

Altered expression of transforming growth factor- β s in chronic renal rejection

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Altered expression of transforming growth factor- β s in chronic renal rejection. We examined the altered expression of transforming growth factor- β s in chronic renal rejection in humans, including transforming growth factor beta-1 (TGF- β 1), TGF- β 2, TGF- β 3 and their receptors, transforming growth factor beta receptor type I (T β R-I) and T β R-II. Using Northern blot analysis and immunohistochemistry, 10 specimens of chronically rejected and 8 normal kidney samples were analyzed. By Northern blot analysis the expression of mRNA encoding TGF- β 1, TGF- β 2, TGF- β 3 ($P < 0.02$), T β R-I and T β R-II ($P < 0.02$) was decreased in chronically rejected renal cortex samples, compared to normal controls. Immunohistochemical analysis of the normal renal cortex showed strong immunostaining for TGF- β 1 and TGF- β 3, and mild immunostaining for TGF- β 2 in the proximal and distal tubulointerstitium, but no signal for any of the TGF- β isoforms in the glomeruli or in the cortical vessels. In sharp contrast, the glomeruli and the cortical vessels of the rejected kidney specimens exhibited strong immunostaining for TGF- β 1 and TGF- β 3, whereas the tubules revealed a decrease in immunoreactivity. T β RI and T β RII immunostaining showed similar changes as observed with TGF- β 1 and TGF- β 3 antibodies. There was a concomitant increase in B-cell accumulation in the glomeruli, while T-cells and macrophages were diffusely abundant in the rejected samples. Since TGF- β s are potent inducers of extracellular matrix proteins and have been shown to be involved in fibrotic disease, the increase in TGF- β 1 and TGF- β 3 immunoreactivity in the glomeruli suggests that there is a redistribution in TGF- β expression in chronic renal allograft rejection. Together with changes affected by B-cell mediated immunity, the above alterations might contribute to the histopathological changes that occur in this disorder, such as intimal fibrosis, arteriosclerosis and glomerular and tubular sclerosis.

Chronic rejection is the most common cause of graft loss in renal transplantation. Despite this fact, research has mainly focused on the prevention of acute rejection with the development of powerful immunosuppressants. To date, no effective treatment has been developed for the irreversible damage associated with chronic rejection. The most characteristic histopathological features of chronic rejection in renal allografts are intimal fibrosis mainly in the cortical arteries, glomerular ischemic simplification, interstitial fibrosis and tubular atrophy.

T cell mediated immunity plays a critical role in allograft rejection [1]. A variety of interactions have been implicated in the rejection process, including cytokines such as IL-1, IL-2, transforming growth factor beta-1 (TGF- β 1), TGF- β 2 and TGF- β 3 [2, 3]. The initial targets of rejection appear to be the graft endothelial structures. Interstitial mononuclear cells (lymphocytes, macrophages, plasma cells, eosinophil cells) infiltrate the rejected graft and serve as histological indicators of chronic cell-mediated rejection.

TGF- β 1, TGF- β 2 and TGF- β 3 belong to a superfamily of multifunctional homologous polypeptide growth factors, which act through pleiotropic effects in various cell types [4, 5]. They play a major role in the regulation of extracellular matrix formation and fibrosis, arteriosclerosis and angiogenesis, immunosuppression, carcinogenesis, inflammation, tissue repair and also in normal differentiation and growth [6–12]. TGF- β 1, TGF- β 2 and TGF- β 3 are the mammalian isoforms of TGF- β . In addition cDNA clones have also been isolated for TGF- β 4 from chicken [13], and TGF- β 5 from frog [14], but these proteins have not been identified in mammalian cells.

TGF- β s bind to specific cell surface binding proteins with high affinity in many different cell types. Two receptors involved in signal transduction have been identified, a 53 kDa (type I TGF- β receptor, T β R-I), and a 70 kDa (type II TGF- β receptor, T β R-II), the cytoplasmic domains have serine threonine kinase activity [15, 16]. In addition, a 200 to 400 kDa (type III TGF- β receptor, T β R-III) non-signaling proteoglycan has been described [15–21]. This receptor, also called betaglycan, is required for the presentation of TGF- β s to the T β R-I/T β R-II complex [16, 19–21]. Studies using deletion mutants have indicated that T β R-I and T β R-II co-operate to initiate a signal [15, 16]. T β R-II binds the ligands and sequesters T β R-I into a complex for signaling [16].

Recent studies indicate that the induction of growth factors may play a pathobiological role in experimental acute and chronic rejection [22–33]. TGF- β 1 has been implicated as a critical regulatory molecule in the cause of renal fibrosis and arteriosclerosis [12, 34]. However, it is not known whether other TGF- β isoforms and their receptors contribute to the perturbations that occur in the renal rejection. Therefore, in the present study, we investigated the expression of all three mammalian TGF- β isoforms (TGF- β 1, TGF- β 2, TGF- β 3) and their signaling receptors

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Table 1. Monoclonal and polyclonal antibodies used in immunohistochemistry on paraffin-embedded material

Cluster	Antibody	Source	Lymphohistiocytic specificity
CD 45	LCA ^a	DAKO	Common lymphocyte marker
CD 20	L 26 ^a	DAKO	B cells, follicular dendritic cells
CD 3	CD 3	DAKO	T cells
Ø	MAC 387 ^a	DAKO	Macrophages, histiocytic cells

^a Monoclonal antibodies DAKO, Dakopatts, Copenhagen, Denmark

(T β R-I, T β R-II) in human chronic renal allograft rejection by Northern blot analysis and immunohistochemical staining.

