

# $\mathbf{TGF}$ - $\beta$ and fibrosis in different organs - molecular pathway imprints

Dirk Pohlers, Julia Brenmoehl, Ivonne Löffler, Cornelia K. Müller, Carola Leipner, Stefan Schultze-Mosgau, Andreas Stallmach, Raimund W. Kinne, Gunter Wolf

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3	Dirk Pohlers <sup>1</sup> , Julia Brenmoehl <sup>2</sup> , Ivonne Löffler <sup>3</sup> , Cornelia K. Müller <sup>4</sup> , Carola Leipner <sup>5</sup> ,
4	Stefan Schultze-Mosgau <sup>4</sup> , Andreas Stallmach <sup>2</sup> , Raimund W. Kinne <sup>1</sup> , Gunter Wolf <sup>3</sup>
5	
6	1 Experimental Rheumatology Group, Department of Orthopedics, Waldkrankenhaus "Rudolf
7	Elle" Eisenberg, University Hospital, Friedrich Schiller University, Jena
8	2 Department of Gastroenterology, Hepatology and Infectious Diseases, Clinic of Internal
9	Medicine II, University Hospital, Friedrich Schiller University, Jena
10	3 Clinic of Internal Medicine III, University Hospital, Friedrich Schiller University, Jena
11	4 Clinic of Oromaxillofacial Surgery/Plastic Surgery, University Hospital, Friedrich Schiller
12	University, Jena
13	5 Institute of Animal Research, University Hospital, Friedrich Schiller University, Jena
14	$\mathcal{A}$
15	Corresponding author:
16	Raimund W. Kinne
17	Experimental Rheumatology Unit, University Hospital Jena
18	Department of Orthopedics, Waldkrankenhaus "Rudolf Elle"
19	Klosterlausnitzer Str. 81
20	07607 Eisenberg
21	e-mail: <u>Raimund.W.Kinne@med.uni-jena.de</u>
22	Tel./Fax +49 36691 81228/6
23	
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25 wound-healing, myocarditis

Review

#### 26 ABSTRACT

The action of transforming-growth-factor (TGF)- $\beta$  following inflammatory responses is 27 28 characterized by increased production of extracellular matrix (ECM) components, as well as mesenchymal cell proliferation, migration, and accumulation. Thus, TGF- $\beta$  is important for 29 30 the induction of fibrosis often associated with chronic phases of inflammatory diseases. This 31 common feature of TGF-related pathologies is observed in many different organs. Therefore, in addition to the description of the common TGF- $\beta$ -pathway, this review focuses on TGF- $\beta$ -32 related pathogenetic effects in different pathologies/organs, i. e., arthritis, diabetic 33 34 nephropathy, colitis/Crohn's disease, radiation-induced fibrosis, and myocarditis (including their similarities and dissimilarities). However, TGF- $\beta$  exhibits both exacerbating and 35 36 ameliorating features, depending on the phase of disease and the site of action. Due to its central role in severe fibrotic diseases, TGF- $\beta$  nevertheless remains an attractive therapeutic 37 target, if targeted locally and during the fibrotic phase of disease. 38

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Review

#### 40 **1. INTRODUCTION**

The fibrotic reaction of the connective tissue following an inflammatory response is mainly 41 42 characterized by an increased production of extracellular matrix (ECM) components and 43 mesenchymal cell proliferation, migration and accumulation. Despite the existence of numerous distinct causes of chronic inflammatory diseases in different organs and tissues, 44 45 these diseases are generally characterized by: i) severe and intermittent progression with phases of acute exacerbation and remission; ii) immigration of inflammatory cells 46 47 (macrophages, granulocytes and T-cells); and iii) increased expression of pro-inflammatory mediators (Figure 1). These processes result in the proliferation of local fibroblasts and, by 48 49 interaction with epithelial cells, in their differentiation into myofibroblasts and can be regarded as a misguided wound healing. Finally, the inflammatory process comes to rest, but 50 51 the massive fibrosis prevents a rebuilding of functionally intact tissue and organs.

Transforming growth factor (TGF)- $\beta$  is an ubiquitously expressed cytokine belonging to a large superfamily of activins/bone morphogenetic proteins [1]. This mediator plays an active role in the processes discussed above, such as proliferation, wound healing [2], and synthesis of ECM molecules [3]. TGF- $\beta$ , therefore, strongly contributes to fibrotic disorders such as diabetic nephropathy, Crohn's disease, rheumatoid arthritis, radiation-induced fibrosis, and myocarditis. However, TGF- $\beta$  is clearly a bi- (or multi-) functional molecule with strong effects on the immune system [4,5].

