Connective tissue growth factor (CTGF/CCN2) is increased in peritoneal dialysis patients with high peritoneal solute transport rate

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Departments of 1Nephrology and Renal Replacement Therapy and 2Urology, Nagoya University Graduate School of Medicine, Nagoya; 3Department of Immunology, Nagoya City University Graduate School of Medical Sciences, Nagoya, Japan; 4FibroGen, Inc., San Francisco, California; 5Department of Pathology, University Medical Center Utrecht, Utrecht; and Departments of 6Pathology and 7Nephrology, Academic Medical Center, University of Amsterdam, Amsterdam, The Netherlands

Submitted 30 June 2009; accepted in final form 10 December 2009

Mizutani M, Ito Y, Mizuno M, Nishimura H, Suzuki Y, Hattori R, Matsukawa Y, Imai M, Oliver N, Goldschmeding R, Aten J, Krediet RT, Yuzawa Y, Matsuo S. Connective tissue growth factor (CTGF/CCN2) is increased in peritoneal dialysis patients with high peritoneal solute transport rate. Am J Physiol Renal Physiol 298: F721–F733, 2010. First published December 23, 2009; doi:10.1152/ajprenal.00368.2009.—Peritoneal fibrosis (PF) is an important complication of peritoneal dialysis (PD) therapy that often occurs in association with peritoneal high transport rate and ultrafiltration failure (UFF). To study the possible pathogenic role of connective tissue growth factor (CTGF) in the relationship of PF and UFF, dialysate CTGF contents (n = 178) and tissue CTGF expression (n = 61) were investigated by ELISA, real-time PCR, immunohistochemistry, and in situ hybridization. CTGF production and with without TGF-$\beta_1$ stimulation in human peritoneal mesothelial cells (HPMC) from the spent patients’ peritoneal dialysate (n = 32) was studied in vitro. The dialysate-to-plasma ratio for creatinine (D/P Cr) was positively correlated to dialysate CTGF concentration and estimated local peritoneal production of CTGF. CTGF mRNA expression was 11.4-fold higher in peritoneal membranes with UFF than in pre-PD renal failure peritoneum and was correlated with thickness of the peritoneum. CTGF protein and mRNA were detected in mesothelium and in fibroblast-like cells. In cultured HPMC, TGF-$\beta_1$-induced expression of CTGF mRNA was increased at 12 and 24 h and was correlated with D/P Cr. In contrast, bone morphogenetic protein-4 mRNA expression was inversely correlated with D/P Cr. Our results suggest that high peritoneal transport state is associated with fibrosis and increased peritoneal CTGF expression and production by mesothelial cells, which can be stimulated by TGF-$\beta_1$. Dialysate CTGF concentration could be a biomarker for both peritoneal fibrosis and membrane function. Functional alteration of mesothelial cells may be involved in progression of peritoneal fibrosis in high transport state.

TGF-$\beta$; BMP-4; BMP-7; fibrosis; ultrafiltration failure

LONG-TERM PERITONEAL DIALYSIS (PD) treatment is accompanied by functional and histopathological alterations in the peritoneum (10, 14, 28). The characteristic feature of chronic peritoneal damage in PD treatment is decreased ultrafiltration capacity associated with submesothelial fibrosis, accumulation of extracellular matrix, and neoangiogenesis leading to a large vessel peritoneal surface area (49). The decrease in ultrafiltration capacity seen after prolonged PD is one of the important reasons for its discontinuation (22). The pathogenesis of peritoneal fibrosis is attributed to a combination of bioincompatible factors in dialysate, including high osmolality, high glucose (10), advanced glycation products (47) and glucose degradation products (48), uremic inflammation (49), and acute peritonitis with inflammation (11, 12, 40). Importantly, peritoneal fibrosis/sclerosis often occurs in association with high transport rate and ultrafiltration failure (UFF). The mechanism of these interactions between peritoneal fibrosis and UFF, which may become a target to prevent the peritoneal damage, is still not clear. In addition, there is no biomarker that reflects both conditions.

Connective tissue growth factor (CTGF; CCN-2) is a 349 amino acid cysteine-rich polypeptide belonging to the CCN (CTGF/Cyr61/Nov) family. CTGF was first identified in conditioned media of endothelial cells as a 36- to 38-kDa polypeptide containing chemotactic activity toward fibroblasts. The CCN family consists of six regulatory proteins, which participate in diverse biological processes such as angiogenesis and wound healing and are involved in control of migration, cell proliferation and differentiation, and epithelial-to-mesenchymal transition (EMT) (7, 39). CTGF is highly expressed during development of various fibrotic disorders and has been acknowledged as one of the key growth factors in extracellular matrix production and other profibrotic activities mediated by transforming growth factor (TGF)-$\beta$ (25, 52, 53). In patients with Type 1 diabetic nephropathy, we observed that plasma CTGF is an independent predictor of end-stage renal disease and mortality (34) and that urinary CTGF excretion is correlated with clinical markers of renal disease (33). CTGF was also detected in peritoneal fluid of patients undergoing peritoneal dialysis (57). However, since these latter studies used small numbers of patients, they were not sufficiently powered to draw conclusions on the potential use of CTGF as biomarker in PD patients and the possible pathophysiological role of CTGF in peritoneal transport. Therefore, we investigated CTGF expression in human peritoneal fibrosis and peritoneal transport dysfunction using human peritoneal tissue, dialysate, and cultured mesothelial cells from continuous ambulatory peritoneal dialysis (CAPD) patients with varying rates of peritoneal transport.