Methods

Patients

Kidney samples of 10 patients (6 female, 4 male; median age 52.7 years; range 45 to 63 years) with chronic renal rejection, established according to clinical records and histopathological analysis, were analyzed. Before these samples were used in our analysis the clinical diagnosis was verified by histopathological examination by two independent pathologists. Immediately after surgical removal of the kidney, the cortex was separated from the medulla in the operating room and a larger representative area of the separated cortex was cut approximately in half and used for both histological fixation and molecular analysis in order to ensure comparison. Tissues destined for histological analysis were fixed in Bouin solution for 12 to 24 hours, then dehydrated through graded alcohol and subsequently embedded in paraffin. For RNA extraction the tissues were snap frozen in liquid nitrogen immediately upon surgical removal, and maintained at -80°C until use. The median range of time between the transplantation and the episode of chronic kidney rejection was 51 months (range 5 months to 9 years). Patients were all nondiabetic adults. From the rejected group one patient was free of immunosuppressive drugs prior to renal explantation, three patients were administered prednisolone and salicylic acid and three patients had a combination of prednisolone and salicylic acid with immunosuppressive agents such as azathioprine and cyclosporine. Normal renal tissues were obtained from six patients undergoing surgery because of renal cell carcinoma and from two previously healthy individual through an organ donor program (4 female, 4 male; median age 54.75 years; range 28 to 80 years). The expression of TGF- β 1, TGF- β 2, TGF- β 3, T β R-I and T β R-II was assessed by Northern blot analysis and immunostaining in all specimens.

Immunohistochemical staining

Paraffin-embedded sections (2 to 4 μ m thick) were immunostained for TGF- β 1, TGF- β 2, TGF- β 3, T β R-I, T β R-II and for lymphocyte and macrophage cell markers (Table 1) using the streptavidin-peroxidase/biotin technique (Kirkegaard & Perry Laboratories, Inc., Gaithersburg, MD, USA). Tissue sections were submerged for 15 minutes in TBS buffer (10 mM Tris-HCl, 0.85% NaCl, pH 7.4) containing 0.1% (vol/vol) Triton X-100 and washed for five minutes in TBS solution, as previously reported [35, 36]. Endogenous peroxidase activity was quenched by incubating the

slides in methanol and in methanol/0.6% hydrogen peroxide, followed by washing in methanol and TBS/0.1% BSA [35, 36]. Following treatment with hyaluronidase (1 mg/ml in 100 mM sodium acetate, 0.85% NaCl), the sections were blocked for 30 minutes at 37°C with 10% normal goat serum prior to overnight incubation at 4°C with isoform specific polyclonal TGF- β 1, TGF- β 2 and TGF- β 3 antibodies (2.5 μ g/ml) diluted in TBS containing 5% normal goat serum and 0.1% BSA [35, 36]. Bound antibody was detected with a biotinylated goat anti-rabbit IgG secondary antibody and streptavidin-peroxidase complex (Kirkegaard & Perry Laboratories), followed by incubation with diaminobenzidine tetrahydrochloride (0.05%) as the substrate and counterstained with Mayer's hematoxylin.

To ensure antibody specificity, control slides were either incubated in the absence of primary antibody or with an irrelevant IgG antibody. In both cases no immunostaining was detected. The isoform specific antibodies to mature TGF- β 1, TGF- β 2 and TGF- β 3 were produced in the laboratory of Leslie Gold, and their preparation and characterization are described in detail by Pelton et al [36]. Briefly, the antibodies were raised in rabbits to synthetic peptides corresponding to amino acid residues 4-19 of TGF- β 1 and TGF- β 2 and 8-29 of TGF- β 3. Each antiserum was purified by ammonium sulfate precipitation followed by peptide affinity chromatography using the respective peptide immunogen. The antisera were shown to be isoform-specific by Western blot analysis using mature recombinant TGF- β 1 and TGF- β 3 and porcine native TGF- β 2, as illustrated [36]. No cross-reactivity among the antisera was observed. All tissue sections that were compared were treated at the same time using identical incubation times and dilutions of all reagents including the antisera. Antibody activity was previously shown to be absorbed with 33 Molar excess of each peptide used as immunogen [36, 37]. Each antiserum absorbed with peptide showed no immunoreactivity, proving antibody specificity. Antibodies against T β R-I and T β R-II were obtained from Santa Cruz Laboratories, California. Denaturation of the tissue by fixation in formalin exposes the epitopes so that immunoreactivity is enhanced. We have observed that frozen sections require ten times more antisera to achieve similar intensity of immunostaining (unpublished observation). This is consistent with the fact that ten times more antisera was required if native TGF- β was not reduced prior to SDS-PAGE in Western blot analysis (unpublished observation).

Both monoclonal and polyclonal antibodies to lymphocyte (CD 45) and macrophage cell markers were used as primary antibodies as detailed in Table 1. The individual antisera of T-cells (CD 3), B-cells (CD 20) and macrophages (MAC 387) showed no cross-reactivity. No immunostaining was detected when the slides were processed either in the absence of the primary antibody or in the presence of affinity purified non-immune rabbit or mouse anti-IgG.

Grading of the immunohistochemical staining was defined on the basis of the percentage of morphological changes occurring over an area of the cortex, and was quantified according to the number of positively stained cells: Ø, no staining; (+) < 10%; + 10 to 30%; ++ 30 to 50%; +++ > 50%.

Probe synthesis

The TGF- β 1 cDNA probe consisted of a 280 bp EcoRI/XbaI fragment of human TGF- β 1 cDNA [38, 39]. The TGF- β 2 cRNA probe consisted of a 600 bp HindIII/PstI fragment of human TGF- β 2 cDNA [38], corresponding to nucleotides 253 to 853 [38,

39]. The TGF- β 3 cRNA consisted of a 125 bp *XbaI/BglII* fragment of human TGF- β 3 cDNA [38], corresponding to nucleotides 917-1042 [38, 39]. T β R-I and T β R-II cRNA probes were generated from a 377 bp and a 476 bp *BamHI* fragment of human T β R-I and T β R-II cDNA [10]. The 7S cDNA probe consisted of a 190 bp fragment of the mouse 7S cytoplasmic cDNA which cross hybridizes with human 7S RNA [9, 10, 40]. The antisense cRNA probes used for Northern blot analysis were radiolabeled with [α - 32 P] CTP (Du Pont, Boston, MA, USA). All the membranes were also hybridized with 7S in order to assess equivalent RNA loading [40-42]. [α - 32 P] dCTP (Du Pont) was incorporated into TGF- β 1 and 7S cDNA probes using a random primer labeling system (Boehringer-Mannheim, Germany) [43].

