# **Chapter 11 How Tubular Epithelial Cell Injury Contributes to Renal Fibrosis**



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**Abstract** The renal tubules are the major component of the kidney and are vulnerable to a variety of injuries including ischemia, proteinuria, toxins, and metabolic disorders. It has long been believed that tubules are the victim of injury. In this review, we shift this concept to renal tubules as a driving force in the progression of kidney disease. In response to injury, tubular epithelial cells (TECs) can synthesize and secrete varieties of bioactive molecules that drive interstitial inflammation and fibrosis. Innate immune-sensing receptors on the TECs also aggravate immune responses. Necroinflammation, an auto-amplification loop between tubular cell death and interstitial inflammation, leads to the exacerbation of renal injury. Furthermore, TECs also play an active role in progressive renal injury via mechanisms associated with the conversion into collagen-producing fibroblast phenotype, cell cycle arrest at both G1/S and G2/M checkpoints, and metabolic disorder. Thus, a better understanding the mechanisms by which tubular injury drives AKI and CKD is necessary for the development of therapeutics to halt the progression of CKD.

**Keywords** Tubular epithelial cells · Renal fibrosis · Renal inflammation · Chronic kidney disease · Acute kidney injury

## 11.1 Introduction

The renal tubules and tubulointerstitium make up a significant portion of the kidney and are the major sites in response to injuries. Increasing evidence shows that tubular epithelial cells (TECs) play diverse roles in renal repair or progression to chronic kidney disease (CKD). The innate immune characteristics demonstrate TECs as immune responders to a wide range of insults, with the consequent production and release of bioactive molecules that drive interstitial inflammation and fibrosis. Accumulating evidence shows that renal function decline correlates better with tubu-

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lointerstitial damage than that of glomerular injury (Risdon et al. 1968; Bohle et al. 1979; Mackensen-Haen et al. 1981). Maladaptive repair of injured tubules after acute kidney injury (AKI) also leads to the progression of CKD (Ferenbach and Bonventre 2015; Venkatachalam et al. 2015). Thus, TECs should be regarded not only as victims in the context of kidney disease but also as key inflammatory and fibrogenic cells that drive the progression from acute to chronic kidney disease, which will be the focus in this review. It should be noted that due to the length limitations, this review focuses on the emerging mechanisms by which TECs play a driving role in renal injury, whereas other potentially important factors/pathways not directly related to this topic are not discussed here.

# 11.2 Tubule-Derived Factors Associated with Tubulointerstitial Inflammation and Fibrosis

In response to stress and injury, TECs can be transformed into a secretory phenotype, with the consequent production and release of various bioactive molecules to favor the recruitment of inflammatory cells, the activation of fibroblasts, and the loss of endothelial cells, which eventually drive tubulointerstitial inflammation and fibrosis.

#### 11.2.1 Pro-inflammatory Cytokines

In response to renal injury, TECs become activated and can actually facilitate the inflammatory response through induction of a variety of pro-inflammatory cytokines (e.g., interleukin, tumor necrosis factor, colony stimulating factor, and growth factor). After the first report of TNF- $\alpha$  and IL-6 produced by TEC following IL-1 stimulation (Jevnikar et al. 1991; Yard et al. 1992), a variety of cytokines produced by activated TECs are known including IL-1 $\beta$ , IL-18, IL-34, IL-16, CSF-1, TWEAK, VEGF, CTGF, and so on. In TECs, NLPR3 inflammasome activation causes the release of mature IL-1 $\beta$  and IL-18 during kidney injury (Leemans et al. 2014; Anders 2016). Observations by Menke and Wang showed that expression of CSF-1 is upregulated in TECs during kidney injury and may be responsible for the polarization of renal macrophages and recovery from AKI (Menke et al. 2009; Wang et al. 2015b; Huen et al. 2015). Baek et al. identified that TEC-derived IL-34 plays a key role in recruiting kidney macrophages and causing persistent kidney injury and the development of CKD (Baek et al. 2015).