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#### 60 **2. TGF-\beta signaling pathway**

61 TGF-β is synthesized as one part of a large molecule, the pro-TGF-β containing the latency-62 associated proteins (LAP; Figure 2). The latter is cleaved from TGF-β in the Golgi apparatus, 63 but remains non-covalently associated with the growth factor. The disulfide-bound latent-

Review

64 TGF- $\beta$ -binding proteins 1/2 (LTBP 1/2) connect the whole complex to the ECM (details described in [6]). Release of TGF- $\beta$  from the pro-TGF- $\beta$  complex can be achieved through 65 66 proteolytic activity by plasmin [7] or matrix-metalloproteinase (MMP)-2 and MMP-9 [8], through integrins [9,10], recently reviewed in [11], treatment with mild acids [12], or through 67 68 the action of thrombospondin (THBS; [13]) by disrupting the non-covalent interactions 69 between LAP and TGF- $\beta$ 1. Once released, TGF- $\beta$  mediates signals through pairs of type I 70 and type II receptors [14]. The type III receptor (betaglycan) acts - probably in conjunction 71 with other heparan sulfate glycans like syndecan [15]- as a co-receptor for binding/presenting 72 TGF and a regulator of TGF- $\beta$  signaling [16]. The result of ligand binding is the activation of 73 the type II receptor (TGFBR2), which then phosphorylates the type I receptor (TGFBR1). The 74 active receptor complex then phosphorylates the so-called R (receptor)-Smad-2 or Smad-3 75 that propagates the signal [17]. The phosphorylation of Smad2/3 decreases the affinity for the Smad-anchor for receptor activation (SARA), which in non-stimulated cells mediates the 76 77 retention of Smad2/3 in the cytoplasma by interaction, and increases the affinity of Smad2/3 for Smad-4 (a so-called co-Smad). This complex is now able to enter the nucleus, to bind 78 79 transcriptional co-activators like p300 and Creb-binding-protein (CBP) or repressors like SkiL 80 or TGIF [18], and to regulate the transcriptional activity of various genes.

81 Mitogen-activated protein kinases (MAPKs) and protein kinase C can also interfere 82 with either the nuclear translocation or binding of Smad3/4 complexes to DNA and regulate 83 TGF-β1 signalling [19,20]. Moreover, the serine-threonine protein kinase B can directly 84 interact with Smad3, thereby preventing its phosphorylation and nuclear translocation [21]. 85 Other pathways can be directly activated by TGF-B1. These include components of the MAPK pathway, such as ras, raf, ERK, p38 and JNK, the phosphatidylinositol-3 kinase 86 cascade, as well as the regulators of cadherin junctions, RhoA and Rac ([19,22,23]; Fig. 1). 87 88 Recently, an involvement of the focal adhesion kinase (FAK) was established in

Review

myofibroblast differentiation and in remodeling of the connective tissue following stimulation with TGF [24,25]. In line with these results, TGF-induced FAK-signaling is required for the activation of TAK [26] or MEKK1 and, subsequently, of JNK [27], all factors shown to be essential for the transcription of pro-fibrotic genes.

Notably, that signal transduction pathways have their own intracellular regulators. An
inhibitory Smad (Smad7) blocks TGF-β1 signaling by physical interaction with the activated
TGFBR1 receptor and prevents the docking and phosphorylation of Smad2/3 [28,29].

96 This complex TGF-β signaling pathway (Figure 2) contains numerous ligands,
97 receptors, and signaling molecules which, as potential targets of dysregulation via increased
98 or decreased expression, activation or interaction, may be partially involved in fibrotic
99 reactions in the diseases discussed below.

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#### 101 **3. TGF-β-related molecules in Rheumatoid Arthritis**

The importance of TGF-B1 in rheumatoid arthritis (RA) ranges from an association with 102 103 certain vascularization patterns in the synovial membrane (SM) [30], and an association of 104 TGF-β polymorphisms with the radiological signs of joint destruction [31] to an induction of 105 pro-inflammatory cytokines, MMP [32], aggreccanase [33] and urokinase-type plasminogen 106 activator [34]. In addition, TGF- $\beta$  plays an important role for the function of regulatory T-107 cells [5] in the suppression of autoimmunity. Indeed, increased levels of TGF- $\beta$ 1 have been 108 found in the synovial membrane of patients with RA by northern blot [35], 109 immunohistochemistry [36,37], western blot [38] and in synovial effusions [39]. Also 110 TGFBR2 was detected at higher levels than in normal synovial tissue [35].

Using "pathway-directed" software following genome-wide comparison between
synovial fibroblasts (SFB) from patients with RA and osteoarthritis (OA) with Affymetrix

113 arrays, gene expression of TGF-\beta1, TGF-\beta3, LTBP1/2, THBS1, TGFBR1, SARA, CBP, SkiL 114 - belonging to the TGF-β-pathway (Figure 2) - was elevated in RA [40]. After validating 115 array data at the mRNA and protein levels using quantitative PCR and western 116 blot/immunohistochemistry, we confirmed an upregulated TGF-β pathway in RA-SFB. The presence of TGF-\u00df1, in conjunction with increased amounts of TGF-\u00bf2-releasing THBS1 and a 117 118 higher expression of TGFBR1, may thus lead to an amplified response of RA-SFB to TGF- $\beta$ . 119 This RA-specific response has been confirmed by increased expression of MMP-11 following TGF-ß stimulation, implying a pathogenetic relevance of the TGF-β-pathway for MMP-120 121 induced degradation or remodeling processes in RA [40].