Northern blot analysis

Total RNA was extracted by the guanidine isothiocyanate method [44], size-fractionated on 1.2% agarose/1.8 M formaldehyde gels, and stained with ethidium bromide for verification of RNA integrity and loading equivalency [40, 45]. The RNA was electro-transferred onto Nylon membranes (GeneScreen; Du Pont) and cross-linked by UV irradiation [40, 45]. The blots were then prehybridized, hybridized and washed under conditions appropriate for antisense cRNA riboprobes (TGF- β 2, TGF- β 3, T β R-I, T β R-II) or cDNA probes (TGF- β 1, 7S), as previously described [9, 10, 35].

For the antisense riboprobes the blots were prehybridized overnight at 65°C in 50% formamide, 0.5% sodium dodecyl sulfate (SDS), 5 \times SSC, 5 \times Denhardt's solution (1 \times Denhardt's = 0.02% ficoll, 0.02% polyvinylpyrrolidone, and 0.02% bovine serum albumin), 250 μ g/ml salmon sperm DNA, and 50 mM Na₂PO₄, pH 6.5. The blots were then hybridized for 18 hours at 65°C in the presence of 1 \times 10⁶ cpm/ml of the labeled antisense riboprobe, washed twice at 65°C in a solution containing 1 \times SSPE (150 mM NaCl, 10 mM NaH₂PO₄, and 1 mM EDTA) and 0.5% SDS, and twice at 65°C in a solution containing 0.1 \times SSPE and 0.5% SDS [40, 45].

For TGF- β 1 and 7S cDNA probes the blots were prehybridized overnight at 42°C in a prehybridization buffer that contained 50% formamide, 1% SDS, 0.75 M NaCl, 5 mM EDTA, 5 \times Denhardt's solution, 100 μ g/ml salmon sperm DNA, 10% Dextran sulfate and 50 mM Na₂PO₄, pH 7.4. The hybridization was carried out at 42°C for 18 hours with the labeled cDNA probe (1 \times 10⁶ cpm/ml), washed twice (23°C) in 2 \times SSC and three times at 55°C in 0.2 \times SSC and 2% SDS [40, 45].

Blots were then exposed at -80°C to Fuji X-ray film using intensifying screens, and the intensity of the radiographic bands was quantified by video densitometry (Biorad 620, USA), as previously reported [40].

Statistical analysis

Results were expressed as mean or as median and range. For statistical analysis the Wilcoxon-test was used [46]. Significance was defined as $P < 0.05$.

Results

Chronically rejected kidney shows increased and redistributed immunoreactivity for TGF- β isoforms compared to normals

TGF- β isoforms are secreted as latent molecules consisting of a precursor, termed latent associated peptide (LAP), covalently

complexed to the mature potentially bioactive dimer (ie pro-TGF- β). Only the active mature dimer can bind to TGF- β receptors. Therefore, any antibodies produced to the mature amino acid sequences of TGF- β isoforms will presumably detect the mature molecules both, complexed to the LAP portion and separated from the complex in its activated form (unless the epitopes on the mature portion are masked by the LAP peptide). For this reason, the antibodies will not be able to distinguish between the latent and active molecules. Thus, the antisera detect potentially active or activated TGF- β isoforms (that may or may not bind to TGF- β receptors).

Figure 1 shows the differences among the immunostaining patterns obtained of TGF- β 1, TGF- β 2 and TGF- β 3 in normal (A, C, E) and rejected (B, D, F) renal samples. Figure 2 shows a higher magnification to emphasize the major structures of immunohistochemical localization of TGF- β 1 in the rejected cortex. Tables 3 and 4 summarize the pathological changes detected in the rejected and the normal group. Grading was defined on the basis of the percentage of morphological changes occurring over an area of the cortex, and was quantified according to the number of positively stained cells: \emptyset , no staining; (+) < 10%; + 10 to 30%; ++ 30 to 50%; +++ > 50%.

Normal kidney samples exhibited intense immunoreactivity for both TGF- β 1 (Fig. 1A) and TGF- β 3 (Fig. 1E) in the proximal and distal tubules in the renal cortex, whereas the interstitial space was devoid of immunoreactivity. Only a few glomeruli showed mild TGF- β 1 immunostaining around the epithelial layer of the Bowman's capsule (Fig. 2 A, B). The endothelium and the mesangium of the normal glomeruli, as well as the large vessels and peritubular capillaries did not exhibit TGF- β 1 immunoreactivity (Fig. 1A; Fig. 2 A, B). TGF- β 2 immunoreactivity was slight in most of the normal tissues (Fig. 1C).

Rejected kidney samples exhibited a decrease in the intensity of TGF- β 1 (Figs. 1B and Fig. 2 C, D) and TGF- β 3 (Fig. 1F) immunoreactivity in the tubules by comparison with the normal specimens (Fig. 2 A, B, and Table 4). A minimal number of the tubules were positively stained, most notably the proximal ones. In contrast, immunoreactivity in the glomeruli for TGF- β 1 (Fig. 1-B; Fig. 2-C,D) and TGF- β 3 (Fig. 1-F) was markedly increased in the epithelial and intraglomerular cells in the chronically rejected kidneys. The peritubular capillaries and the characteristically thickened intimal layer of the cortical vessels in the rejected kidney were also positively immunostained for TGF- β 1, TGF- β 2 and for TGF- β 3 in contrast to the normal tissues (Fig. 1 B, D, F). Moreover, strong immunoreactivity for TGF- β 1 and TGF- β 3 was detected among the infiltrating lymphocytes, macrophages and other inflammatory cells of the grafted kidney (Table 3). TGF- β 2 immunostaining in the rejected kidney showed less differentiated changes compared to normal samples. The intensity of immunostaining was mild and more intense staining was only detected in 2 out of the 10 rejected specimens. As shown in Figure 3, T β RI and T β RII immunoreactivity exhibited the same pattern of distribution as TGF- β 1 and TGF- β 3 in the rejected renal tissue.

