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Interleukin-6 and TNF α production in human renal cell carcinoma

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Interleukin-6 and TNF α production in human renal cell carcinoma. Several clinical and biological features suggest that cytokines implicated in the inflammatory response are produced by renal cell carcinoma (RCC). To define if alterations of tumor necrosis factor alpha (TNF α), interleukin 1 alpha (IL-1 α), IL-1 β and IL-6 gene expression are present in this malignancy, samples from 19 tumors as well as samples from seven paired normal renal tissue were examined using Northern blot and immunohistochemical analysis. In addition, the expression of these cytokines was evaluated in seven RCC-derived cell cultures using Northern blot or RT-PCR. TNF α and IL-6 proteins were measured in culture supernatants using specific bio- and immunoassays. Consistent levels of IL-6 mRNA were detected in 17 of the 19 tested tumors whereas $TNF\alpha$ specific transcripts were present in seven of eight available RNA samples. TNF α and IL-6 mRNA were also detected in five of the seven paired normal kidneys. By immunolabeling, IL-6 antigen was not detected in RCC cells in any of the 19 studied samples. In contrast, using anti-TNF α antibody a strong labeling of stromal endothelia and macrophage cells was detected in all the 19 cases, and evident TNF α staining of the carcinoma cells themselves was observed in eight cases. Spontaneous IL-6 mRNA expression was detected in five RCC cell cultures and TNF α mRNA in four. The cultured cells exhibited positive $TNF\alpha$ immunolabeling in six of seven cases but were always IL-6 negative. Bioactive IL-6 was detected in all culture supernatants while bioactive $TNF\alpha$ was not detected. However, immunoreactive TNF α protein was measured in two of three supernatants tested. Altogether these data indicate that RCC cells produce TNF α and IL-6 in vivo and in vitro at the RNA and protein level.

Renal cell carcinomas (RCC) are the most frequent kidney tumors in adults. Recent studies have described cell differentiation in these tumors, suggesting that clear cell type carcinomas differentiate more or less towards the proximal tubule, whereas basophilic cell type carcinomas share similarities with the blastematous tubules [1–6]. It is well known that growing RCC almost always present areas of necrosis and of hemorrhage even when the tumors are of small size, and comprise abundant inflammatory cells in the stroma [7]. Clinically, RCC may be associated with fever, increased acute phase reactant blood proteins in serum and, in some cases, with secondary AA amyloidosis [7]. These features suggest, as has been observed in other human tumors, that RCC may produce increased levels of tumor necrosis factor alpha (TNF α), interleukin-1 and -6 (IL-1 and IL-6) cytokines known to be implicated in the inflammatory response. In this regard it has been reported that IL-6, TNF α , IL-1 α and IL-1 β genes are expressed in normal renal tissue at the RNA level [8]. More recently, IL-6 expression has been observed in RCC and it has been suggested that IL-6 may act as a growth factor in these tumors [9–11].

The aim of the present study was to determine whether the synthesis of these cytokines ($TNF\alpha$, IL-1, IL-6) occurs in RCC and to define the cell type involved in that production. Therefore, we examined the expression of the specific mRNA for each cytokine on one hand and their tissular localization on the other hand, in neoplastic and normal kidney specimens. On the basis of the RCC features observed *in vivo*, we studied in a second step, the production of $TNF\alpha$ and IL-6 by tumor-derived cell cultures using Northern blot and RT-PCR, immunocytochemistry and specific assays.

Methods

Tumor samples

Nineteen renal cell carcinomas obtained from total nephrectomy were examined including 17 cases of clear cell type and two tubulopapillary carcinomas with basophilic cells. Specimens from the tumorous areas were frozen in isopentane precooled by liquid nitrogen. In seven cases a nontumorous area, taken at the opposite pole of the same kidney, was studied using the same procedures.