SUBJECTS AND METHODS

Patients and Experimental Design

All studies were approved by the Ethics Committee for Human Research of the Faculty of Medicine, Nagoya University (approval no.
CTGF IS ASSOCIATED WITH HIGH PERITONEAL TRANSPORT

Table 1. Peritoneal biopsy cases evaluated for CTGF mRNA expression

<table>
<thead>
<tr>
<th>Control</th>
<th>UFF</th>
<th>Peritonitis</th>
<th>Incidental</th>
</tr>
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<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>n</td>
<td>26</td>
<td>7</td>
<td>5</td>
</tr>
<tr>
<td>Male</td>
<td>17</td>
<td>3</td>
<td>5</td>
</tr>
<tr>
<td>Female</td>
<td>9</td>
<td>4</td>
<td>0</td>
</tr>
<tr>
<td>Age, yr</td>
<td>62.0 ± 12.8</td>
<td>55.9 ± 11.6</td>
<td>72.5 ± 12.8</td>
</tr>
<tr>
<td>Duration of treatment, yr</td>
<td>9.4 ± 6.6</td>
<td>2.4 ± 1.8</td>
<td>3.7 ± 3.0</td>
</tr>
<tr>
<td>Average thickness of peritoneum, μm</td>
<td>157.9 ± 62.1</td>
<td>308.6 ± 129.2</td>
<td>432.1 ± 322.8</td>
</tr>
</tbody>
</table>

Values are means ± SD. CTGF, connective tissue growth factor; Control, peritoneal tissues were taken at time when a peritoneal dialysis (PD) catheter was inserted because of renal failure; UFF, cases of ultrafiltration failure; incidental, peritoneal tissues were taken when the catheter was removed because of reasons other than UFF.

Table 2. Patient profiles of the culture studies

<table>
<thead>
<tr>
<th>PD Duration (&lt; 2 yr)</th>
<th>All Patients</th>
</tr>
</thead>
<tbody>
<tr>
<td>D/P Cr</td>
<td></td>
</tr>
<tr>
<td>Low</td>
<td>11</td>
</tr>
<tr>
<td>Low average</td>
<td>-0.5–0.64</td>
</tr>
<tr>
<td>High average</td>
<td>-0.65–0.81</td>
</tr>
<tr>
<td>High</td>
<td>-0.82</td>
</tr>
<tr>
<td>D/P Cr ratio of creatinine concentrations in dialysate and plasma, an index of the peritoneal transport.</td>
<td></td>
</tr>
</tbody>
</table>

CTGF production in human mesothelial cells. Human peritoneal mesothelial cells (HPMC) were isolated from spent glucose-based peritoneal dialysis fluid (Dianeal-N PD-4, pH 6.5–7.5, Baxter, Tokyo, Japan) taken from 32 clinically stable patients (Table 2) and cultured by use of a modified method described previously (5, 26). Basal and TGF-β1-induced CTGF mRNA expression in both HPMC and human mesothelial cell line, Met-5A, were studied as detailed below.

Processing of Biopsy Samples and Morphological Analysis

Samples of parietal peritoneum were biopsied in the standard manner and processed as reported previously (17, 35, 49). The tissue samples were fixed with 10% buffered formalin overnight, routinely processed for light microscopy, and embedded in paraffin. The 4-μm-thick sections were cut and stained with hematoxylin and eosin and Masson’s trichrome. Before analysis of peritoneal thickness, each specimen was assessed for size, site, and direction of the peritoneum, then judged adequate as described by Honda et al. (17). In 40 of 61 samples, thickness and the number of the vessels could be measured. To assess the extent of peritoneal thickening, the submesothelial compact zone was identified as the peritoneal fibrosis between basal border of the surface mesothelial cells and upper border of the peritoneal adipose tissues (17, 49). We measured peritoneal thickness at five random points using a Zeiss Z1 microscope and Axiostar software version 4.4 (Carl Zeiss, Oberkochen, Germany), and mean thickness was calculated.