122 The importance of TGF- $\beta$  for the pathogenesis of arthritis is emphasized by a number of animal models. The abundant expression of TGF- $\beta$ 1, 2, and 3 as well as the TGFBR1 and -123 2 in rat synovium was increased after onset of the collagen-induced arthritis (CIA) [41], and 124 direct intra-articular injection of TGF-B1 or TGF-B2 induced synovial erythema, swelling, 125 126 and cellular infiltration resulting in synovial inflammation and hyperplasia [42]. Conversely, neutralization of TGF- $\beta$  inhibited acute and chronic arthritis induced by streptococcal cell 127 128 wall (SCW) [43]. In line with these observations, an adenovirus-mediated overexpression of TGF-\beta1 in rabbit knees led to an increased glycosaminoglycan release, nitric oxide 129 130 production and, most notably, to fibrosis and muscle edema [44]. The prevention of CIA by administration of a TGFBR1 inhibitor (HTS466284), which concomitantly reduced the 131 132 expression of vascular endothelial growth factor (VEGF), platelet-derived growth factor 133 (PDGF)-AA, TNF- $\alpha$ , and cellular proliferation [45], further underlines the pathogenetic role of TGF- $\beta$  in arthritis. 134

In contrast to the above-mentioned studies, numerous observations show beneficial
effects of TGF-β in arthritis. If administered systemically, TGF-β1 suppressed SCW-induced

Review

137 arthritis, as measured by cellular infiltration and joint erosion [46]. In addition, investigation 138 of the cytokine expression during CIA demonstrated a strong upregulation of TGF- $\beta$ 1/2 in the 139 remission state of disease, possibly refelecting the anti-inflammatory regulation of T-cells by TGF- $\beta$  in arthritis. If TGF- $\beta$  signaling was inhibited by expression of dominant-negative 140 TGFBR2 in T-cells [47] the susceptibility and the clinical severity of CIA was strongly 141 increased. Likewise, if TGF-B1 was retrovirally overexpressed in arthritogenic splenocytes, 142 143 CIA could not be transferred to SCID mice and established disease was ameliorated [48]. Therefore, it may be important to inhibit TGF- $\beta$  only at the site of inflammation without 144 targeting regulatory lymphocytes at extra-articular sites. 145

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#### 147 **4. TGF-β-RELATED MOLECULES IN DIABETIC NEPHROPATHY**

148 TGF- $\beta$  and its signal transduction play a major role in diabetic nephropathy and have 149 therefore been thoroughly studied [49-53]. Among the features of the diabetic milieu, 150 hyperglycemia, increased non-enzymatic glycation of proteins, *de novo* synthesis of 151 diacylglycerol and subsequent activation of protein kinase C, increased intracellular 152 glucosamine production, and enhanced renal production of vasoactive agents (angiotensin II, 153 endothelins, thromboxane) have all been shown to increase the expression of TGF- $\beta$  in 154 cultured renal cells and animal models of diabetic nephropathy [50,52,54].

155 The TGF- $\beta$  level is elevated in the kidneys of insulin-dependent diabetic animals 156 during both early and late stages of disease [53,54]. Treatment of the streptozotocin (STZ)-157 diabetic rat with sufficient insulin to reduce hyperglycemia suppressed the enhanced 158 expression of TGF- $\beta$  and matrix components in the glomeruli. In the STZ-diabetic rat and 159 mouse, increased TGF- $\beta$ 1 expression in the renal cortex and glomeruli as well as up-160 regulation of the TGFBR2 mRNA and protein was noted early after the onset of diabetes

Review

161 [53].. The *db/db* mouse, a model of type 2 diabetes, characterized by hyperglycemia, obesity, 162 and insulin resistance, develops increased amounts of TGF-B1 localized in the glomerular compartments [55]. In contrast, the mRNA and protein levels of the TGFBR2 are 163 significantly up-regulated in both the glomerular and the tubulointerstitial compartments [55]. 164 The development of diabetic renal hypertrophy and glomerulosclerosis is likely caused 165 by heightened activity of the TGF-β system [56-63]. Short-term treatment of the STZ-diabetic 166 167 mouse with a neutralizing monoclonal antibody against all three isoforms of TGF- $\beta$  prevented 168 glomerular hypertrophy, reduced the increment in kidney weight by 50%, and significantly attenuated the increase in TGF- $\beta$ 1,  $\alpha$ 1(IV) collagen, and fibronectin mRNAs without 169 170 affecting glycemic control [56]. The results of this study suggested a cause-and-effect 171 relationship between the renal TGF- $\beta$  system and the development of early structural changes in diabetic nephropathy. Systemic anti-TGF- $\beta$  therapy for eight weeks prevented the 172 173 mesangial matrix expansion of diabetic glomerulosclerosis and, most importantly, preserved 174 kidney function, showing for the first time that neutralization of TGF-B activity prevents the progression of renal failure in diabetes [57]. However, the anti-TGF-β antibody did not reduce 175 albuminuria, which itself may promote the progression of renal insufficiency [57]. The 176 177 paradox of preserved renal function in view of persistent albuminuria may be explained by 178 postulating that the deleterious effects of proteinuria are themselves mediated by the TGF- $\beta$ 179 system [63-65].

In mouse mesangial and tubular cells, high glucose stimulates the transcription of fibronectin and, in addition, potentiates the transcriptional activation of fibronectin by TGF- $\beta$ 1 [58,59]. This particular effect of TGF- $\beta$ 1 appears to be mediated by Smad3, because overexpression of Smad3 alone was able to induce fibronectin promoter activity [66]. In conjunction with exogenous TGF- $\beta$ 1, Smad3 over-expression synergistically increased

Review

185 fibronectin expression, as if the extra Smad3 had increased the efficiency of TGF-β signaling [66]. Finally, transfection of a Smad3-dominant-negative construct inhibited TGF-β1 186 187 stimulated fibronectin promoter activity [67,68]. However, part of the TGF-B1-induced 188 fibronectin expression may be mediated in parallel by the p38MAPK pathway [68,69]. Finally, there is evidence that Smad3 is a central mediator in the TGF-B1-induced increase of 189 190 mRNA expression for  $\alpha 1(I)$  collagen [68,70]. TGF- $\beta$ -induced MAPK activation also leads to 191 N-terminal phosphorylation of p53 that enables its interaction with TGF-β-activated Smads [64], an indication for cross-talk between the various TGF- $\beta$  signaling pathways. 192