Tumor derived cell cultures

Cell cultures were obtained from seven tumors [6 clear cell type RCC and one tubulopapillary RCC (case no. 5, Table 1)]. Immediately after surgical removal, a fragment (1 cm³) of the tumoral mass chosen in a non-necrotic area was minced and trypsinized to obtain single cell suspension. These cells were cultured in complete medium consisting of RPMI-1640 medium supplemented with 10% fetal calf serum, 100 U/ml of penicillin, 100 μ I/ml of streptomycin and 2 mM L-glutamine. Initial complete growth medium contained insulin 5 μ g/ml and 10 ng/ml of EGF. The last two additives were removed from the medium after the second passage. The renal epithelial nature of the RCC cultures was confirmed by immunostaining for cytokeratin, vimentin, and CD24 as previously described [6]. Human skin fibroblasts cultured under the same conditions were used as controls.

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Case	Tumoral cell cultures									
	Immunocytochemistry					mRNA		Bioassays U/ml		ELISA TNFa
	CytoK	vim	CD24	IL-6	TNFα	IL-6	TNFα	IL-6	TNFα	pg/ml
1	+	+	+	0	+	0	0	> 1400	0	ND
2	_	ND	+	0	+	+	0	> 620	0	ND
3	+	ND	+	0	+	+	0	> 500	0	ND
4	+	+	+	0	+	0	+	> 1000	0	ND
5	+	+	+	0	+	+ ^a	+ ^a	> 500	0	24
6	+	+	+	0	+	+ ^a	+ ^a	> 500	0	74
7	+	+	+	0	0	+ ^a	$+^{a}$	> 500	0	0
Fibroblasts	0	+	0	0	0				-	-

 Table 1. Immunocytochemical, mRNAs cytokine expression and supernatants bio and immunoassays in 7 RCC derived cell cultures (cases 1-4, 6 and 7 derived from clear cell type RCC and case 5 derived from tubulopapillary RCC)

Abbreviations are: cytoK, cytokeratin; vim, vimentin; ND, not determined.

^a RT-PCR

Isolation of RNA, Northern blot and RT-PCR

Total cellular and tissue RNA were purified by the guanidinium isothyocyanate/cesium chloride method as described by Chirgwin et al [12], followed by precipitation with 3 M sodium acetate and ethanol. Concentration and purity were determined by absorbance at 260 and 280 nm. The integrity of total RNA was evaluated after fractionation of ethidium bromide stained RNA bands on 1% agarose gel electrophoresis containing 2.2 M formaldehyde.

For Northern blot analysis, aliquots (20 μ g) of total cellular RNA were electrophoresed through 1% agarose-formaldehyde gels followed by transfer to nylon membranes (Hybond, Amersham, UK) and hybridization with appropriate probes. The following cDNA fragments were used: the 1.1 kb Pst I fragment of PE4 plasmid containing human TNF α cDNA insert [13], the 1.7 kb IL-1a cDNA obtained from Xho I digested pXM plasmid, the 1.3 kb IL-1 β insert obtained by Pst I digestion of pSP64 vector, the 1.2 kb IL-6 fragment obtained by EcoRI digestion of pM2T vector, and the chicken β -actin cDNA purified from PA1 plasmid [14]. All probes were labeled with ³²P dCTP using the multiprime DNA labeling system (Amersham, UK) as described by Feinberg and Vogeslstein [15]. The membranes were prehybridized at 42°C for 12 hours in buffer consisting of 50% formamide, $5 \times$ standard saline citrate (SSC) (0.15 M NaCl; 0.015 M Na3 citrate = $1 \times SSC$), 0.1% SDS, $5 \times Denhardt's$ solution and 200 μ g/ml salmon sperm DNA. The filters were then incubated for an additional 16 hours in the same buffer with 2×10^6 cmp/ml of labeled probe. After hybridization, the blots were washed twice in 0.1% SDS, $2 \times$ SSC for 60 minutes at room temperature, and then washed two more times with 0.1% SDS, $0.1 \times$ SSC at 55°C. The blots were then dried and exposed to X-ray films for 12 to 24 hours with an intensifying screen at -80°C.