#### 11.2.2 Chemokines

Chemokines are a family of small molecular cytokines with chemotactic activity. TECs are rich sources of CCL subfamily (including MCP-1/CCL2, RANTES/CCL5, and MIP-1/CCL3) and CX3CL subfamily (fractalkine/CX3CL1), which have specific effects on monocytes and monocyte-derived lineages (Chung and Lan 2011). MCP-1/CCL2 is one of the most widely studied chemokines in AKI and CKD (Wang et al. 1997, 2000; Furuichi et al. 2003). CXCL8/IL-8 and CLCL12/SDF-1 are overexpressed after TECs injury and are chemotactic for a number of leukocyte populations (Li and Nord 2002, 2009; Zuk et al. 2014). A recent study reported that CXCL5 is increased in tubular cells following the induction of nephrotoxic nephritis and is responsible for the recruitment of neutrophils during acute renal tissue injury (Disteldorf et al. 2015).

#### 11.2.3 ROS

It has become clear that oxidative stress contributes to CKD progression via myriad effects (Small et al. 2012; Massy et al. 2009; Nie and Hou 2012). Oxidative stress implies an increased production of reactive oxygen species (ROS), including superoxide anion  $(O_2^-)$ , hydrogen peroxide $(H_2O_2)$ , and hydroxyl anion  $(OH^-)$ . In response to multiple stimuli and agonists, mitochondrial dysfunction and NADPH oxidases have been recognized as the major contributors to ROS generation in TECs (Tang and Lai 2012; Sedeek et al. 2013). For instance, Ang II leads to tubular hypertrophy and TECs apoptosis via ROS-dependent mechanisms (Wolf et al. 2001; Leung et al. 2011). Albumin acts through epidermal growth factor receptor to stimulate NADPH oxidase to activation of ERK1/ERK2 pathway (Reich et al. 2005). In addition, albumin has also been shown to stimulate tubulointerstitial inflammation via the mROS-mediated activation of NIrp3 inflammasome (Liu et al. 2014).

## 11.2.4 CRP

C-reactive protein (CRP) is an acute-phase protein, which is rapidly synthesized by the liver in response to infection, inflammation, and tissue damage. Besides its use as a biomarker of inflammation, CRP has been recognized as a pathogenic mediator in diabetic kidney disease (Liu et al. 2011), obstructive nephropathy (Li et al. 2011), and AKI (Pegues et al. 2013; Tang et al. 2014; Lai et al. 2016). CRP is also inducible by high glucose in human TECs and promotes renal inflammation and fibrosis through activation of TGF- $\beta$ /SMAD and NF- $\kappa$ B signaling pathways under diabetic conditions and unilateral ureteral obstructive nephropathy (Liu et al. 2011). Recent

studies have demonstrated that CRP promotes AKI by causing TEC G1 cell-cycle arrest via CD32-Smad3–dependent p27-driven inhibition of the cyclin-dependent kinase 2/cyclin E mechanism (Tang et al. 2014; Lai et al. 2016).

#### 11.2.5 Growth Factors

Transforming growth factor (TGF- $\beta$ ), connective tissue growth factor (CTGF), platelet-derived growth factor (PDGF), and vascular endothelial growth factor (VEGF) are the best-described growth factors involved in the tubulointerstitial fibrosis, of which TGF-B derived from injured TECs has long been considered as one of the most important pro-fibrotic growth factors (Yang et al. 2010; Lan et al. 2012; Geng et al. 2012; Meng et al. 2016; Wu et al. 2013; Grande et al. 2015). Both Ang II exposure and Snail 1 overexpression can induce TGF-B1 production by TECs (Grande et al. 2015; Macconi et al. 2014). After the hypoxic injury, TECs undergo cell cycle arrest. Particularly when cells are under arrest in the G2/M phase, these cells produce large amounts of TGF-β1 (Yang et al. 2010). Increased TGF-β production by TECs can promote TIF through paracrine signaling to activate adjacent fibroblasts and pericytes transforming into myofibroblast-type cells (Wu et al. 2013; Ignotz et al. 1987; Roberts et al. 1986). Interestingly, TEC is also a target of TGF-β1. TGFβ1 can induce cultured TECs to differentiate into cells with distinct myofibroblast morphology and marked upregulation of collagen production (Zeisberg et al. 2003; Fan et al. 1999). Meanwhile, autocrine TGF- $\beta$  signaling increases TEC production of PDGF- $\beta$  and CTGF/CCN2 that can signal on neighboring fibroblasts (Geng et al. 2012).