Figure 4 illustrates the immunostaining of the various immunocells infiltrating the graft. Chronically rejected samples were characterized by a strong infiltration of T-lymphocytes (CD 3) and macrophages (MAC 387) localized diffusely throughout the whole tissue (Fig. 4 C, E). In contrast, B-lymphocytes (CD 20) were

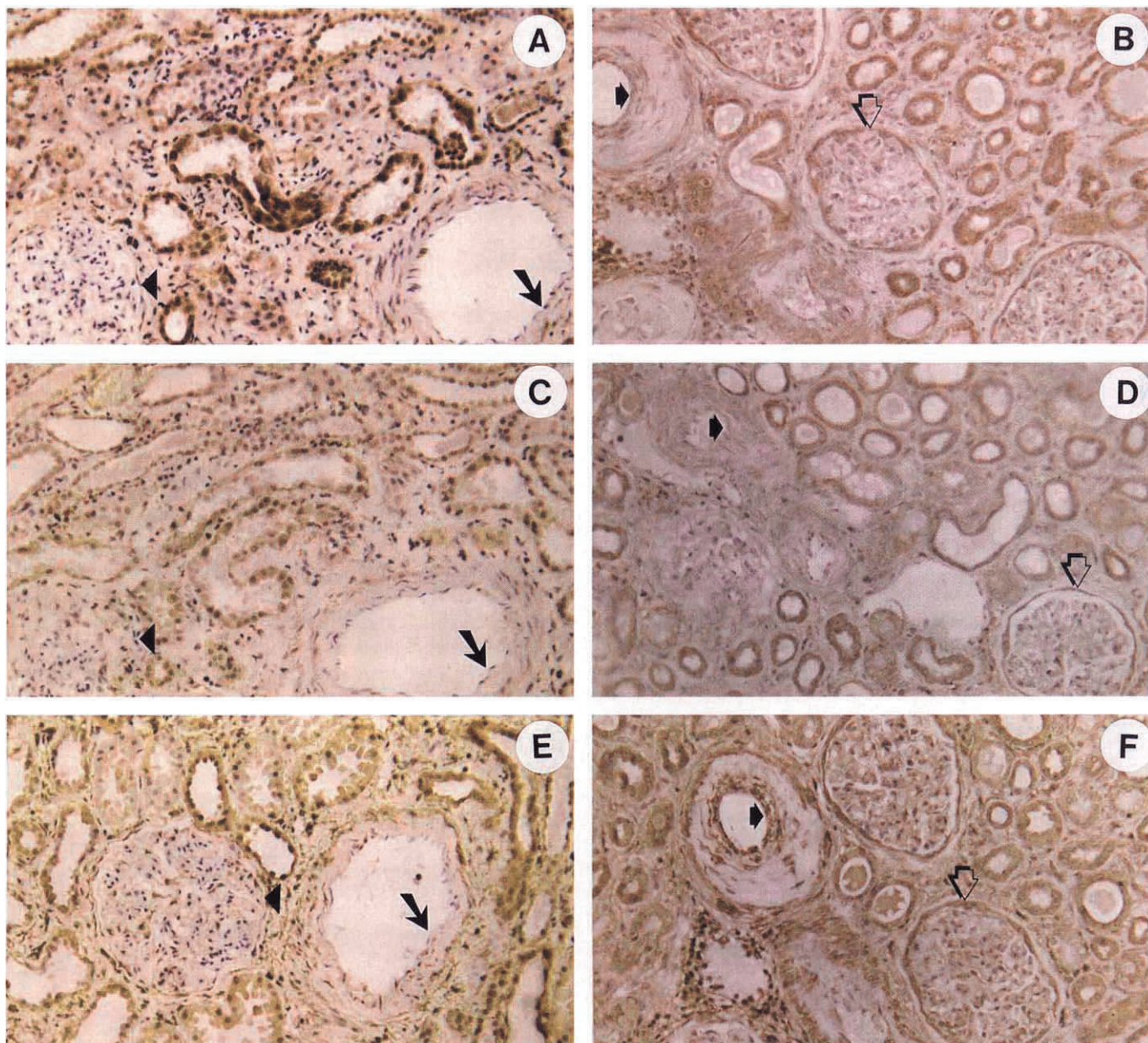


Fig. 1. TGF- β immunostaining in normal (A, C, E) and rejected (B, D, F) renal tissues. The same area is examined in consecutive slides. Symbols are: (black arrow) nonstaining arteries in normal renal tissue; (black triangle) intact glomeruli in normal cortex; (white arrowhead) positive staining in the epithelial and mesangial part of the rejected glomeruli; (black arrowhead) positive staining in the intimal layer and endothelial cells of the sclerotic arteries in rejected grafts. Original magnification is $\times 200$.

found focally, accumulating around and in the damaged glomeruli but were not associating with the intact glomeruli of the rejected specimens, as shown in Figure 4D.

TGF- β isoform and receptor mRNA levels are decreased in rejected kidney specimens

Northern blot analysis of total renal RNA was performed to determine the levels of TGF- β 1, TGF- β 2, TGF- β 3, T β R-I and T β R-II mRNA in both rejected and normal renal cortices (Fig. 5). As shown in Figure 6, densitometric scanning of all the

rejected tissues compared to normal samples indicated an overall decrease in mRNA for TGF- β 1, TGF- β 2, TGF- β 3, T β R-I and T β R-II in the rejected specimens. Furthermore, this decrease tended to vary directly with the general fibrosis in rejection. In the rejected tissues there was a 1.41-, 1.95- and 2-fold decrease in TGF- β 1, TGF- β 2 and TGF- β 3 mRNA levels respectively, compared to the corresponding levels in the normal controls (Fig. 6). T β R-I and T β R-II mRNA levels were 1.3-fold and 3.61-fold decreased in rejection. However, these differences were statistically significant only in the case of TGF- β 3 ($P < 0.02$) and T β R-II ($P < 0.02$) mRNA levels.