Reverse transcription of 1 μ g of total cellular RNA was performed using superscript reverse transcriptase and random primers according to the manufacturer's instructions (Gibco-BRL, Bethesda, Maryland, USA). The obtained cDNA was processed for PCR using TNF α and IL-6 specific primers purchased from Stratagene (La Jolla, California, USA) at a final concentration of 1 μ M. PCR reaction was achieved in a final volume of 100 μ l (1 cycle at 94°C for 5 min and 5 min at 60°C), followed by 30 cycles of 1.5 minutes at 72°C, 45 seconds at 94°C and 45 seconds at 60°C, with a final extension of 10 minutes at 72°C.

In order to assess specificity of the hybridization signal, RNAs extracted from phorbol ester stimulated hematopoietic DEL cell line, expressing TNF α , IL-1 α , IL-1 β and IL-6 were used as positive control.

Immunohistochemistry

Cryostat sections (2 μ) were fixed in methanol for 10 minutes and processed using an indirect immunoperoxidase technique as described previously [6]. Cell cultures for immunolabeling were plated in microwell chamber slides (LabTek chambers, NUNC Inc., Illinois, USA) at a density of 1×10^4 cells/ml. Growing cells were arrested at 80 to 90% confluence, washed in PBS, and after fixation in cold methanol (10 min) used for immunocytochemical staining.

The following primary antibodies (ab) were used: monoclonal anti-CD14 (macrophages) from Becton-Dickinson; monoclonal anti-CD35 (CR1), monoclonal anti-CD57 specific for natural killer (NK) cells and monoclonal anti-endothelial F-VIII antigen from Immunotech (Luminy, France). Rabbit polyclonal abs anti-human TNF α (IP-310), anti-human IL-1 (EP-200) and anti-human IL-6 (LP-716) were purchased from Genzyme (Cambridge, Massachusetts, USA). EP-200 ab consisted of anti-IL-1 α and anti-IL-1 β in approximately a 1:3 mixture. Anti-TNF α ab was used at a dilution of 1/160° and anti-IL-1 and anti-IL-6 at a dilution of 1/20°.

Monoclonal abs were revealed using rabbit anti-mouse and goat anti-rabbit IgG peroxydase conjugated antibodies (Dako, Denmark). For polyclonal ab we used goat anti-rabbit peroxydase conjugated IgG (Dako). Sections incubated with PBS or with normal rabbit IgG and second ab were used in each case as negative controls.

IL-6 and TNFa assays

IL-6 bioactivity of RCC culture supernatants was measured using the IL-6 dependent murine hybridoma cell line B9 [16, 17]. Proliferation of the B9 cells was determined by the MTT colorimetric assay as described by Mosmann [18]. The specificity of the B9 response to IL-6 was tested with a polyclonal

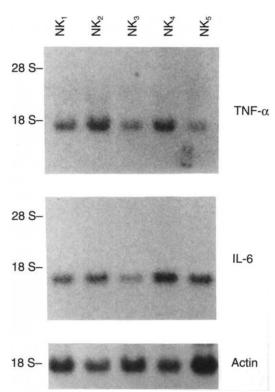


Fig. 1. Expression of $TNF\alpha$ and IL-6 mRNA in 5 normal kidneys (NK). Total cellular RNA (20 μ g) extracted from primary tissue was fractionated on 1% agarose/formaldehyde gels, transferred to nylon membrane and hybridized to 32P-labeled $TNF\alpha$ and IL-6 cDNA probes. The same membrane was rehybridized with β -actin cDNA.

anti-human IL-6 antibody. In the neuralization experiments, supernatants collected five days after passage were incubated during four hours at 37°C with a concentration of 2 μ g/ml of the anti-IL-6 ab or murine unrelated immunoglobulin antibody as control. In these conditions we found that this antibody abrogated the biological activity mediated by more then 100 pg/ml of rHu IL-6.

TNF α was evaluated in culture supernatants using bio- and immunoassays. The biological activity of TNF α was determined on actinomycin D-treated murine L929 cells as described [19]. Immunoreactive TNF α protein was measured using specific ELISA kit with detection limit at 15 pg/ml (Medgenics, Fleurus, Belgium).