193 TGF- $\beta$ 1 may have additional effects besides the stimulation of extracellular matrix 194 production. In podocytes, TGF- $\beta$ 1 induces apoptosis through Smad7 by inhibiting nuclear 195 translocation of the cell survival factor NF- $\kappa$ B [70]. TGF- $\beta$ 1-mediated activation of Smad7 is 196 specific for podocytes and is not found in mesangial cells in a limited series of biopsies from 197 patients with diabetic nephropathy [64]. Since podocytes are terminally differentiated cells 198 unable to undergo cell division due to the up-regulation of the cell cycle inhibitory proteins 199 p57 and p27<sup>Kip1</sup>, apoptotic loss of cells was not replaced.

Studies performed in diabetic patients with various degrees of nephropathy also underline the importance of the renal TGF- $\beta$  system in disease development [71-73]. All three isoforms of TGF- $\beta$  are elevated in both the glomerular and the tubulointerstitial compartments of patients with established diabetic nephropathy [71,72]. Furthermore, glomerular TGF- $\beta$ 1 mRNA is markedly increased in biopsy specimens from patients with proven diabetic kidney disease. These investigations suggests that increased renal TGF- $\beta$  levels closely correlate with the degree of mesangial matrix expansion, interstitial fibrosis, and renal insufficiency.

Review

207 Another study, designed to assess renal production of TGF- $\beta$  [73] measured aortic, renal vein, and urinary levels of TGF- $\beta$  in 14 type 2 diabetic and 11 non-diabetic control 208 209 patients undergoing elective coronary artery catheterization [73]. Both groups were roughly 210 matched with regard to the range of renal function and the presence of hypertension and 211 proteinuria. Renal blood flow was measured to calculate the net mass balance across the 212 kidney. The gradient of TGF-\beta1 concentration across the renal vascular bed was negative in the non-diabetic patients indicating net renal extraction of TGF- $\beta$ 1, whereas the gradient was 213 214 positive in the diabetic patients indicating net renal production of TGF-β1. When the renal TGF-β1 mass balance was calculated, a similar pattern was observed with the non-diabetic 215 kidney removing approximately 3500 ng/min of TGF-β1 from the circulation, and the diabetic 216 217 kidney adding approximately 1000 ng/min of TGF-\beta1 [73]. In addition, the level of bioassayable TGF-B was increased four-fold in the urine of diabetic versus non-diabetic 218 219 patients. This was not simply a function of enhanced glomerular permeability to protein since 220 diabetic patients both with and without microalbuminuria displayed similarly high rates of urinary TGF-β excretion [73]. These results demonstrated that the kidneys of diabetic patients 221 222 overproduce TGF-B1 protein; further details, e. g., the exact contribution of the different renal cell types, need to be investigated. 223

224 An interesting *post-hoc* study assessed whether treatment with the angiotensin 225 converting enzyme inhibitor captopril would lower serum TGF- $\beta$ 1 levels in a small subset of 226 patients with diabetic nephropathy who had been enrolled in the Collaborative Study Group 227 [74,75]. After six months, the serum TGF- $\beta$ 1 level decreased significantly by 21% in the 228 captopril-treated group, whereas it increased slightly by 11% in the placebo-treated group 229 [75]. Interestingly, the captopril-treated patients with decreased serum TGF- $\beta$ 1 levels tended 230 to have better preserved renal function over the ensuing two-year period [75]. This association

Review

was even more pronounced in the subset of patients with an initial glomerular filtration rate of less than 75 ml/min. These results suggest that TGF- $\beta$ 1 plays a pivotal role in the progression of diabetic nephropathy and that angiotensin converting enzyme inhibitor therapy may protect the kidney by lowering TGF- $\beta$ 1 production.

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# 236 5. TGF-β-RELATED MOLECULES IN INTESTINAL INFLAMMATION – A DOUBLE237 SIDED SWORD

TGF- $\beta$  is constitutively expressed by epithelial cells, fibroblasts, and mononuclear cells in the 238 239 gastrointestinal tract [76]. Its critical role in intestinal homeostasis as a negative master regulator of inflammation is well-established [77,78] and indisputable. However, translation 240 241 of elegant mouse experiments into therapeutic interventions in humans requires a clearer understanding of TGF- $\beta$  activity in the human gut. Mice with global TGF- $\beta$  defects, such as 242 243 TGF-β-null mice or transgenic mice expressing a dominant negative TGFBR2 chain, are unresponsive to TGF-B1 signaling. The former die soon after birth due to systemic 244 245 inflammation, and the latter develop severe colonic and pulmonary inflammation [79,80]. These manifestations of global TGF-β1 defects are mirrored in mouse models of colitis in that 246 the secretion of TGF-β1 is consistently associated with either the protection from colitis or a 247 248 greatly diminished severity of colitis. This is seen both in the T<sub>H</sub>1 model of colitis induced by 249 the haptenating reagent trinitrobenzene sulfonic acid (TNBS), which mimics Crohn's disease (CD), or the T<sub>H</sub>2 model of colitis induced by the haptenating agent oxazolone, which mimics 250 251 ulcerative colitis (UC) [81,82]. In addition, it is seen in the colitis of SCID or RAG2-deficient mice receiving CD45RB<sup>high</sup> (naive) T cells in which the protective effect of the cotransfer of 252 CD45RB<sup>low</sup> T (memory) cells is abolished by concomitant administration of a neutralizing 253 254 TGF-β1 antibody [83]. These and other studies quite conclusively establish that TGF-β1 plays