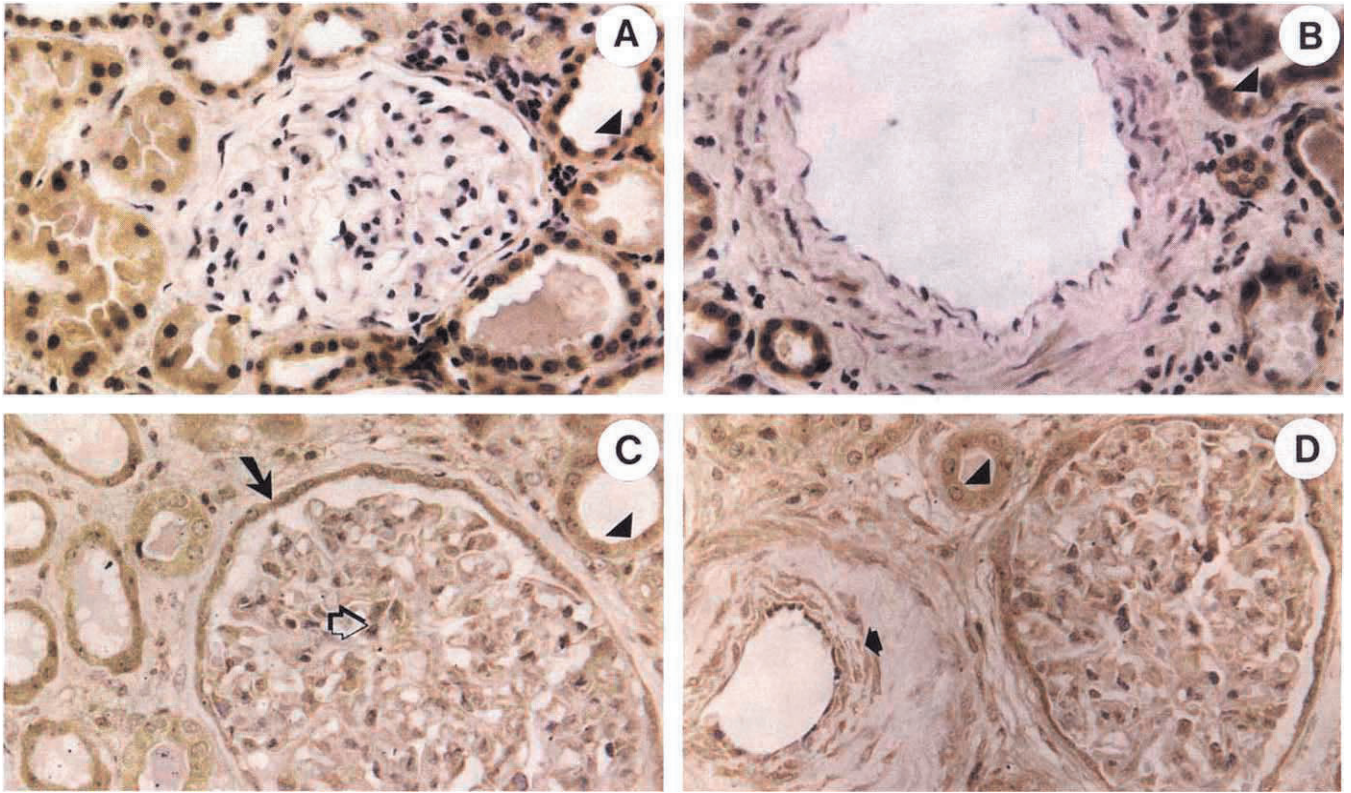


Fig. 2. Significant characteristic localization of TGF- β 1 in the normal kidney (A, B) compared to chronic allograft rejection (C, D) detected by immunohistochemical analysis. A nonstaining intact glomeruli (A) and an intact artery in normal tissue (B). Symbols are: (black arrow) positive glomerular epithelial staining; (white arrowhead) positive intraglomerular mesangial staining; (black arrowhead) positive staining in the intimal layer of the arteries; (black triangle) positive tubular staining. Original magnification $\times 400$.

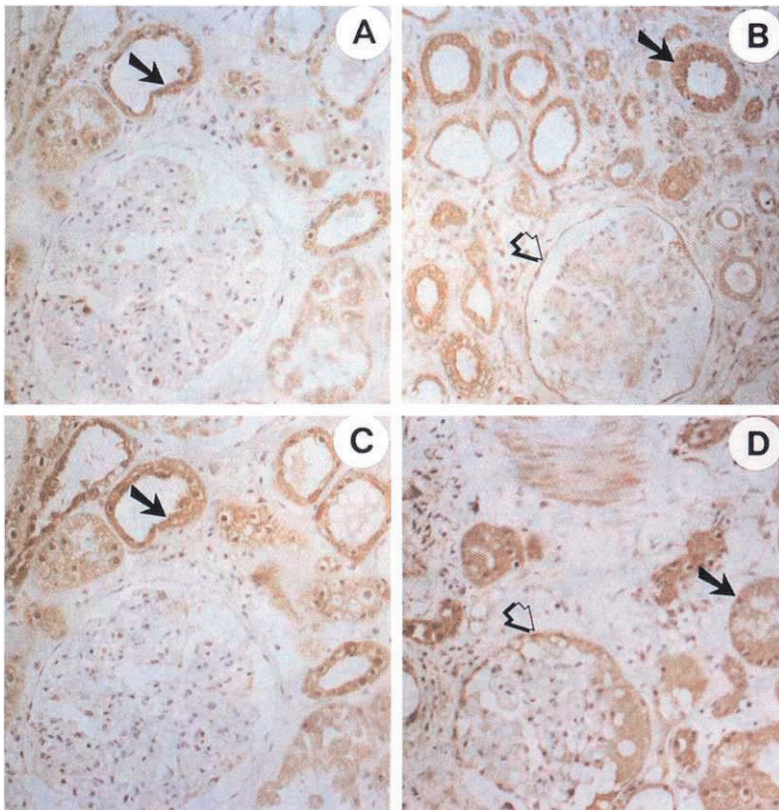


Fig. 3. T β RI (A, B) and T β RII (C, D) immunostaining in normal (A, C) and rejected (B, D) renal tissues. The same area is examined in consecutive slides. black arrow: positive tubular staining, white arrowhead: positive glomerular epithelial staining. Original magnification is $\times 200$.