HIC and ISH for CTGF and α-SMA

In total 44 tissue samples from 32 PD patients and 12 predialysis control patients were performed for immunohistochemistry (IHC). The 4-μm-thick sections of formalin-fixed, paraffin-embedded tissues were deparaffinized and rehydrated. The slides were boiled in 0.04 M citrate, 0.12 M, phosphate, pH 5.8, for 10 min at 100°C. After washing, sections were incubated in 0.3% hydrogen peroxide in methanol to block endogenous peroxidase and were incubated in 10% normal goat serum (Dako, Glostrup, Denmark) in PBS to block nonspecific binding. Afterward, the sections were incubated with mouse monoclonal anti-human CTGF antibody (FibroGen, San Francisco, CA).
cisco, CA) at 1 µg/ml in PBS for 16 h at 4°C, followed by reaction with a conjugate of polyclonal goat anti-mouse IgG antibody and horseradish peroxidase-labeled polymer (Histofine Simple Stain, Nichirei, Tokyo, Japan) as a secondary reagent. Enzyme activity was detected by use of a 3,3′-diaminobenzidine tetrahydrochloride liquid system (Dako) (30, 32). Immunostaining for α-SMA was performed by using mouse monoclonal α-SMA antibody (1A3; Dako) as we described previously (16–18). Counterstaining with hematoxylin was done on the IHC sections of CTGF and α-SMA.

In situ hybridization (ISH) to detect CTGF mRNA was performed on the 10% buffered formalin-fixed paraffin-embedded human peritoneal biopsy tissues by using previously described methods (19, 20). Counterstaining with hematoxylin was not performed on the ISH sections.

ELISA for CTGF

CTGF protein was measured in Na2EDTA-plasma and peritoneal dialysate (PD fluid) samples. Samples were frozen at the time of collection, stored at −80°C, and not subjected to freeze-thaw cycles. CTGF was detected by sandwich ELISAs using monoclonal antibodies against distinct epitopes on the NH2-terminal and COOH-terminal halves of human CTGF (FibroGen) with similar protocols as we have described previously (33, 34). The same preparation of full-length recombinant human CTGF (rhCTGF, FibroGen) in appropriate matrixes was used for standards in all assays, making the results of the different ELISAs comparable and obviating the need to equalize concentration of the different CTGF forms by molarity. Low-, medium-, and high-concentration rhCTGF quality control samples, prepared by using matrixes similar to that of the experimental samples, were included in each assay plate to identify quantitation and detection limits. Acceptable coefficients of variation for the quality control replicates were set to be ≤20% for medium and high concentration quality control samples and ≤25% for the lowest concentration quality control samples. In some of the PD fluid analyses, values were extrapolated from the calibration curve to report “low” values that are above the lower limit of detection (LLOQ) but below the lower limit of quantitation (LLOQ). The assays used detected NH2-terminal half fragments of CTGF (N-CTGF, domains 1 and 2) and/or full-length CTGF (W-CTGF, consisting of domains 1–4). We determined sample concentrations of CTGF N-half fragments plus W-CTGF with CTGF ELISAs that use monoclonal antibodies directed against epitopes in domains 1 and 2. For these assays, the LOD for PD fluid was 1.6 ng/ml and the LLOQ was ~14 ng/ml. For Na2EDTA plasma, the LLOQ = 4.7 ng/ml. We determined sample concentrations of W-CTGF with a CTGF ELISA that uses monoclonal antibodies directed against epitopes in domains 1 and 3. The LOD for PD fluid was 3.2 ng/ml and the LLOQ was 4.7 ng/ml. For Na2EDTA plasma, the LLOQ = 4.7 ng/ml. The intra- and interassay coefficients of variation were 6 and 20%, respectively.

Calculations for Local Peritoneal Production of CTGF

Local peritoneal production of CTGF was defined as the difference between the measured and expected dialysate concentration calculated from the peritoneal transport line of each patient by using the methods by Zweers et al. (59, 60). The peritoneal transport line was computed for each patient based on the least squares regression analysis of the dialysate-to-serum (D/S) ratio of β2-microglobulin [molecular weight (MW) 11,800 Da], albumin (MW 69,000), IgG (MW 150,000) and α2-macroglobulin (MW 820,000) and their MWs when plotted on a double logarithmic scale. The expected amount of CTGF protein (MW 22,000 as described below) transported from the circulation to the peritoneal cavity was estimated by using the peritoneal transport line of each patient. The slope of this line represents the size selectivity of the peritoneal membrane. “Local peritoneal CTGF production index” of each individual is calculated from the difference between measured dialysate-to-plasma ratio for CTGF (D/P CTGF) and expected D/P CTGF values transported from the circulation to the peritoneal cavity.
plied Biosystems Sequence Detection Software version 1.3.1 (Applied Biosystems). To normalize the relative expression of the CTGF mRNA against the 18S ribosomal RNA control, standard curves were prepared in each experiment.