Results

Cytokine gene expression

Nondegraded RNA material was obtained from five of the seven normal kidney fragments. After hybridization with specific probes, transcripts corresponding to IL-6 and TNF α were detected in all five cases (Fig. 1). In contrast, lower levels of IL-1 β mRNAs were detected in three of five while IL-1 α transcripts were not observed (data not shown).

To evaluate the presence of IL-6 mRNA in tumors, total RNAs extracted from nineteen RCC samples were hybridized with IL-6 specific probe. Specific transcript of 1.6 kb was detected in 17 of 19 samples, including 16 of clear cell type and one of basophilic cell type tumors. Eight available RNAs

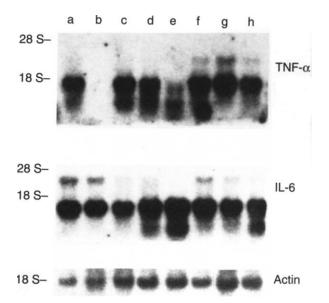


Fig. 2. Northern blot analysis of $TNF\alpha$ and IL-6 mRNA content from 8 primary RCC. The membrane was hybridized with IL-6, $TNF\alpha$ and β -actin probes. No $TNF\alpha$ transcripts were detected in lane b and there was a weak signal in lane e. Supplementary bands of lower molecular weight are due to nonspecific hybridization signals.

samples were further hybridized with $TNF\alpha$ cDNA fragment and a corresponding transcript of 1.7 kb was detected in seven of them (Fig. 2). All these samples were obtained from clear cell type carcinomas.

A low level of IL-1 β mRNA transcripts were detected in the seven tested tumors whereas IL-1 α mRNA was not detected (data not shown).

To further investigate if IL-6 and TNF α were expressed in tumor cultured cells, Northern blots or RT-PCR were performed on total cellular RNA extracted from seven RCC derived cell cultures. As shown in Table 1, IL-6 mRNAs were detected in five cases and TNF α mRNAs in four cases. It is of note that all the three cases tested by RT-PCR expressed consistent levels of IL-6 and TNF α specific mRNAs (Fig. 3). Alcaline Southern transfer and probing with ³²P-end-labeled oligonucleotides identified the fragments as TNF α (355 pb) and IL-6 (628 pb), respectively.

Immunohistochemistry

Normal kidney areas. Light microscopy examination did not reveal any inflammatory or tumoral changes in these sections. A low number of CD 14 positive interstitial macrophages was present (less than 1 cell per microscopic field at ×40 magnification). CR1 antigen was detected at the membrane of glomerular podocytes and on sparse interstitial cells. NK cells were not detected. A faint staining was obtained with anti-IL-1 ab on the arteriolar endothelial cells. Vascular myocytes and glomerular mesangial cell were positively stained. Anti-TNF α ab stained arteriolar endothelia and smooth muscle cells, as well as glomerular mesangial cells. Endothelial cells from peritubular capillaries and tubular epithelial cells were negative. Anti-IL-6 ab stained smooth muscle cells in arterioles and glomerular mesangial cells. Questionable staining was noted on some glomerular parietal epithelial cells.

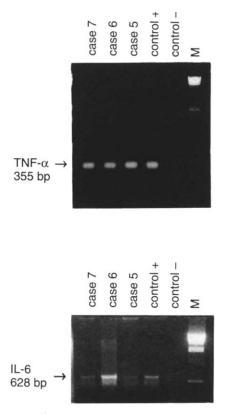


Fig. 3. Detection of $TNF\alpha$ and IL-6 mRNAs in three RCC-derived cell cultures (cases 5, 6 and 7) by RT-PCR. Total RNA (1 µg) was extracted and reverse-transcribed using random primers. The expected sizes of PCR products for $TNF\alpha$ and IL-6 were 355 and 628 bp, respectively.

Tumors. Variable numbers of CD14 immunoreactive macrophages were detected in the stroma in all the 19 tumors; in 11 cases they were numerous (1 macrophage/5 to 10 tumoral cells). Some NK cells (less than 6 cells per field at \times 40) were present in eight cases. Anti-F VIII antibody staining showed a rich capillary network between the tumoral clumps in all cases (Fig. 4).

