IGF-I E peptides remains as yet unclear (24), nevertheless initial evidence was provided recently that Ec peptide is differentially regulated during muscle regeneration in humans (40), while synthetic Ec peptide was documented to possess bioactivity (11, 18-20, 44, 59) and its overexpression in PC-3 prostate cancer cells was found to increase their oncogenic potential in mice (46).

Specifically, the mitogenic effect of an E domain-related product of the IGF-IEc isoform in human prostate cancer, breast cancer, endometrial and osteosarcoma cells has been documented in previous studies of our group *in vitro* (18, 33-35, 46). Moreover, a potential role of the IGF-IEc isoform in the pathophysiology of bladder cancer (13), thyroid cancer (38) and neuroendocrine neoplasms (37) has also been shown, *in vivo*. In particular, differential expression of the IGF-IEc isoform was detected in PCa and prostatic intraepithelial neoplasia, as well as in bladder cancer (13, 33), compared to the corresponding normal tissues. In addition, IGF-IEc expression was found to be significantly related to TNM staging and the presence of muscular and capsule

cancerous invasion in thyroid cancer, exhibiting increased levels in more aggressive compared with the non-aggressive types of cancer. Moreover, there was a positive association between the expression level of this IGF-I isoform and the risk of disease recurrence (38). Furthermore, these findings were in line with previous *in vivo* studies showing that IGF-IEc expression was increased in secondary compared to primary foci in neuroendocrine neoplasms (37), and that its expression was positively correlated with prostate cancer stage and Gleason's score (31). Overall, these findings imply a possible gradual increase of IGF-IEc expression during the progress of this disease.

In the present study, we did not find any association between IGF-IEc expression and overall survival of patients with RCC, nevertheless we did demonstrate that its expression is associated with clear cell RCC independently of tumor pathological stage, grade, size, and mitotic index.

Previous studies have reported that IGF-IR overexpression is associated with increased risk of death in patients with clear cell RCC compared to those who had tumors without IGF-IR expression, while the chemosensitivity of clear cell RCC cells was found to increase after silencing of IGF-IR (2, 60). However, the IGF system components have been shown to be differentially expressed among specific tumor types and particularly in clear cell RCC, where IGF-IR expression was found to be expressed in a disproportionately lower percentage of cases compared to the percentage with IGF-I expression (61), while a recent study further confirmed that the expression of IGF-IR is not related to the expression of its ligands, neither in papillary nor in clear cell RCC tumors (54). Moreover, the expression of IGF-I system components was not found to be related to tumor stage, grade, or prognosis of the disease in clear cell RCC (61). Our study, for the first time, revealed a differential regulation of the specific IGF-IEc isoform among different histological types of RCC, while we found no associations of this particular component with the prognosis of the disease, specifically with the overall survival of patients with RCC.

In conclusion, the present study characterized the expression/localization of IGF-IEc isoform in human RCC tissues, showing a significantly lower expression in clear cell RCC *versus* all other RCC histological types. This differential expression of IGF-IEc remained significant after adjusting for other clinicopathological characteristics, such as tumor grade or stage, while it was not found to be associated with the overall survival of those patients. Further studies are needed to investigate the possible tumor type-specific regulation of the IGF-I isoforms in the pathophysiology of RCC, as previously shown in other cancer types.

Conflicts of Interest

The Authors declare no conflicts of interest.

Authors' Contributions

FM contributed to the experimental design, carried out the experiments, analyzed data and reviewed the article; CP analyzed data and reviewed the article; AP analyzed data and wrote the article; AA analyzed data, performed the statistical analysis and reviewed the article; PM analyzed data, contributed to the statistical analysis and reviewed the article; MK conceived and designed the study, analyzed data and reviewed the article. All Authors read and approved the final version of article.

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