Review

an essential, regulatory role in the control of colitis. On the other hand, in mice TGF- $\beta$ 1 in combination with IL-6 induces a strong pro-inflammatory T<sub>H</sub>17 cell differentiation [84-86]. Notably, in humans TGF- $\beta$ 1 does not have a direct effect on the development of human T<sub>H</sub>17 cells, but it can indirectly favour the development of these cells by suppressing the expression of T-bet and selectively inhibiting the expansion of IFN- $\gamma$ -producing T cells [87-89].

260 The important role of Smad3 as an essential mediator of TGF-B1-induced antiinflammatory and suppressive activities at the mucosal level emerges from studies in mice 261 262 with targeted deletion of the Smad3 gene. The animals are viable, but die from defects in mucosal immunity at 1–6 months of age. Mutant mice show diminished cell responsiveness to 263 TGF-\beta1, massive infiltration of T cells, and multiple pyogenic abscesses in the stomach and 264 intestine [87,90]. When Smad signaling was studied in normal human gut mucosa, whole 265 266 biopsies or isolated lamina propria mononuclear cells, a basal level of phosphorylated (phospho-) Smad3 was observed which was rapidly upregulated by the addition of exogenous 267 268 TGF-*β*1 [91].

269 TGF-β has been also implicated as a key inducer of epithelial-mesenchymal transition (EMT) [92-97]. Amongst others, EMT is an essential component of tissue remodeling and 270 271 wound repair (reviewed in [98,99]) and fibrosis (reviewed in [100]). During this transition, 272 the epithelial phenotype, characterized by strong cell-cell junctions and polarity, is replaced 273 by a mesenchymal phenotype, with reduced cell-cell interactions, a fibroblastic morphology 274 and increased motility. TGF- $\beta$  stimulates the proliferation of many cell types, particularly 275 those of mesenchymal origin, and it is also a potent inhibitor of epithelial cell proliferation. 276 EMT in response to TGF-β1 and in fibrosis is mediated predominantly via Smad-dependent (mainly Smad3) pathways [101,102]. A loss of Smad3 in mice blocked both morphological 277

Review

changes of lens epithelium to a mesenchymal phenotype and expression of EMT markers in
response to injury *in vivo* or to exposure to exogenous TGF-β in organ culture [101].

CD is a chronic, progressive disease of the gastrointestinal tract with an unknown 280 281 etiology. It is characterized by transmural inflammation of all layers of the bowel wall. The 282 formation of stenoses and strictures is common in this disease, which causes abdominal pain, anorexia, and weight loss. Approximately 50% of CD patients undergo surgery for this type 283 284 of complication during a 10-year course; however, the recurrence rate after surgery is high. In contrast, UC rarely causes intestinal stenosis. Cytokines released from inflammatory cells 285 286 have long been implicated in the pathogenesis of intestinal fibrosis. TGF-β/Smad signaling 287 plays an important role in CD [103-105]. The transmural infiltrate of CD is responsible for 288 initiating and maintaining a series of connective tissue changes not only involving the 289 mucosa, but also the submucosa and muscularis mucosae and muscularis propria, where a 290 marked increase of collagen type I, III, and V mRNA is observed [106,107]. TGF-β has been 291 identified as one of the central growth factors/cytokines that specifically induces a fibrotic 292 response after inflammatory injury in the intestinal tract. In CD, there is a marked 293 overexpression of TGF-β1 and TGFBRs in the colonic mucosa [76,108]. Fibrosis in CD can therefore be interpreted as an aberrant healing response to mucosal injury [109]. In addition, 294 295 TGF- $\beta$  appears to be involved in intestinal fibrosis in other enteropathies, such as radiation 296 enteritis, collageneous colitis, and intestinal graft-versus host disease [110-112]. Both TGF-β 297 and its receptors are overexpressed in the intestine of patients with CD [113]. Intestinal 298 fibroblast expression of TGF-β isoforms varies according to the nature of tissue. Fibroblasts 299 from normal and inflamed mucosa both express the TGF-β1 and TGF-β3 isoforms, while those from fibrotic tissue show reduced expression of TGF- $\beta$ 3, but enhanced expression of 300 301 TGF-B2 and TGF-B1 [114]. This is remarkable, since the TGF-B1 and TGF-B2 isoforms have