Negative staining using anti-IL-1 ab was observed in 12 out of 19 cases. In the other seven cases some faint fixation was observed on the endothelium of stromal blood capillaries; in three of these cases some CD14 immunoreactive interstitial cells were also IL-1 positive. IL-6 immunoreactivity was totally negative in all cases except for the vascular myocytes. In contrast, consistent staining was observed with anti-TNF α ab. In all cases the endothelium of the stromal capillaries was strongly labeled as well as some macrophages or other interstitial cells (Fig. 4). In addition, staining of the tumoral cells themselves was clearly observed in eight cases (2 basophilic cell types and 6 clear cell types) predominantly localized at the basal pole of the cells (Fig. 5). In the 11 remaining cases the topography of anti-TNF α ab staining was difficult to define since it delineated a branching network between the tumoral clumps. In all the 19 cases we noted that the staining exhibited with anti-TNF α ab was more diffuse compared to the specific labeling of macrophages and vessels (Fig. 4c).

RCC cultures. The results of the immunochemical analysis summarized in Table 1 show that in all cases the majority of the

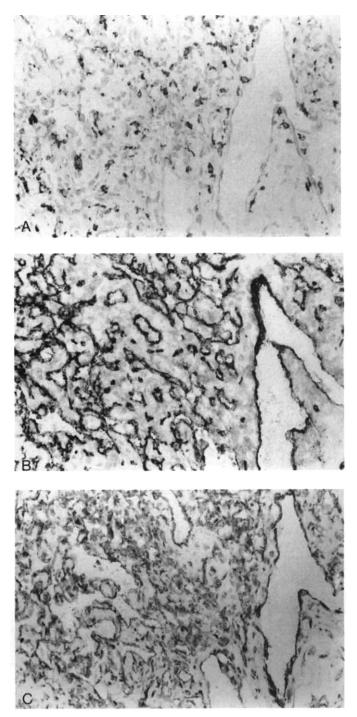


Fig. 4. Frozen sections of RCC immunostained for CD14, FVIII and $TNF\alpha$ antibodies. Immunoreactivity was examined on serial sections from the same area. A. CD14 immunoreactivity (original magnification $\times 250$). Note specific labeling of numerous macrophages present in the supportive stroma. B. FVIII immunoreactivity (original magnification $\times 250$). Staining pattern delineating the rich capillary network. C. TNF α immunoreactivity (original magnification $\times 250$). Evidence for positive staining of vessels, macrophages and tumor cells.

cells were CD24 positive. Cytokeratine immunoreactivity was observed in six of the seven cell cultures (Fig. 6). IL-6 was not detected, whereas in six cases the cells stained with anti-TNF α

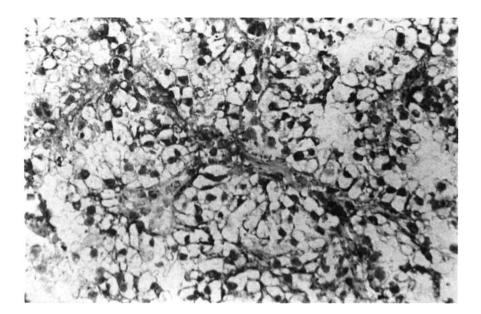


Fig. 5. TNF α immunoreactivity in clear cell type carcinoma (original magnification ×400). Note the labeling of the tumor cell membrane.

ab (Fig. 6). The cultured skin fibroblasts were vimentin positive and were not stained with anti-IL-6 or anti-TNF α ab.

Levels of IL-6 and TNF α in culture supernatants

The seven culture supernatants collected at the second or third passage were monitored for the production of IL-6. The concentrations ranged from 500 to more than 1400 U/ml as detected by the B9 bioassay (Table 1). To ascertain that supernatant-induced B9 cell proliferation was due to IL-6, samples with IL-6 activity were tested in the presence of anti-IL-6 polyclonal antibody. Preincubation of the seven culture supernatants with this anti-IL-6 ab significantly reduced (77 to 85% of inhibition) the proliferation of the B9 cells, giving evidence that the activity detected in supernatants was attributable to IL-6.