# 11.2.6 Intrarenal RAS

Renal local renin–angiotensin system (RAS) activation plays a pivotal role in the progression of CKD. Blockade of the RAS has become the mainstay therapy for the preservation of CKD (Hou et al. 2006). Ang II is the major bioactive product of the RAS driving renal fibrosis. There is substantial evidence that the major fraction of Ang II present in renal tissues is generated from angiotensinogen (AGT) and subsequently delivered to the kidney, as well as from AGT produced by the PTECs. Ang I delivered to the kidney can also be converted to Ang II (Kobori et al. 2007). Renin mRNA and renin-like activity have been observed in cultured PTECs (Henrich et al. 1996). The brush border membrane of proximal human kidney tubules also expresses abundant levels of angiotensin-converting enzyme (ACE) mRNA (Sibony et al. 1993) and protein (Vío and Jeanneret 2003). ACE has been detected in the proximal and distal tubular fluids (Casarini et al. 1997). Therefore, all of the major components required to generate Ang II are expressed within the renal tubules (Urushihara and Kagami 2017; Kobori and Urushihara 2013). And the upregulation of these RAS

components may be in a Wnt/ $\beta$ -catenin-dependent manner (Zhou et al. 2015). Studies have demonstrated that Ang II stimulates TGF- $\beta$  expression in cultured murine PTECs and upregulates specific receptors for TGF- $\beta$  to further enhance its proinflammatory and fibrogenic action (Wolf et al. 1993, 1999; Liu et al. 2009). Ang II is also able to induce CTGF to mediate the fibrotic phenotype change (Liu et al. 2006, 2007; Chen et al. 2006). Moreover, we also proposed the interaction of Ang II and inflammation might be the critical node in the pathogenic tubuloglomerular feedback loop (Zhang and Liu 2011).

#### 11.2.7 Wnt and Hh

The Wnt pathway has been implicated in the epithelial repair process, but an abundance of evidence also supports Wnt/ $\beta$ -catenin signaling in tubulointerstitial fibrosis (Kang et al. 2016; Kawakami et al. 2013; Tan et al. 2016; Edeling et al. 2016). There are 19 Wnt ligands, and all of them can bind to Frizzled and LRP5/6 receptors at the cell surface, leading to canonical signaling through  $\beta$ -catenin activation (Tan et al. 2014). Wnt proteins and receptors are upregulated after renal injury, and  $\beta$ -catenin activity appears to be increased in injured TECs (Zhou et al. 2012; He et al. 2009). Overexpression of Wnt1 in proximal tubules is sufficient to cause TIF and activate myofibroblasts to produce ECM, suggesting paracrine signaling (Maarouf et al. 2016). It is likely that injured TECs can produce Wnt ligands which then activate the neighboring fibroblasts to promote TIF (Gewin et al. 2017).

Hedgehog (Hh) signaling is a key mammalian developmental pathway and regulates tissue patterning, cell growth, and differentiation (Cain and Rosenblum 2011; Mao et al. 2010). Of three Hh ligands (Sonic Hh [Shh], Desert Hh [Dhh], and Indian Hh [Ihh]), Shh is well studied. Lineage tracing studies indicate that Shh and Ihh expression are upregulated in renal tubules after UUO (Fabian et al. 2012; Ding et al. 2012; Zhou et al. 2014). Interstitial fibroblasts and pericytes are the cells supposed to respond to these ligands. Shh induces fibroblast activation, manifested as an expression of  $\alpha$ -SMA, fibronectin, collagen, and desmin (Ding et al. 2012).