Review

302 been specifically implicated in pathogenic fibrosis, while TGF-β3 appears to have antifibrotic properties [115]. Monteleone and colleagues have provided insight into the failure of TGF- $\beta$ 303 304 down-regulation in CD. Despite the abundant expression of TGF- $\beta$  in the mucosa of patients 305 with CD, phospho-Smad3 is diminished in the mucosa compared to control mucosal samples, as is the complex of Smad3 with Smad4. This may be due to the induction and overexpression 306 307 of Smad7 in the mucosa of patients with CD and UCs [116]. However, upregulation of Smad7 308 is not specific for inflammatory bowel disease (IBD), but also occurs in Helicobacter pylori-309 induced gastritis [117]. In addition, mucosal T cells in both whole tissue and isolated cells 310 show defective TGF-B1 signaling as measured by reduced immuno-reactivity against 311 phospho-Smad3 [117]. Specific anti-sense oligonucleotides for Smad7 reduce expression of 312 Smad7 in cells isolated from IBD patients which then become responsive to exogenous TGFβ1. TGF-β1 cannot inhibit pro-inflammatory cytokine production in isolated lamina propria 313 mononuclear cells from CD patients, but inhibition of Smad7 with anti-sense oligonucleotides 314 restores TGF-B1 signaling and allows TGF-B1 to inhibit cytokine production. In inflamed 315 316 mucosal tissue explants from CD patients, inhibition of Smad7 also restores phospho-Smad3 317 and decreases pro-inflammatory cytokine production, an effect which is partially blocked by anti-TGF-\beta1. The extension of these studies examined the interactions between Smad 318 319 signaling and NF-κB activation in inflamed gut: While TGF-β1 is a potent inhibitor of TNF-320  $\alpha$ -induced NF- $\kappa$ B activation in normal gut, it has no activity in inflamed gut. This can be 321 attributed to over-expression of Smad7, since treatment of cells from inflamed gut with antisense to Smad7 allows TGF-β1 to rapidly down-regulate NF-κB activation [117]. 322

323 If it becomes possible to specifically inhibit Smad7, endogenous TGF- $\beta$ 1 in the 324 inflamed gut may negatively regulate pro-inflammatory cytokine production and NF- $\kappa$ B 325 activation, the major components of the immune overactivity which drives tissue injury in

Review

326 IBD. At the same time, however, it is important to discover the factors which control Smad7 327 expression in the inflamed gut. Furthermore, cell-specific expression of Smad7 will be 328 important because TGF-β1 has different effects on different cell types. Thus, while blocking 329 Smad7 will allow TGF-B1 to reduce pro-inflammatory cytokine production by T cells and 330 macrophages, it may allow TGF-B1 to increase collagen production in myofibroblasts, 331 resulting in fibrosis. However, at the moment the relative importance of the known inducers of Smad7 in the gut, such as IFN- $\gamma$  or TNF- $\alpha$ , or even whether TGF- $\beta$ 1 itself induces Smad7 332 333 in a negative regulatory loop, is still unclear.

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#### 335 6. TGF-β-RELATED MOLECULES IN RADIATION-INDUCED FIBROSIS

336 TGF-\beta1 levels are increased in irradiated mouse skin [118,119] and decrease slowly after irradiation in both pig and human skin [120,121]. Following microvascular hard or soft tissue 337 338 transfer, TGF-\beta1 is again upregulated in a biphasic manner. The first expression peak on day 339 3 post operation is due to enhanced activation of latent TGF-B1 by extracellular enzymes while the second between day 14 and 28 after surgery is a result of *de novo* synthesis [122]. 340 341 Its most important signaling receptor TGFBR2 is upregulated in irradiated graft beds as well 342 [123]. Signaling leads to increased nucleoplasmatic shuttling of active Smad2/3 and induction of TGF- $\beta$ 1 target genes in fibrotic healing, which is mainly due to decrease in cytoplasmatic 343 344 levels of the inhibitory Smad7 [124].

As a consequence, the extracellular matrix is qualitatively and quantitatively altered [125]. Prolyl-hydroxyprolinase- $\beta$  overexpression [126] promotes synthesis of collagen I, III and IV [124], while repression of degrading enzymes, such as MMP-1 and induction of tissue inhibitors [127] suppresses the degrading pathways. Moreover, integrin surface receptors, such as  $\alpha 2\beta 1$  integrin are up-regulated as well and modulate transmission of tensile forces

Review

350 [128]. In the presence of such forces fibroblasts differentiate into myofibroblasts resulting in351 constrictive fibrosis [129].

Irradiation-induced fibrosis and damage to the microvasculature lead to wound healing disorders following surgery in previously irradiated areas. Such disorders are dependent, in part, on the radiation dosage and the timing of surgery after irradiation [130,131] and reduce the success rate of free flaps to 90% compared with 94% in non-irradiated graft beds [132].

Taking the central role of TGF-B1 in radiation-impaired wound healing into account, 356 the question of whether TGF-\beta1-levels differ in the healthy tissue between different patients 357 is of utmost importance. It has been demonstrated that patients with an increased TGF-B1 358 plasma level exhibit an increased risk of developing skin fibrosis following irradiation [133]. 359 To find a particular predictor which sufficiently corresponds with the frequency to develop 360 361 wound healing complications following surgery in previously irradiated graft beds would give 362 a large clinical impact on planning individual treatment protocols. The availability of reliable markers may eventually allow the prediction of outcome prior to commencement of treatment, 363 364 and thus allow modification of combined protocols to minimize late adverse effects without 365 compromising tumor control.

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#### **367 7. TGF-β-RELATED MOLECULES IN MYOCARDITIS**

Heart fibrosis is a hallmark feature of the chronic stage of viral myocarditis [134,135]. Human pathogenic coxsackievirus B3 (CVB3) is considered the most frequent viral cause of chronic myocarditis in men [136]. Clinical manifestations of acute myocarditis vary from flu-like symptoms to the fulminant fatal forms. Frequently, acute myocarditis, with distinct onset, follows a monophasic clinical course, and the majority of patients recover spontaneously after several days of congestive heart failure. Some patients progress into subacute or chronic

Review

forms, which ultimately lead to death. The molecular mechanisms underlying fibrosisdevelopment in chronic myocarditis are currently not well understood.