Determination of secreted $\text{TNF}\alpha$ in culture supernatants by biological activity or immunoreactivity is shown in Table 1. Measurable $\text{TNF}\alpha$ cytotoxic activity could not be detected in any of the supernatants tested. However, significant levels of immunoreactive $\text{TNF}\alpha$ protein was measured in two of three unconcentrated supernatants (Table 1). Remarkably, $\text{TNF}\alpha$ protein was not detected by ELISA and immunocytochemistry in case 7.

Discussion

The present study demonstrates that the normal human kidney constitutively expresses significant levels of $\text{TNF}\alpha$ and IL-6 mRNA. Lower amounts of IL-1 β specific mRNA were also detectable. Immunoreactive IL-6, $\text{TNF}\alpha$ and IL-1 β were observed in the renal parenchyma mainly in the arteriole walls and in the glomerular mesangial cells, but not in the tubular cells. These findings are in agreement with those previously reported concerning IL-6, $\text{TNF}\alpha$ and IL-1 β expression in normal kidney tissue at the RNA [8, 20] or protein level [21]. In addition, it has recently been shown that normal renal tubular epithelial cells *in vitro* spontaneously express IL-6 mRNA but neither IL-1 nor TNF α transcripts [22].

In RCC, we observed significant levels of $TNF\alpha$ and IL-6

RNA transcripts compared to the paired normal tissue, whereas similar low levels of IL-1 β specific transcripts were present in both normal and tumoral tissue.

Although consistent levels of IL-6 RNA were observed in the tumors, immunoreactive IL-6 was not detected in the RCC *in vivo*, except in the normal arterial walls included in the tumor. Likewise, cultured RCC cells were not stained with anti-IL-6 ab, in spite of the presence of IL-6 mRNA and of the measurable amounts of bioactive IL-6 protein in the culture supernatants. These data suggest that RCC cells produce IL-6 protein both *in vivo* and *in vitro*, which is not stored in the producing cells.

Constitutive production of IL-6 has been found in various human tumors, including adenocarcinomas, soft tissue tumors and lymphomas [23], as well as in epidermoid, ovarian and bladder carcinoma cell lines [17, 24, 25]. In studies using cell cultures derived from human RCC, it was found that tumoral cells produce significant amounts of bioactive IL-6 protein in vitro [9, 10, 26, 27], which is in agreement with our results. However, these authors reported that variable percentages of the tumoral cells either in vivo [26] or in vitro [9, 11] were IL-6 immunoreactive, which is in disagreement with our observations. This discrepancy could be due to the different origins or specificities of the anti-IL-6 antibodies. Whatever the reasons for these discordant immunohistochemical results, it can be concluded that RCC cells produce IL-6 in vivo. In this regard, the increased levels of serum acute phase reactant proteins frequently observed in patients with RCC [7] could be related to the IL-6 production by the neoplastic cells.

Concerning TNF α expression, our results indicate that the consistent levels of TNF α mRNA detected in RCC are, at least in part, related to the supportive stroma. Indeed, we observed that infiltrating macrophages and the vascular network of the supportive stroma were clearly stained by the anti-TNF α ab. Similarly, TNF α mRNA synthesis has been evidenced by *in situ* hybridization in activated macrophages present in colorectal cancer stroma but not in the neoplastic cells [28]. The strong