#### 11.2.8 Exosomes

Exosomes are small (30–100 nm in diameter), lipid bilayer membrane vesicles of endocytic origin. They can shuttle bioactive molecules including proteins, lipids, DNA, mRNA, and microRNAs (Zhang et al. 2016; Morrison et al. 2016). In kidneys, renal exosomes are produced and secreted by kidney cells which have been implicated in renal function and diseases via cell–cell communication (Krause et al. 2015). It is known that injured TECs can release exosomes containing TGF- $\beta$  mRNA to activate fibroblasts, contributing to the development of renal fibrosis in post-AKI kidneys (Borges et al. 2013). We recently demonstrated that in the setting of pro-

teinuric kidney disease, albumin triggered TECs to release exosomes packaged with CCL-2 mRNA, which was delivered to macrophages and led to interstitial inflammation (Lv et al. 2018). In addition, we also found that the HIF-1 $\alpha$ -dependent release of miRNA-23a-enriched exosomes from hypoxic TECs activates macrophages to promote tubulointerstitial inflammation (Li et al. 2019).

# 11.3 Abnormal Repair of TECs: The Central Pathology Linking AKI to CKD

An increasing number of epidemiological studies have suggested that incomplete recovery from AKI can lead to progressive CKD (Waikar and Winkelmayer 2009; Okusa et al. 2009; Hsu 2012; Coca et al. 2012). This is supported by the finding that the incomplete tubular repair is tightly associated with persistent tubulointerstitial inflammation, proliferation of fibroblasts, and excessive deposition of extracellular matrix (Yang et al. 2010; Grgic et al. 2012). A number of recent studies have also demonstrated that tubule selective injury is sufficient to drive fibrosis, inflammation, and capillary rarefaction, which is making it to be a central link between AKI and CKD (Grgic et al. 2012; Takaori et al. 2016; Zhou et al. 2014; Humphreys et al. 2013).

In general, primary tubular injuries have a very good chance of recovery. The surviving cells dedifferentiate, migrate along the basement membrane, proliferate to restore cell number, and then restore the functional integrity of the nephron (Thadhani et al. 1996). However, some damaged TECs become atrophic or gain the fibrotic phenotype after AKI. This may be tightly associated with the abnormal repair process in response to the injuries. For example, in the initial repair phase after injury, TECs may become arrested in the G2/M phase, which may be associated with the activation of JNK signaling production of pro-fibrotic cytokine (Yang et al. 2010; Ferenbach and Bonventre 2015). This is confirmed by the ability of using pharmacological inhibition of G2/M-arrested cells with histone deacetylase inhibitors or p53 inhibition to block the process of fibrosis (Cianciolo Cosentino et al. 2013; Zhou et al. 2010). Recent studies also found that aging can sensitize TECs to be arrested at the cell cycle G2/M in response to cell stress and DNA damage, which provides a potential explanation for the increased risk of CKD progression after AKI in the elderly (Ferenbach and Bonventre 2015; Verzola et al. 2008; Liu et al. 2012; Yang and Fogo 2010). In addition, CRP-induced G1/S cell cycle arrest may also contribute to progressive TIF via the Smad3-p21/p27-dependent mechanism (Tang et al. 2014; Lai et al. 2016).

Wnt/ $\beta$ -catenin signaling is a pathway involving the recovery from AKI. In the acute phase of injury, Wnt/ $\beta$ -catenin is likely to be protective. In both IRI and folic acid nephropathy, tubule-specific ablation of  $\beta$ -catenin has been shown to aggravate kidney injury by increasing TEC apoptosis (Zhou et al. 2012). Activation of Wnt-4/ $\beta$ -catenin signaling allows entry into the cell cycle via the upregulation of cyclin D1 and cyclin A, two of the most crucial proteins in regulating cell proliferation and cell