**SDS-PAGE and Western Blotting Analyses**

**CTGF.** CTGFs present in PD fluid samples from 2 different patients were isolated by immunoprecipitation (IP), resolved by SDS-PAGE and detected by Western blotting to determine MWs. A CTGF monoclonal antibody against domain 1 (2 μg/ml in 1% BSA-0.05% Tween; FibroGen) was added to 0.5-ml samples of PD fluid and immune complexes were allowed to form by rotating the samples at 4°C for 30 min. Immune complexes were collected on Protein A Sepharose (Sigma, St. Louis, Mo; cat. no. P-9424) after 6 h at 4°C with rotation, washed twice with 1-PBS (Ca²⁺, Mg²⁺-free, Mediatech, Herndon, VA; cat. no. 21-031-CV), and eluted by use of Laemml sample buffer without DTT or β-mercaptoethanol. Unreduced samples were heated at 70°C for 10 min and resolved by SDS-PAGE (4–12% nonreducing gradient gel, Invitrogen, Carlsbad, CA; cat. no. NP0335BOX), and proteins were transferred to nitrocellulose (8-min transfer, Invitrogen iBlot). Blots were blocked with 1% BSA-0.05% Tween 20 at 4°C overnight and total CTGF species (W-CTGF and N-CTGF) were detected by exposing the blot to a CTGF monoclonal antibody against domain 2 (Fibro-...
Gen) at 2 μg/ml in 1% BSA-0.05% Tween 20 in n-PBS for 4 h at room temperature with agitation. CTGF bands were visualized by treating blots with goat anti-mouse IgG-horseradish peroxidase (1:5,000) and Pierce Luminescence reagents (Pierce, Rockford, IL) at room temperature followed by exposing blots to X-ray film. For comparison, Chinese hamster ovary (CHO) cell-derived W- and N-rhCTGFs were included on the gel, and MWs were determined by comparing mobilities of CTGF bands and MW standards (Bio-Rad Laboratories, Hercules, CA, cat. no. 161-0374).

**TGF-β type II receptor.** To detect TGF-β type II receptor on HPMC from six patients in the highest and lowest PET category each, we modified our previously reported technique (21). Briefly, protein amount of lysates was measured by BCA protein assay kit (Pierce). Lysates, in which protein amounts were adjusted, were mixed with sample buffer for SDS-PAGE and separated under nonreducing condition on 20% gels. Separated proteins were transferred to nitrocellulose membrane (Bio-Rad Laboratories), and membranes were blocked with 5% (wt/vol) nonfat milk in PBS (PBS-M). Membranes were then probed with a polyclonal goat anti-TGF-β type II receptor polyclonal antibody (R&D Systems) diluted in PBS-M, washed in PBS containing 0.1% Tween 20, and then probed with horseradish peroxidase-conjugated rabbit anti-goat IgG (Cappel, Durham, NC) absorbed with normal human serum (1:1 vol/vol). After they were washed again in PBS containing 0.1% Tween 20, bands were developed using enhanced chemiluminescence (GE Healthcare Bio-Sciences KK, Tokyo, Japan) and captured on LAS-300 image analysis system (FujiFilm, Tokyo, Japan).

**Statistical Analysis**

Values are expressed as means ± SD. Differences between groups were analyzed by Student’s *t*-test or one-way ANOVA followed by Dunnnett’s multiple comparison tests. Correlations were assessed by the linear regression. Differences were considered to be statistically significant if *P* < 0.05. All analyses were performed using SPSS (Chicago, IL). Polynomial regression analysis was performed by using Prism 5 (GraphPad Software, La Jolla, CA).

**RESULTS**

**CTGF Concentration in the Plasma and Peritoneal Effluent and Local Peritoneal CTGF Production in the PET**

To address the possibility that CTGF content in the PD effluent could be a biomarker of peritoneal dialysis, we measured both plasma and dialysate CTGF (N-CTGF and/or W-CTGF) by sandwich ELISA. Plasma CTGF levels were significantly increased in PD patients compared with healthy controls (121.97 ± 47.36 vs. 5.76 ± 1.50 ng/ml, *P* < 0.0001, Fig. 1A). There was no correlation between plasma CTGF levels and the peritoneal transport rate D/P Cr in the PD patients (Fig. 1B). We found a positive correlation between CTGF concentration in PD effluent from 4-h dwelling times and D/P Cr, an index of peritoneal transport rate (Fig. 1C). For calculation of peritoneal transport of CTGF, we performed IP and Western blot analysis to determine MWs and species of CTGF in peritoneal effluent. The intact form of CTGF (36–38 kDa) was not identified, whereas CTGF reactive fragments of 22 kDa and diffuse 25–28 kDa were demonstrated (Fig. 1D). Most of the measured CTGF effluent dialysate concentrations (point a of Fig. 1E) were significantly greater than CTGF levels that could be expected due to simple diffusion from circulation to the dialysate using the peritoneal transport line (point b). The difference defines the potential extent of local peritoneal CTGF production, designated as “local CTGF production index” (Fig. 1E). Local CTGF production indexes correlated well with D/P Cr (Fig. 1F). W-CTGF in the spent PD effluent was not detected by ELISA, which is consistent with IP and Western blot results.

**Concentration of CTGF in the Overnight Human PD Effluent**

We further assessed CTGF concentration in overnight dwelled peritoneal dialysis effluent of 155 patients and evaluated relationships with peritoneal transport rate and duration of treatment. There was a positive correlation between dialysate CTGF concentration and the D/P Cr ratio (Fig. 2A, *R* = 0.603), and a correlation with duration of PD treatment (Fig. 2B, *R* = 0.264).