Table 2. Role of growth factors after different organ transplantations

Transplanted tissue	Growth factor	Correlation with rejection-CAV	Author, date, source, [Ref]
1. Cornea—human	EGF	<i>In vitro</i> pre-treated tissue prevents rejection	Lass, 1994 <i>Ophthalmology</i> [24]
2. Langerhans islet—mouse	TGF- β	Elevated. Prevention of rejection?	Gill, 1991 <i>Transplant Proc</i> [25]
3. Langerhans islet—rat to mouse	TGF- β	<i>In vitro</i> pre-treated tissue prevents rejection	Carel, 1993 <i>Transplantation</i> [26]
4. Liver—human	bFGF	Elevated. Chronic rejection identification?	Bishop, 1992 <i>Transplant Proc</i> [27]
5. Aorta—rat	PDGF, EGF, IGF-1	Elevated in CAV/chronic rejection	Häyry, 1993 <i>FASEB J</i> [28]
6. Heart—rat	TGF- β 1,2,3, LTBP	Elevated. Responsible for rejection?	Waltenberger, 1993 <i>J Immunol</i> [29]
7. Heart & kidney—rat	PDGF- β	Elevated. Cause of CAV?	Higgy, 1991 <i>Transplant Proc</i> [30]
8. Heart—human	TGF- β , FGF	Elevated. Cause of CAV?	Zhao, 1993 <i>Clin Exp Immunol</i> [22]
			Zhao, 1993 <i>Transplant</i> [23]
9. Heart—human	PDGF	Elevated. Cause of CAV?	Shaddy, 1992 <i>J Heart Lung Trans</i> [31]
10. Renal—rat	EGF	Decreased in chronic rejection.	Stein, 1993 <i>Transplant Proc</i> [32]
11. Renal—human	LMW-GF serum ultrafiltrate	Decreased to 0 level in CRF or rejection, back to normal in good renal function	Jacob, 1993 <i>Clin Nephrol</i> [33]
12. Renal—human	TGF- β 1	Increased TGF- β 1, PAI-1 and fibronectin in glomeruli	Shihab, 1995 <i>J Am Soc Nephrol</i> [34]

Abbreviations are CRF, chronic renal failure; CAV, chronic arterial vasculopathy.

Table 3. Grading of the pathological changes and staining intensity of the graft infiltrating immune cells in renal cortex in the rejected and normal kidney specimens

	Normal	Rejected
Glomeruli	Ø	++
Arteriosclerosis	Ø; (+)	++
Fibrosis	Ø	++
Necrosis	Ø	+
Lymphocytes	+	++
Macrophages	(+)	+++

Grading was defined on the basis of the percentage of morphological changes occurring over an area of the cortex, and was quantified according to the number of positively stained cells: Ø, no staining; (+), <10%; +, 10–30%; ++, 30–50%; +++, > 50%.

Discussion

Characteristic pathological changes of chronic renal allograft rejection include the presence of interstitial fibrosis, arteriosclerosis and necrosis, glomerular ischemic simplification and tubular atrophy. TGF- β isoforms especially TGF- β 1 has been implicated as a critical regulatory molecule in the cause of fibrosis and arteriosclerosis [11, 12]. The role for TGF- β in the fibrotic response is due to its ability to stimulate the production of proteins that compose the extracellular matrix, including fibronectin, collagens and proteoglycans. Moreover, TGF- β stimulates the production of protease inhibitors to prevent breakdown of the deposited matrix components. The most significant studies indicating a causative role for TGF- β in an animal model of glomerulonephritis were those of Border et al [12]. In these studies neutralizing antibodies to TGF- β completely obviated the fibrotic response in experimentally induced glomerulonephritis in rats [12]. Similar pathological changes were observed in the glomerular epithelium and mesangium in glomerulonephritis and progressive kidney fibrosis [47, 48]. The increased expression of TGF- β 1 and TGF- β 3 in the vasculature most likely mediates the intimal proliferation, which causes arteriosclerosis, thereby accelerating the process of chronic renal allograft rejection.

An important function of TGF- β s which may effect chronic renal allograft rejection is their role in the regulation of the immune response [6–8]. TGF- β s furthermore have immunosuppressive effects upon various target cells within the immune system *in vivo* [49, 50], which would have an effect in preventing

Table 4. Staining intensity of TGF- β s and graft infiltrating cell markers in renal cortex

	Normal	Rejected
TGF- β 1		
BC	Ø	++
TUB	++	+
TGF- β 2		
BC	Ø	+
TUB	+	+
TGF- β 3		
BC	Ø	+++
TUB	++	+
Lymphocytes (CD 45)	+	+++
T cells (CD 3)	(+); +	++
B cells (CD 20)	Ø; (+)	+++
Macrophages (MAC-387)	(+)	+++

Abbreviations are: BC, Bowman's capsule; TUB, tubules; CD 45, general lymphocyte marker; CD 3, T cell marker; CD 20, B cell marker; MAC 387, macrophage marker. Grading was defined on the basis of the percentage of morphological changes occurring over an area of the cortex, and was quantified according to the number of positively stained cells: Ø, no staining; (+), <10%; +, 10–30%; ++, 30–50%; +++, > 50%.

rejection. For example a possible mechanism could be the suppression of T-cell activation by antagonizing the function of IL-1 and IL-2 [2, 3]. TGF- β s can also inhibit B-lymphocyte differentiation and proliferation [8, 51]. However, TGF- β s also demonstrate other effects on immune cells, which would promote the process of rejection such as chemotactic effects on monocytes and macrophages [6–8].