cycle progression (Terada et al. 2003; Angers and Moon 2009; Clevers and Nusse 2012). Therefore, an early and appropriate activation of Wnt/ $\beta$ -catenin signaling is required for minimizing the initial renal damages after AKI (Zhou et al. 2016). However, persistent activation of Wnt signaling has a decisive role in driving AKI to CKD progression because sustained Wnt signaling causes uncontrolled fibroblast activation, RAS activation, inflammation, and excessive deposition of ECM (Tan et al. 2014; Xiao et al. 2016). It is well known that tissue injury and inflammation are closely linked and interact with each other (Wallach et al. 2014). While initial renal inflammation may be protective in favoring the repair process in response to AKI, unresolved and prolonged renal inflammation may cause progressive renal fibrosis. Thus, better understanding the mechanisms by which tubular injury drives interstitial inflammation and renal fibrosis is of paramount importance.

# 11.4 Emerging Mechanisms of Tubule Injury Driving the Progression of CKD

## 11.4.1 Inflammation: Innate Immune-Sensing Receptors in TECs Activation

Uncontrolled or excessive inflammatory responses can lead to progressive kidney injury. In view of the immune characteristics of TECs, substantial information indicates that Toll-like receptors (TLRs), Nod-like receptors (NLRs) and the NACHT, LRR, and PYD domain-containing protein 3 (NLRP3) inflammasome have important roles in the pathogenesis of multiple renal disorders (Leemans et al. 2014). TLRs are a family of transmembrane receptors and the signal transduction initiated from TLRs activates effector cells via several kinases and NF-KB-dependent mechanisms (Gluba et al. 2010). TLRs are widely expressed in TECs. For instance, TECs are known to express both TLR2 and TLR4, and both TLR2 and TLR4 signaling are activated during IRI (Wu et al. 2010; Allam et al. 2012; Wolfs et al. 2002), sepsis-induced AKI (El-Achkar and Dagher 2006; El-Achkar et al. 2006; Dear et al. 2006), diabetic nephropathy (Lin et al. 2012, 2013; Mudaliar et al. 2013; Devaraj et al. 2011), unilateral ureter obstruction (Pulskens et al. 2010; Leemans et al. 2009; Campbell et al. 2011; Skuginna et al. 2011). Necrotic tubular cells release high-mobility group box1 protein (HMGB1), histones, heat-shock proteins, and other DAMPs that activate TLR2 and TLR4 on renal parenchymal cells and drive inflammation (Wu et al. 2010; Allam et al. 2012; Leemans et al. 2005). We also found that albumin might serve as an endogenous DAMP to trigger the activation of TLR2-MyD88-NF-κB pathway and pro-inflammatory cytokine TNF- $\alpha$  and IL-6 secretion (Ding et al. 2015) (Fig. 11.1). NLRs are cytoplasmic receptors. Shigeoka and co-workers showed that Nod1 and Nod2 are present in TECs in both mouse and human kidneys and that the absence of these receptors can protect the kidney from AKI by inhibiting TEC apoptosis and inflammation (Shigeoka et al. 2010).

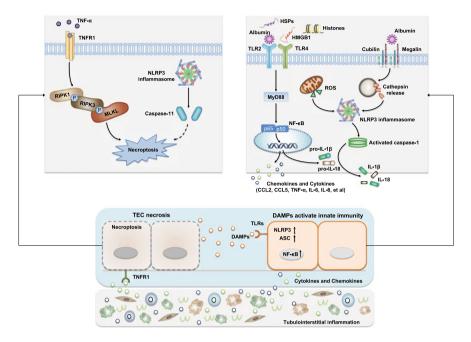


Fig. 11.1 Landscape of interstitial inflammation caused by damaged TECs. In response to injury, damaged TECs release various kinds of DAMPs that activate innate immunity through identical pattern recognition receptors including TLRs and inflammasomes, with the consequent production and release of cytokines and chemokines to recruit inflammatory cell infiltration in the interstitium, which eventually drive interstitial inflammation and fibrosis. Some injury factors can also be seen as DAMPs (such as albumin). In addition, TNF- $\alpha$  and possibly other cytokines drive necroptosis as a secondary cell death category contributing to tubular necrosis and renal dysfunction. This sets up the auto-amplification loop of necroinflammation