**CTGF mRNA Expression and Correlation With Peritoneal Thickness and the Number of Blood Vessels in Human Peritoneal Biopsy Samples**

We next investigated CTGF expression in the peritoneal membrane before and after treatment with PD. Peritoneal
membrane in the group of pre-PD renal failure (157.9 ± 17.9 μm) was thicker compared with the normal peritoneum reported by Williams et al. (49) (50 μm) and Honda et al. (17) (62.4 ± 52.0 μm). In UFF and peritonitis conditions, the peritoneum was remarkably thickened (308.6 ± 48.8 and 432.1 ± 144.4 μm, respectively). CTGF mRNA expression assessed by real-time PCR was 11.4-fold higher in peritoneal membranes with UFF vs. biopsy samples at insertion of PD catheter (pre-PD renal failure peritoneum) (Fig. 3A). There was a correlation between CTGF mRNA expression and thickness of submesothelial compact zone of the peritoneum in the groups of control and incidental patients (R = 0.61, P < 0.0001) and in all patients other than peritonitis (R = 0.57, P < 0.0001) (Fig. 3, B and C). However, we could not find a relationship between CTGF mRNA expression and blood vessel density of the peritoneum in either group (Fig. 3, D and E).

Fig. 3. CTGF mRNA expression detected by real-time PCR in human peritoneal biopsy samples and correlation with peritoneal thickness and the number of blood vessels. A: CTGF mRNA expression in peritoneal biopsy samples (n = 61) was assessed by real-time PCR. Control, peritoneal tissues were taken at the time when PD catheter was inserted because of renal failure; UFF, cases of ultrafiltration failure; incidental, peritoneal tissues were taken when the catheter was removed because of reasons other than UFF; ##P < 0.001 compared against controls. B: correlation between CTGF mRNA expression and thickness of submesothelial compact zone in the groups of control and incidental patients. C: correlation between CTGF mRNA expression and thickness of submesothelial compact zone in all groups other than peritonitis group. D: there is no correlation between CTGF mRNA expression and density of blood vessels of the peritoneum in the groups of control and incidental patients. E: there is no correlation between CTGF mRNA expression and density of blood vessels of the peritoneum in all groups other than peritonitis group.
Localization of CTGF mRNA and Protein Expression in the Peritoneal Tissues

ISH and IHC weakly detected CTGF mRNA and protein in the mesothelial cells and vascular wall of peritoneal tissues from patients with chronic renal failure before initiation of dialysis (Fig. 4, A and B). In the patients whose catheters were removed incidentally, CTGF was identified in the mesothelial cells and vessel walls (Fig. 4, C and D). The extent of CTGF expression was similar or slightly increased when compared with pre-PD renal failure group. In the advanced fibrotic peritoneum, mesothelial cells were partially detached from the surface of the peritoneum. However, CTGF mRNA and protein were strongly detected in the mesothelial cells and in fibroblast-like spindle-shaped cells (Fig. 4, E and F). Immunostaining for α-SMA suggested these CTGF-positive spindle-shaped cells were fibroblasts (Fig. 4E, inset).

Morphological Features and CTGF mRNA Expression in the Cultured HPMC Under Basal Condition

Human mesothelial cells (HPMC) were isolated from the spent peritoneal dialysis effluent of 32 PD patients and cultured on the collagen-I coated dish. We could not find obvious morphological differences in cells from patients of variable peritoneal transport rates (Fig. 5A; PET low, 5B; PET high). All cells appeared cobblestone shaped and were positive for ZO-1 and cytokeratin-18 but negative for α-SMA, CD68, CD31, and factor VIII by IHC analysis. In contrast, HPMC grew rapidly in culture on the noncoated dishes in the presence of EGF, adopting a spindle fibroblast-like shape as previously reported (26). We studied the CTGF mRNA content of HPMC in both culture conditions. There was no significant correlation between the rate of peritoneal membrane transport (D/P Cr) in the PD patient of origin and the basal CTGF mRNA expression under EGF-positive (P = 0.601) or -negative (P = 0.452) culture conditions with or without type I collagen. Also no correlation between basal CTGF mRNA expression and duration of PD treatment (EGF-positive condition; P = 0.748, EGF-negative condition; P = 0.822) was found. We confirmed that all of the spindle-shaped HPMC cultured in EGF-containing medium reversibly modified into the polygonal, cobblestone-shaped, epithelioid morphology after seeding and culture on collagen dishes.