Like humans, mice develop a marked age-related susceptibility to CVB infections [137]. The myocardial lesions in mice closely resemble those seen in human disease [138]; therefore, experimental murine models of coxsackievirus-induced myocarditis have been developed to investigate the pathogenesis of this disease. Although chronic inflammation is characteristic for the human disease as well as for our mouse model, fibrosis is more prevalent in the latter.

Excessive fibrosis, as it occurs under conditions of chronic myocarditis, can be 382 classified as either replacement fibrosis, when functional tissue is replaced by connective 383 384 tissue, or as reactive fibrosis, which is part of an adaptive process [139]. In addition to collagen, tenascin C, and fibronectin, splice variants of these molecules are often part of the 385 386 fibrotic tissue [140,141]. Various cytokines and growth factors are believed to contribute to 387 the induction of fibrosis, including TGF- $\beta$  [142], IL-1, [143], TNF- $\alpha$  [144,145], and PDGFs [146.147]. For example, persistent expression of cytokines in the chronic stage of CVB3-388 induced myocarditis has been described for various mouse models [148-150], as well as for 389 390 human dilatative cardiomyopathy [151]. New observations suggest that sustained pro-391 inflammatory signaling is associated with a pro-fibrotic phenotype based on TGF- $\beta$ -mediated 392 signaling [152].

For fibrogenesis in the heart, members of the PDGF family are apparently important mediators. Transgenic overexpression of PDGF-C and PDGF-D, two more recently discovered PDGF isoforms [153], in the heart leads to massive cardiac fibrosis [146,147]. Therefore, the importance of PDGF for the pathology of chronic myocarditis was investigated in mice with CVB3-induced myocarditis. Interestingly, all analysed isoforms of PDGF-A, -B, and -C were upregulated in close correlation with the inflammatory process. High levels of

Review

the growth factors persisted only in MHC class II knockout mice, which develop a chronic
myocarditis upon CVB3 infection, whereas immunocompetent C57BL/6 wild-type mice
exhibit only an acute, completely reversible myocarditis [154,155].

Furthermore, it has been shown that the PDGF-receptor (PDGFR) blocker Imatinib 402 403 inhibits activation of resident PDGFR, and attenuates fibrosis in this mouse model 404 significantly [156]. These data strongly suggest that elevation of PDGF levels and subsequent activation of PDGFR causally contribute to the type of cardiac fibrosis which occurs in this 405 406 model. Efficacy of Imatinib for attenuation of fibrosis has recently been reported also for 407 other organs, i.e., liver, joints, and kidney [157-159]. It can therefore be assumed that Imatinib-sensitive tyrosine kinases play a more general role in fibrogenesis. In addition to the 408 409 PDGFR [157,160], the Abelson tyrosine kinase, a mediator of TGF-β-signaling (c-Abl) [161], 410 has also been proposed as a relevant target for Imatinib in the inhibition of fibrogenesis [159,162]. While our data [156], and data of others [146,147] strongly suggest a causal 411 412 involvement of the PDGFR in fibrogenesis, they do not exclude that c-Abl activity is also involved in fibrogenetic signalling. It could function downstream of TGFBRs, but also 413 partially mediate signalling of the activated PDGFR [163]. It is known that TGF-β can drive 414 cardiac fibrosis when overexpressed in the mouse heart [164] and the use of genetic mouse 415 416 models to understand the role of TGF- $\beta$  signalling in the heart is reviewed in [165]. But the 417 relative contribution of the different TGF- $\beta$ -mediated signalling mechanisms to fibrosis in our 418 model of CVB3-induced chronic myocarditis remains to be fully elucidated.

419

#### 420 8. DIFFERENCES AND SIMILARITIES OF TGF-β IN DIFFERENT ORGANS

421 As presented in Table 1, numerous molecules have similar expression patterns in the diseases 422 mentioned in this review. Due to limited information from the human system, some data were 423 replaced by results derived from the respective animal model (fibrosis following irradiation).

Review

424 TGF-B1 is elevated in most pathologies in its active or latent form and shows similarities with the isoform TGF- $\beta$ 2 in most cases. In contrast, the expression of TGF- $\beta$ 3 425 426 varies from down-regulation during wound healing and CD, abundance without regulation in 427 rheumatoid arthritis and UC, to up-regulation during diabetic nephropathy. If determined, the 428 expression of TGFBR2 is often enhanced during disease. The widespread appearance of the 429 term "n.d." points out the urgent need for further investigation of the expression and the 430 effects of TGF-B-related molecules in human diseases associated with fibrosis, particularly at 431 the stage of signaling and transcriptional regulation.

432

#### 433 **9. THERAPEUTIC STRATEGIES**

434 As either increased or decreased activity of the TGF- $\beta$  pathway has been implicated in the 435 pathogenesis of different human diseases, methods for increasing or decreasing signaling 436 through these pathways are required [166]. There are some tools for enhancing TGF- $\beta$ 437 signals, e. g., direct administration of the ligand, usage of agonists, and increased expression 438 of receptors or decreased expression of signaling antagonists.

On the other hand, there are different ways to inhibit TGF-β signaling, e. g.,
administration of neutralizing antibodies, application of soluble receptors, usage of antisense
nucleotides, and chemically synthesized inhibitors of the receptor serine/threonine kinases.