In addition, emerging evidence suggests an important role for NLRP3 inflammasome and IL-1 $\beta$ /IL-18 in the pathogenesis of acute and chronic inflammation and tissue remodeling in the kidney (Anders and Muruve 2011; Chang et al. 2014) (Fig. 11.1). Upregulation of the NLRP3 inflammasome is demonstrated in both classical immune cells as well as in TECs in a wide variety of tubulointerstitial disease (Anders and Muruve 2011; Chang et al. 2014). We recently found that proteinuria causes NLRP3 inflammasome activation and IL-1 $\beta$ /IL-18 maturation in a time course and dose-dependent manner in the proximal tubules (Liu et al. 2014). Further investigation indicated that megalin/cubilin-mediated albumin retention and lysosomal rupture are involved in the activation of NLRP3 inflammasome and interstitial inflammation (Liu et al. 2015). Moreover, Ang II has also been shown to induce NLRP3 inflammasome activation in TECs, which is associated with mitochondrial dysfunction or ER stress (Wang et al. 2015a; Wen et al. 2016). Thus, activation of the inflammasome pathway may represent a new mechanism of tubulointerstitial inflammation.

# 11.4.2 Necroinflammation: An Auto-Amplification Loop Between Tubular Injury and Tubulointerstitial Inflammation

Necroinflammation is a new pathological auto-amplification loop driven by necrosis (defined by cell death involving rupture of the plasma membrane) and inflammation (defined by cytokine release, increased vascular permeability, and recruitment of immune effector cells) (Linkermann et al. 2014; Mulay et al. 2016b). Following this pathological process, ischemia, toxins, and proteinuria can trigger tubulointerstitial inflammation, and in turn, tubulointerstitial inflammation causes TECs injury, which leads to an aggravation of interstitial inflammation (Fig. 11.1).

*How TECs necrosis induces tubulointerstitial inflammation?* In the last decade, it was unraveled that injured cells release DAMPs that activate innate immunity through identical pattern recognition receptors including TLRs and inflammasomes (Anders and Schaefer 2014). As mentioned above, this process is also involved in kidney inflammation and immunopathology (Anders and Muruve 2011; Anders et al. 2004; Anders 2010). AKI is most frequently associated with cell necrosis that implies DAMPs release. For example, ischemic, septic, or toxic forms of tubular necrosis can induce HMGB1, histones, heat-shock proteins, and other DAMPs release, which activate TLR2 and TLR4 on renal parenchymal cells and inflammatory cells to drive inflammation (Allam et al. 2012; Leelahavanichkul et al. 2011; Rabadi et al. 2012; Wu et al. 2010; Arumugam et al. 2009). Deficiency of receptor-interacting protein kinase 3 (RIPK3) or mixed lineage kinase domain-like (MLKL), two core proteins of the necroptosis pathway, blocks oxalate crystal-induced AKI and inflammation (Mulay et al. 2016a).

*How tubulointerstitial inflammation induces TECs necrosis?* DAMPs released by dying cells activate the pattern recognition receptors of infiltrating immune cells and intrinsic renal parenchymal cells and induce the release of numerous proinflammatory mediators. In particular, TNF-α and IFN-γ can induce necroptosis via two distinct pathways (Dannappel et al. 2014; Takahashi et al. 2014; Vanden Berghe et al. 2014). Mulay et al. showed that oxalate crystal formation inside tubules induced TNF-α secretion, which could activate the RIPK1, RIPK3, and MLKL pathway of necroptosis via TNFR1. And blocking either TNF-α or TNFR1 could abrogate kidney injury and dysfunction (Mulay et al. 2016a). Furthermore, the NLRP3 inflammasome activation not only triggers cytokine release but also pyroptosis, as a consequence of inflammasome-driven caspase-11 activation (Bergsbaken et al. 2009; Case et al. 2013). But if pyroptosis can occur in TECs is under debate (Krautwald and Linkermann 2014; Yang et al. 2014) (Fig. 11.1).