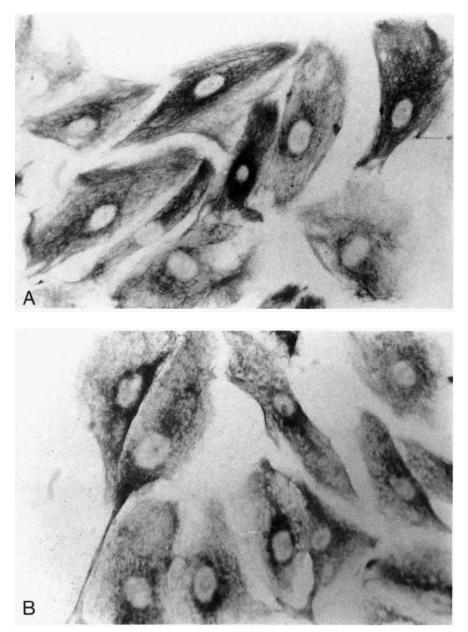


Fig. 6. Cytokeratin and $TNF\alpha$ immunostaining of RCC cultures cells (Table 1, case 1) (original magnification ×400). A. Anticytokeratin immunoreactivity: evidence of filamentous cytoplasmic staining. B. $TNF\alpha$ immunoreactivity showing fine granular pattern.

TNF α immunostaining of the stromal capillary vessels observed in RCC is intriguing, since it was not observed in the nontumoral areas of the corresponding kidney. Moreover, using the same antibody and the same technical procedure, TNF α staining of the renal blood capillaries was not observed in inflammatory conditions, such as renal transplant acute rejection crisis or glomerulonephritis, while it was detected in tubular cells (unpublished observations). Therefore, TNF α immunostaining of capillary endothelial cells appears as particular feature of the RCC supportive stroma and could be related to the intense neoangiogenesis present in these tumors. In this respect, it has been reported that TNF α [29, 30] is a potent activator of endothelial cells *in vitro* and plays a major role in angiogenesis *in vivo* [31].

In addition to the observation that $TNF\alpha$ is produced by the

supportive stroma our results argue for tumoral cell production of this cytokine. Indeed, in tumors, TNF α positive RCC cells were clearly detected in 40% of the studied cases. Furthermore, TNF α producing cells were directly identified by immunostaining utilizing anti-TNF α ab in six of seven RCC derived cultures, whereas specific TNF α transcripts were detected in four cases. This discrepancy between the TNF α mRNA levels and the presence of TNF α antigen in the cells might be related to the transcriptional and post-transcriptional regulation of this molecule [32]. It is of note that in our material the TNF α production was evidenced in clear cell type tumors as well as in tubulopapillary tumors with basophilic cells.

Within the limits of the L929 assay, TNF α biological activity was not detected in RCC culture supernatants while immunoreactive TNF α could be measured in two cases. These data suggest that either RCC cells in vitro synthesize inactive $TNF\alpha$ or that the released active protein is rapidly inactivated or degraded. It has recently been reported that normal renal tubular epithelial cells, when stimulated by LPS, are able to express TNF α transcripts [33, 34], whereas the levels of bioactive TNF α measured in supernatants remained remarkably low, suggesting that the cells express cell membrane associated and secreted TNF α molecule [34]. Expression of TNF α mRNA has also been documented in several long-term cultured epithelial tumor cell lines, especially in those resistant to $TNF\alpha$ induced cytotoxicity [35, 36]. Interestingly, it was observed that the cell lines resistant to $TNF\alpha$ did not produce detectable amounts of TNF α protein in vitro as evaluated by the L929 assay. However, after protein labeling and immunoprecipitation, TNF product was detectable in supernatants and cell lysates from ovarian carcinoma cells [37]. One hypothesis to explain all these data would be that the TNF α molecule produced by the cultured cells is complexed to its soluble receptors, and thus has lost its biological activity [38]. Whether the $TNF\alpha$ protein produced by the RCC cells in vivo is bioactive or not remains unsolved. However, in addition to the frequency of tumor necrosis, several facts such as the modulation of the expression of HLA class I antigen [6], EGF-receptor [39] or ICAM-1 and VCAM adhesion molecules (unpublished observations) by the tumor cells, could be related to the presence of bioactive $TNF\alpha$ molecule.

In conclusion, we emphasize the $TNF\alpha$ and IL-6 cytokine gene expression by RCC cells themselves as well as by the supportive stroma. These findings may explain some of the histopathological and clinical features observed in patients with this malignancy, and highlight their involvement in RCC growth and spread.

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