Table 2 summarizes certain growth factors studied, and their possible or putative function in both ameliorating or causing rejection in the transplantation of various organs. Several studies reported upregulation of TGF- β , EGF, FGF or PDGF both in human and animal models of chronic rejection after cornea, Langerhans islet, liver, aorta or heart transplantation [24–31]. Only three have studied kidney allograft rejection, and in contrast to our studies, in chronic renal allograft rejection down-regulation of epidermal growth factor (EGF) and other growth factors such as IGF-I and IGF-II were found. Stein-Oakley et al reported lower EGF levels in a rat model of chronic kidney rejection, detected by Northern blot and immunohistochemical analysis [32]. In humans, Jacob et al measured decreased low molecular

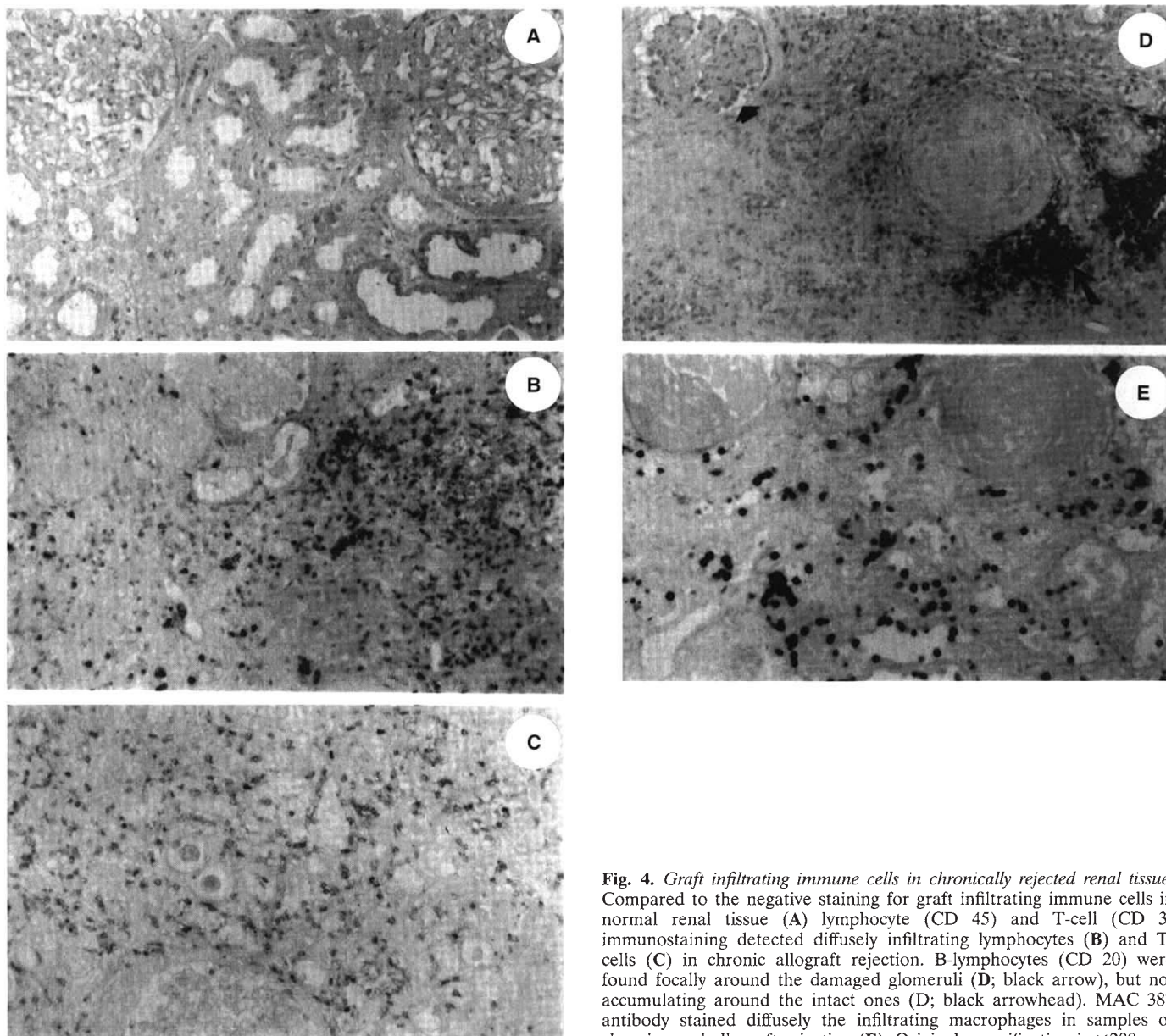


Fig. 4. Graft infiltrating immune cells in chronically rejected renal tissue. Compared to the negative staining for graft infiltrating immune cells in normal renal tissue (A) lymphocyte (CD 45) and T-cell (CD 3) immunostaining detected diffusely infiltrating lymphocytes (B) and T-cells (C) in chronic allograft rejection. B-lymphocytes (CD 20) were found focally around the damaged glomeruli (D; black arrow), but not accumulating around the intact ones (D; black arrowhead). MAC 387 antibody stained diffusely the infiltrating macrophages in samples of chronic renal allograft rejection (E). Original magnification is $\times 200$.

weight growth factor levels (IGF-I, IGF-II) in serum ultrafiltrates with bioassay technique [33]. Shihab et al found an increase in TGF- β 1 mRNA and protein in glomeruli of chronically rejected human kidney allografts when needle biopsies were taken [34]. However, they did not examine the other TGF- β isoforms and their receptors and the concomitant localization of immune cells in kidney rejection in their studies.