#### 11.4.3 Partial Epithelial–Mesenchymal Transition (EMT)

TECs might directly contribute to renal fibrosis via EMT, a phenotypic conversion program that is characterized by the loss of epithelial markers (such as E-cadherin, zonula occludens-1 [ZO-1] and cytokeratin) and gain of mesenchymal features (including vimentin,  $\alpha$ -smooth muscle actin [ $\alpha$ -SMA], fibroblast-specific protein-1 [FSP1], interstitial matrix components type I collagen, and fibronectin) (Liu 2004; Strutz 2009). Historical data and recent new findings have suggested that renal fibrosis might occur as a result of the tubular epithelial cells injury. In response to this, TECs produce various chemokines and cytokines around peritubular compartments to attract and direct the influx of inflammatory cells to the tubulointerstitial space. Infiltrating cells in turn activate and produce a mixture of soluble factors, including pro-inflammatory, pro-fibrotic cytokines, and MMPs. Altered microenvironment contributes to the reshaping of the mesenchymal cell phenotype, and rendering TECs adaptable to changing cell phenotype for the sake of escaping apoptosis (Prunotto et al. 2012; Liu 2010).

However, the precise contribution of the EMT to kidney fibrosis remains a subject of debate, as studies using genetic cell lineage tracing could not find evidence of a direct contribution of epithelial cells to the myofibroblast population in the fibrotic kidney (Humphreys et al. 2010). Two studies recently addressed this dispute and offered new insights into the potential role of tubular EMT in the development and progression of renal fibrosis (Ovadya and Krizhanovsky 2015; Zhou and Liu 2016). The transcription factors Snail 1 and Twist are the main regulators of the EMT program. Grande et al. (2015) focus on Snail 1, whereas Lovisa et al. (2015) carried out experiments with both Snail 1 and Twist. By conditional deletion of Snail 1 or Twist in TECs, the EMT is specifically inhibited. As a result, fibrosis is reduced in several CKD models, including unilateral ureter obstruction, nephrotoxic seruminduced nephritis, and folic acid-induced nephropathy. And improvement of renal fibrosis also led to the preservation of tubular cell integrity and function. Interestingly, both studies found that TECs undergo incomplete EMT during renal fibrosis-the cells express markers of both epithelial and mesenchymal cells and remain associated with their basement membrane. In this respect, these observations are in harmony with earlier genetic cell lineage tracing studies and demonstrate that partial EMT is sufficient to induce tubular function impairment, triggering cell cycle arrest, and promoting the release of critical fibrogenic cytokines, although evidence for partial EMT in human CKD is rare.

## 11.4.4 Cell Cycle Arrest

A series of elegant studies have identified that G1/S and G2/M arrest in TECs is an important driver of maladaptive TECs repair and renal fibrosis, providing a link between AKI and CKD (Yang et al. 2010; Cianciolo Cosentino et al. 2013; Tang et al. 2013). Yang et al. demonstrated a causal association between epithelial cell cycle G2/M arrest and a fibrotic outcome in toxic and obstructive models of AKI. G2/M-arrested PTECs activate JNK signaling, which acts to upregulate pro-fibrotic cytokine (TGF- $\beta$ 1 and CTGF) production (Yang et al. 2010). Canaud et al. further identified PTECs in the G2/M phase form target of rapamycin-autophagy spatial coupling compartments, which facilitate pro-fibrotic secretion similar to the senescenceassociated secretory phenotype (Canaud et al. 2019). Targeting the G2/M checkpoint to maintain the proper progression of TECs through the cell cycle during the injury phase has been proposed as an attractive therapeutic target to prevent the progression of CKD (Canaud and Bonventre 2015). Cianciolo Cosentino et al. reported that a histone acetylase inhibitor could reduce the number of cells in G2/M arrest and reduce post-injury tubular atrophy and interstitial fibrosis (Cianciolo Cosentino et al. 2013). Jenkins et al. suggested that miR-192 has an important role in aristolochic acidinduced G2/M arrest (Jenkins et al. 2014). Interestingly, the induction of a transient G0/G1 arrest in TECs with the CDK4/6 inhibitor PD0332991 before IRI ameliorated kidney injury by preventing apoptosis and pro-fibrotic cytokine production (DiRocco et al. 2014).