CTGF mRNA Expression After Incubation With TGF-β1 in Cultured HPMC and Met-5A Mesothelial Cell Line

The time course of CTGF mRNA expression in response to TGF-β1 treatment was studied in both HPMC and Met-5A
cells. Samples were taken after 3, 6, 12, and 24 h of exposure to TGF-β1 (5 ng/ml). In 24 HPMC derived from 32 patients and Met-5A cells, CTGF mRNA expression was increased and peaked at 12 h. In another eight strains of HPMC CTGF mRNA expression peaked at 24 h after incubation with TGF-β1 (Fig. 6, A and B). Therefore, we evaluated the increment of CTGF induction by TGF-β1 at both 12 and 24 h post-TGF-β1 exposure. Increase of CTGF mRNA at 12 h (fold) showed a good correlation with D/P Cr in both the PD patient group treated less than 2 yr with PD (r = 0.802, P < 0.0001) and all-patients group (r = 0.668, P < 0.0001, Fig. 7, A and B). This suggests that mesothelial cells from high peritoneal solute transport groups induce higher levels of CTGF by TGF-β1. Correlation was weaker at 12 h than at 24 h (Fig. 7). No significant correlation between the extent of TGF-β1-induced increase of CTGF mRNA expression in HPMC and the duration of PD treatment of the patients from which the HPMC were derived was found (Fig. 8). Western blotting did not reveal differences in the levels of TGF-β type II receptor expression on the HPMC of patients with high peritoneal transport compared with those with low peritoneal transport, therefore excluding this as a possible factor in differential induction of CTGF expression by TGF-β1 in these groups of HPMC (Fig. 9).

**BMP-4 mRNA Expression Before and After Incubation With TGF-β1 In HPMC**

To characterize the BMP-4 expression after exposure to TGF-β1, we examined the time course of BMP-4 mRNA in HPMC. TGF-β1-induced a transient decrease of BMP-4 expression in HPMC of patients with low/low average peritoneal transport. In contrast, BMP-4 mRNA expression continued to be downregulated at 12–24 h after incubation with TGF-β1 in HPMC from the high peritoneal transport patients (Fig. 10A). We found a good inverse correlation between D/P Cr and BMP-4 mRNA levels 12 h after exposure to TGF-β1 in both the PD patient groups treated less than 2 yr (R = 0.678, P < 0.001) and all-patients group (R = 0.500, P < 0.01), which was reciprocal to the CTGF response on TGF-β1 exposure (Fig. 10, B and C). No correlation was observed between D/P Cr and basal BMP-4 mRNA expression both with and without presence of EGF (P = 0.474).

**DISCUSSION**

Although there is increasing evidence that peritoneal membrane failure is associated with fibrosis and neoangiogenesis, the precise mechanisms of interactions between peritoneal fibrosis and ultrafiltration failure have not been defined. Peritoneal dialysis treatment itself had a strong impact on the progression of peritoneal fibrosis/sclerosis (17), and the submesothelial compact zone thickness increased significantly with duration of PD therapy and was remarkable in the state of UFF (49). In our analysis, CTGF mRNA was significantly increased in the UFF group and was correlated with thickness of the peritoneum in all groups other than peritonitis. We excluded the cases with peritonitis in this analysis, because peritonitis can be thickened by the acute inflammatory changes with strong cell infiltration, exudation of fibrin, and edema (13a, 35). By IHC and ISH, CTGF protein and mRNA were detected in the mesothelial cells and fibroblasts in the thickened peritoneal membrane associated with high peritoneal transport. These findings indicate that CTGF is likely to be involved in peritoneal fibrosis and UFF.
Higher levels of plasma CTGF in PD patients may be affected by several factors, such as 1) accumulation by reduced renal clearance; 2) production by proliferative renal cells, periternal tissues, blood vessel endothelial cells, and peritoneal tissues (16, 33, 34, 36); 3) absorption of PD fluid, which contains CTGF, through lymphatic vessels (29, 42). In this respect, local peritoneal CTGF production may contribute to the high levels of plasma CTGF. CTGF in PD effluent might be derived from the circulation and/or be locally produced in the peritoneum, especially by mesothelial cells and fibroblasts, which is consistent with the ISH and IHC results. In contrast to the rapid removal of the small-molecular-weight solutes such as urea and creatinine into the PD fluid, the extent of low MW protein transfer from circulation to PD fluid is dependent on several factors including dwelling time and MW (23). Diffusion of full-length and fragmentary CTGF from circulation to PD fluid can be expected to increase linearly with time. Based on these concepts, local peritoneal production of CTGF can be calculated by the difference between the measured and expected dialysate concentration by using the peritoneal transport line determined for each patient. IP/Western blotting showed that CTGF proteins in the peritoneal effluent were 22-kDa and 25- to 28-kDa peptides, a proteolytically processed form of CTGF. Smaller fragments of CTGF can more easily diffuse from the circulation to the peritoneal fluid. Therefore, local production of CTGF using individual peritoneal transport lines was calculated at the MW 22 kDa to estimate the minimum local production rate. In addition, charge may affect the D/P ratio. β2-Microglobulin, albumin, and α2-macroglobulin are negatively charged, and their isoelectric points are 6.5, 6.2, and 6.4, respectively. In contrast, CTGF is positively charged with an isoelectric point of 8.0 (http://www.ensembl.org/index.html) and therefore is prone to adhere to the peritoneal membrane, which is negatively charged by glycosaminoglycans and proteoglycans (14, 55). CTGF is generally considered to be a “sticky” protein and the COOH-terminal half of CTGF is known to bind heparin sulfate proteoglycans (15). A recent report has further shown that the NH2-terminal half of CTGF can bind aggrecan (2). In this respect, the actual local CTGF production may be even higher than the calculated local production of CTGF. Another complication to consider is that after initiation of PD, the amount of glycosaminoglycans and proteoglycans may change (55). Presently it is not possible to correct for these factors in the formula of calculation. Nevertheless, our calculations indicate that local peritoneal CTGF production correlates well with peritoneal transport D/P Cr (R = 0.723, P < 0.0001), suggesting that peritoneal membranes in patients with higher peritoneal transport rates are characterized by production of larger amounts of CTGF. This is consistent with the positive correlation between D/P Cr and TGF-β-induced
CTGF production that we observed in cultured mesothelial cells from spent effluents and strong expression of CTGF demonstrated by IHC and ISH in the UFF group. Therefore, because abnormally elevated CTGF production correlates with peritoneal fibrosis, use of CTGF as a biomarker by measuring CTGF content in PD effluent could provide important information about peritoneal transport abnormalities and activity of the peritoneal fibrotic process. TGF-β was also reported to be elevated in the PD effluent and was correlated with peritoneal transport D/P (24). There are many mechanisms including exposure to glucose, advanced glycation end products (AGE), glucose degradation products, IL-1, and angiotensin II, to upregulate TGF-β in the mesothelial cells of the PD patients (3, 27, 47). Thus high levels of both TGF-β and CTGF in PD effluent of high transport patients might strongly enhance profibrotic activity in the peritoneal cavity.