The tendency for TGF- β s and T β Rs mRNA levels to be decreased in the rejected kidneys was not statistically significant with the exception of TGF- β 3 and T β R-II mRNA levels. This decreased expression paralleled the general cell and tissue destruction associated with chronic renal rejection, and was most likely due to the marked loss of tubular cells in the rejected samples. In contrast, Shihab et al found increased TGF- β 1 mRNA (and protein) in the tissue specimens of chronically rejected kidney

allografts compared to normal. The difference between the two studies may be due to the presence of less necrosis in their samples which may have been derived from kidney with less severe disease [34]. In our study, the increase in TGF- β 1 and TGF- β 3 immunoreactivity was limited to the less abundant glomeruli and vascular structures. Thus, there was a redistribution of TGF- β 1 and TGF- β 3 expression in the rejected kidney from the tubular cells to the glomeruli. Since the glomerular epithelial and mesangial cells are most likely responsible for the extracellular matrix production in the kidney [47], our findings raise the possibility that enhanced expression of TGF- β 1 and TGF- β 3 within the glomeruli contribute to the fibrosis in chronically rejected renal allografts.

Immune cell staining (detected by markers) revealed the distribution pattern of lymphocytes (CD 45), T-cells (CD 3) and

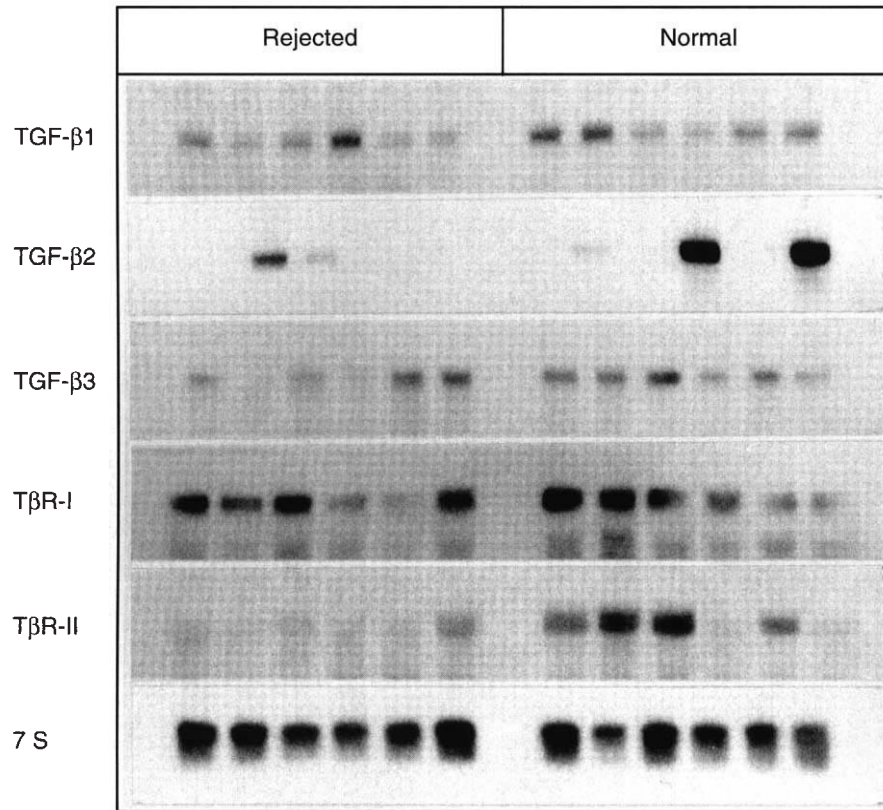


Fig. 5. Northern blot analysis of TGF- β 1, TGF- β 2, TGF- β 3 and T β R-I and T β R-II mRNA in 6 rejected and in 6 normal kidney samples. The same samples were run in all blots in the same order. 7S RNA was used to verify equal RNA loading.

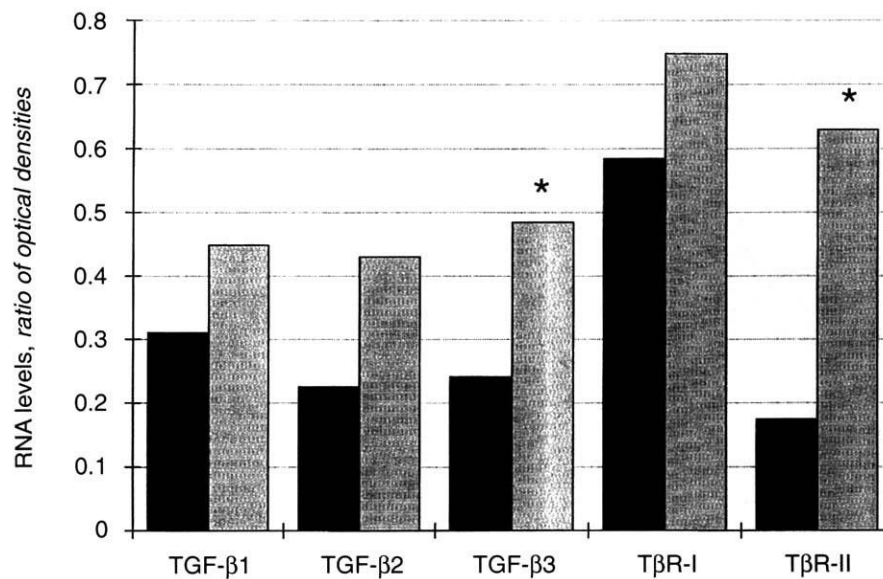


Fig. 6. Densitometric analysis. The ratio of optical density between TGF- β 1, TGF- β 2, TGF- β 3, T β R-I, T β R-II and the corresponding 7S signals were calculated. Bars represent the mean values: (▨) rejected; (■) normal. * $P < 0.02$

macrophages (MAC-387) showed diffuse localization in the rejected kidney samples. Specific immunostaining for CD 20 detected B-lymphocytes accumulating focally around the glomeruli in the chronically rejected allografts, whereas in the normal tissues there was no immunoreactivity for TGF- β s in the glomerular structures, consistent with no evidence of B-cell infiltration.

Cell mediated immunity has been shown to be involved in host

versus graft reaction of tissue rejection. Therefore, it is interesting that both TGF- β , a potent immunosuppressive agent, and B-cells co-localized to the glomeruli involved in apparent tissue destruction. This observation raises the possibility that TGF- β 1 and TGF- β 3 may also participate in the regulation of B-cell mediated immune responses involved in glomerular destruction. Further studies are necessary to evaluate this possibility.

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