As previously discussed, the functional consequences of EMT during fibrotic injury are the induction of the G2 phase arrest of TECs (Lovisa et al. 2015). Genetic inhibition of EMT by knocking out Twist and Snail 1, resulted in a substantial decrease in the G2/M-arrested TECs. In vitro induction of EMT with TGF-  $\beta$ 1 also induced G2/M arrest in TECs (Wu et al. 2013; Lovisa et al. 2015). Furthermore, it was found that the G2 arrest was mediated by the cell cycle inhibitor p21 (Lovisa et al. 2015). And it is in line with a finding that p21 in kidney proximal tubules mediates fibrosis (Megyesi et al. 2015).

## 11.4.5 Metabolic Disorder

The intracellular accumulation of excess non-esterified fatty acid (NEFA) and metabolites in TECs, namely lipotoxicity, can result in renal dysfunction, especially in the context of diabetic nephropathy (Schelling 2016; Kimmelstiel and Wilson 1936; Oliver et al. 1954; Herman-Edelstein et al. 2014). Several groups have shown that proximal tubule uptake of filtered NEFAs is the source of tubular toxicity in case of glomerular damage. Tubulointerstitial damage can be induced in rats by infusion of NEFA-loaded albumin and in vitro incubation with albumin-bound NEFAs stimulate PTEC apoptosis (Thomas et al. 2002; Kamijo et al. 2002; van Timmeren et al. 2005). Tubular cells have a high level of energy demand and the ATP that they use is mostly produced by fatty acid oxidation. New findings indicate that dysregulation of fatty acid oxidation followed intracellular lipid accumulation profoundly affects the fate of TECs, by promoting EMT, inflammation, and eventually interstitial fibrosis (Kang et al. 2015). They also investigated the mechanisms behind the depressed metabolic pathways in fibrotic kidney disease and further demonstrated that TGF- $\beta$ 1 inhibits the expression of carnitine palmitoyltransferase 1 (CPT1), the rate-limiting

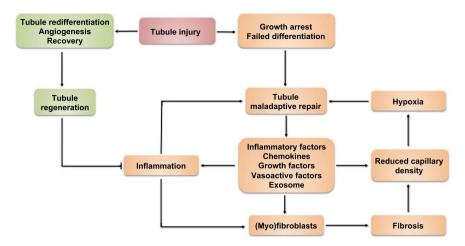


Fig. 11.2 Schematic diagram illustrating cycle feedback interactions between tubule pathology and interstitial pathology

enzyme in FAO, and thereby decreases fatty acid metabolism (Kang et al. 2015). Furthermore, miR-21 is shown to be implicated in the regulation of metabolic pathways recently (Trionfini et al. 2015; Chau et al. 2012). miR-21 promotes tubular injury and fibrosis by downregulating PPAR $\alpha$ , with consequent alterations of TEC lipid metabolism. Inhibition of miR-21 reduces TGF- $\beta$ -induced fibrogenesis and inflammation, preserves tubular integrity, as a result of enhanced PPAR $\alpha$ /RXR activity and improved mitochondrial function (Gomez et al. 2015).

## 11.5 Conclusion

In this review, we shift TECs from the victim of injury to a driving force in the progression from AKI to CKD. Damaged TECs can contribute directly to interstitial inflammation and fibrosis through various kinds of mechanisms (Fig. 11.2). Thus, protecting tubules from repeated injury and restoring healthy tubular function may be the priority of treatment of kidney diseases. Although the mechanisms of tubular injury remain to be elucidated, the G1/S and G2/M cell cycle arrest may be a pivotal obstacle to the adaptive repair of injured TECs and targeting the G1/S and G2/M checkpoint to maintain the proper cell cycle transition may be an attractive therapeutic target to prevent the progression of CKD.

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