Mesothelial cells are the main components of peritoneum and play an important role in peritoneal homeostasis including antigen presentation, clearance of fibrin, synthesis of cytokines, growth factors, and matrix proteins (56). There are increasing data about the role of mesothelial cells in determining the functional alteration of peritoneum during PD. HPMC isolated from spent dialysate of PD patients cannot be termed "normal." Nevertheless, studies using PD-derived HPMC may provide essential data of the physiological status of renal failure and the patient’s own peritoneal status during PD (56). Cells obtained from spent dialysis effluent from PD patients were reported to be enlarged and multivacuolated and to have reduced microvilli density and dysfunctional mitochondria in long-term PD therapy (8, 51, 56). Investigations into the role of mesothelial cells in the structural and functional alterations of the peritoneum during PD have shown that mesothelial cells lose epithelial phenotype and acquire myofibroblast phenotype by an EMT (3, 50). The prevalence of nonepithelioid cells by culture on the type I collagen plates in the absence of EGF conditions was reported to be related to the duration of CAPD (50). During the first 2 yr of PD, EMT of mesothelial cells is

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**Fig. 8.** Relationship between “CTGF amplification ratio” and duration of PD treatment. Relationship between duration of treatment with PD and increment of CTGF mRNA expression in cultured mesothelial cells from the spent PD effluent. A: 12 h after stimulation with TGF-β1 (5 ng/ml), treatment for less than 2 yr. B: 12 h after stimulation with TGF-β1 (5 ng/ml), all patients. C: 24 h after stimulation with TGF-β1 (5 ng/ml), treatment for less than 2 yr. D: 24 h after stimulation with TGF-β1 (5 ng/ml), all patients.

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**Fig. 9.** Western blotting of TGF-β type II receptor on the cultured HPMC. Lanes 1 to 4 are from different patients with the high category and lanes 5 to 8 were from the low category of the PET. There are no differences between 2 groups. Representative cases are shown.
a frequent morphological change in the peritoneal membrane (50). In addition, the prevalence of nonepithelioid cells was detected in the high transport status (13). However, in our experiments all patients’ mesothelial cells from the spent dialysis fluid cultured on the type I collagen dishes showed a cobblestone-like appearance with positive staining for cytokeratin and ZO-1, which suggests that mesothelial cells in our experimental setup display a reduced fibrogenic phenotype compared with those in previous reports (50). These differences may be related to the usage of neutral pH dialysate in our patient groups. In contrast, mesothelial cells grew rapidly in culture when provided with serum, EGF, and hydrocortisone, adopting a fibroblast shape and forming parallel, multilayered arrays as reported previously (9). EGF was reported to transform cultured HPMC to fibroblast phenotype (26). When cells were split and subsequently cultured on a collagen matrix in absence of EGF, we established that these cells reverse their phenotype into polygonal, cobblestone epithelioid morphology with positive cytokeratin and ZO-1 staining. These findings suggest that EMT of mesothelial cells is reversible and may be followed by mesenchymal-to-epithelial transition under proper conditions. Therefore, we explored basal CTGF expression in both mesothelial cells cultured on the type I collagen dishes without EGF conditions and cultured on the noncoated dishes with EGF-positive conditions. In both conditions CTGF basal expression before TGF-β1 stimulation was not different for mesothelial cells from patients with either high or low peritoneal solute transport. However, CTGF induction by TGF-β is quite different for these two groups.