442 Regarding TGF-β inhibition, some clinical trials have been performed with 443 neutralizing antibodies, especially in fibrotic diseases, including a TGF-β2 neutralizing 444 antibody (lerdelimumab) which effectively decreased the amount of scarring after glaucoma 445 surgery [167]. A TGF-β1 neutralizing antibody (CAT-192, metelimumab) has been 446 administered intravenously to patients with systemic sclerosis, which causes scarring in skin 447 and internal organs, however, without any evidence of efficacy and with more adverse events

Review

and serious adverse events in *verum* than in placebo patients [168]. This raises the question of whether broader or even complete blockade of the TGF- $\beta$  axis will be safe or rather associated with substantial toxicity [168]. Despite these concerns, a pan-TGF- $\beta$  (GC-1008) neutralizing antibody has recently being administered to patients with idiopathic pulmonary fibrosis in a phase I clinical trial for safety evaluation [169] and is being administered to patients with focal segmental glomerulosclerosis [170], renal cell carcinoma, and malignant melanoma [171]; however, safety and efficacy data from these studies are not yet available.

Similar to neutralizing antibodies, soluble TGF- $\beta$  superfamily receptors abrogate signaling at the ligand level by binding the ligand and preventing it from binding to its cell surface receptors. Due to the lack of studies in humans, only data from animal models are available. For example, soluble TGFBR3 has demonstrated efficacy against renal damage progression associated with diabetes in mice [172]. Similarly, soluble TGFBR2 has anti-cancer effects in mice, as it suppresses the growth and metastasis of pancreatic cancer cells [173] and also inhibits breast cancer cell growth, migration, invasion, and metastasis [174].

Using anti-sense oligonucleotides to reduce the expression of TGF-β superfamily members is a relatively new therapeutic tool that has been already successful applied in clinical trials for cancer treatment [175,176]. Also, small molecule inhibitors have been introduced to block TGF-β signaling. The TGFBR1-inhibitor Ly573636, which blocks intrinsic receptor-kinase activity, is currently being assessed in patients with certain cancers (see [176]), whereas other TGFBR1-inhibitors have shown to be efficient in mouse tumor models [177].

468

#### 469 **10. CONCLUSIONS**

470 Due to the central role of TGF- $\beta$  in severe fibrotic diseases (with similarities and 471 dissimilarities among organs/diseases) it is an attractive therapeutic target, as already shown 472 in several clinical trials (see above).

Review

473 The strongly bifunctional role of TGF- $\beta$ , however (pro-fibrotic, but anti-inflammatory), 474 requires great care for the application of TGF-β-directed treatments. Future strategies will 475 therefore have to focus on developing suitable tools to address this bifunctionality such as: 476 1) locally or regionally restricted administration of agonists or antagonists (in particular, 477 broad TGF-B blockade by agents such as TGF-B antibodies, TGF-B receptors (soluble/anti-478 sense), latency-associated peptide or Smad7; 2) phase-dependent application in those periods of disease dominated by the critical pathogenetic features of TGF-B; and 3) development of 479 480 local or systemic biomarkers indicative of a future favorable response. The systemic applicability of broad TGF- $\beta$  blockade will have to await the safety date from ongoing trials. 481

482

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Review

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Review

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41

Organ	Irradiated skin	Heart	Synovial membrane	•	Gut	, , , , , , , , , , , , , , , , , , ,	Kidney
Disease	Wound healing	Fibrotic heart diseases*	RA	CD inflamed	CD fibrotic	UC	Diabetic nephropathy
Molecule					$\mathbf{O}$		
THBS1	n.d.	↑[178,179]	[40,180]	↓[181]	n.d.	↔[181]	↑[182]
Latent- TGF-β	<b>↑</b> [122]	n.d.	↔[183], ↑[39]	n.d.	n.d.	n.d.	<b>↑</b> [182]
TGF-β1	<b>†</b> [122]	<b>†</b> [184,185]	↔[35,36,40,183], ↑[37,38]	↑[76,108,114]	↑[108,114]	↑[76,108,114]	↔[186], <b>†</b> [53,72]
TGF-β2	↑[122]	↔[185]	↔[35,183]	<b>↑</b> [114]	<b>†</b> [114]	↔[114]	<b>†</b> [72]
TGF-β3	↓[187]	<b>†</b> [185]	↔[35,183]	↓[114]	↓[114]	↔[114]	↔[186], ↑[72]
TGFBR1	n.d.	↓[184]	<b>↑</b> [40]	↔[113]	n.d.	n.d.	n.d.
TGFBR2	<b>†</b> [188]	↔[184]	↑[35,183]	↑[113]	n.d.	n.d.	n.d.

Table 1. Expression of TGF-β related proteins in human disease compared to controls (normal or inflammatory)

 $\uparrow$  increased,  $\downarrow$  decreased,  $\leftrightarrow$  no change, **n.d.** not determined; \*mostly following myocardial infarction

#### **FIGURE LEGENDS**

**Figure 1:** TGF-β1 induces different, but overlapping response in different organ systems.

**Figure 2:** Molecules of the TGF- $\beta$ -pathway ranging from the release of TGF- $\beta$ , binding of receptors, signaling through Smads, FAK and MAPK to its entry into the nucleus and the regulation of the transcriptional activity (adapted from [40]).