CTGF mRNA is shown to be upregulated by TGF-β in the cultured mesothelial cells from spent PD effluent in our experiments as previously reported for rat (44) and human mesothelial cells derived from omentum (57). These findings are consistent with the notion that TGF-β is an important inducer of CTGF expression in mesothelial cells. An increased susceptibility to TGF-β exposure, leading to increased production of CTGF in mesothelial cells, may be related to the extent of fibrosis of the peritoneal membrane and corresponds with the observed phenotypic changes in patients with high peritoneal solute transport. Identification of the factors that regulate enhanced responsiveness to TGF-β may help to identify new strategies to prevent peritoneal fibrosis. First, we examined the expression of TGF-β type II receptor in the HPMC and found no differences between high and low peritoneal transport categories. To further characterize the difference we evaluated BMP-4 expression in HPMC. We demonstrated reciprocal expression patterns of BMP-4 and CTGF after exposure to TGF-β1. CTGF was previously shown to bind directly to TGF-β through its CR domain (i.e., domain 2) and regulate opposite effects. Recently BMP-4 was reported to inhibit TGF-β2-induced expression of extracellular matrix protein and to have antagonistic effects on aldosterone signaling in the mesangial cells (1, 31, 32, 37, 58). Imbalance of TGF-β signaling leading to altered CTGF and BMP-4 expression in

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**Fig. 10.** BMP-4 mRNA expression after incubation with TGF-β1 in the cultured HPMC. **A:** BMP-4 mRNA expression is downregulated from 3 to 24 h after incubation with TGF-β1 in the PET high category patient. In contrast, BMP-4 is decreased transiently and recovered at 12 and 24 h in the PET low category patient. Representative cases are shown. *P < 0.05, **P < 0.005, ***P < 0.001, ****P < 0.0001 vs. 0 h. **B:** relationship between peritoneal permeability (D/P Cr) and increment of BMP-4 mRNA expression in cultured mesothelial cells from the spent PD effluent. 12 h after stimulation with TGF-β1 (5 ng/ml), treatment for less than 2 yr. **C:** relationship between peritoneal permeability (D/P Cr) and increment of BMP-4 mRNA expression in cultured mesothelial cells from the spent PD effluent. 12 h after stimulation with TGF-β1 (5 ng/ml), all patients.
the mesothelial cells may play an important role in the regulation of fibrogenic and antifibrogenic activity in the different PET category. Future studies are necessary to investigate whether overexpression of BMP-4 can compensate the dysregulation of TGF-β and CTGF signaling pathway in vitro and in vivo, which may lead to new strategies to control peritoneal transport. In addition, regulation with other antifibrogenic factors including BMP-7 and hepatocyte growth factor will have to be established in the future (46, 54).

Peritoneal neoangiogenesis is a major factor in development of peritoneal membrane failure, and local production of VEGF during PD has been proposed to play a central role in increased solute transport and ultrafiltration failure. VEGF has been shown to stimulate CTGF mRNA and protein production in bovine retinal endothelial cells and pericytes (43), and under certain circumstances CTGF also can exert angiogenic effects, as was demonstrated by the induction of neovascularization in rat corneal micropocket implants (4) and in chicken chorioallantoic membranes (41). In contrast, Inoki and colleagues (18) reported that CTGF inhibited VEGF-induced angiogenesis. In our studies, we did not observe any relation between CTGF expression and the number of vessels in the peritoneal membrane. This suggests that CTGF expression level may not be a major determinant of angiogenesis in the peritoneal membrane.

In summary, we report that high peritoneal transport state correlates with increased peritoneal CTGF expression and higher CTGF expression in response to TGF-β in mesothelial cells. CTGF content in spent dialysate might be a biomarker for development of peritoneal fibrosis in PD patients. Functional alteration of mesothelial cells, as exemplified by the altered balance of CTGF and BMP-4 expression induced by TGF-β, may be involved in progression of peritoneal fibrosis in the high transport state. Phenotypic control of the mesothelial cells could be a potential therapeutic target of peritoneal fibrosis and membrane failure.

ACKNOWLEDGMENTS

The technical assistance of Norihiko Suzuki, Keiko Higashide, Naoko Asano, and Yuriko Sawa (Department of Nephrology, Nagoya University, Nagoya, Japan) is gratefully acknowledged. We thank Dongxia Li, Dan Yi, Thomas Crowley, and Jay Leone (FibroGen) for the technical assistance on the ELISA and Western blotting analysis.

GRANTS

This work was supported by in part by a grant-in-aid for Scientific Research from the Ministry Education, Science, and Culture, Japan (no. 20590972), the 2007 research grant from the Aichi Kidney Foundation and Baxter Japan PD Grant 2009.

DISCLOSURES

N. Oliver is an employee of FibroGen, Inc. (San Francisco, CA), supplier of anti-CTGF antibodies; R. Goldschmeding has received research support grants and is currently also an employee of FibroGen, Inc.

REFERENCES


