

# Application of Histone Deacetylase Inhibitors in Renal Interstitial Fibrosis

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## Keywords

Renal interstitial fibrosis · Histone deacetylases · Signaling pathway · Inhibitor

## Abstract

**Background:** Renal interstitial fibrosis is characterized by the accumulation of extracellular matrix proteins, which is a common feature of chronic kidney diseases. **Summary:** Increasing evidence has shown the aberrant expression of histone deacetylases (HDACs) in the development and progression of renal fibrosis, suggesting the possibility of utilizing HDAC inhibitor (HDACi) as therapeutics for renal fibrosis. Recent studies have successfully demonstrated the antifibrotic effects of HDACis in various animal models, which are associated with multiple signaling pathways including TGF- $\beta$  signaling, EGRF signaling, signal transducer and activator of transcription 3 pathway, and JNK/Notch2 signaling. This review will focus on the utilization of HDACi as antifibrotic agents and its relative molecular mechanisms. **Key Messages:** HDACis have shown promising results in antifibrotic therapy, and it is rational to anticipate that HDACis will improve clinical outcomes of renal fibrosis in the future.

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## Introduction

Renal interstitial fibrosis, characterized by the activation and proliferation of fibroblasts, and subsequent production of excessive amounts of extracellular matrix (ECM) deposition in response to acute and chronic damage, is a common feature of chronic kidney diseases (CKD) and contributes to the deterioration of renal function [1–3]. Many cytokines participate in this process, leading to differentiation of renal interstitial fibroblasts into the activated myofibroblast phenotype, which can be identified by markable expression of  $\alpha$ -smooth muscle actin ( $\alpha$ -SMA) [4–7]. Of those cytokines, transforming growth factor- $\beta$ 1 (TGF- $\beta$ 1) is considered as the master regulator in renal fibrosis [8]. TGF- $\beta$ 1 is mainly secreted by macrophages responding to inflammation in injured tissues, and its interaction with receptor leads to activation of signal transducer and activator of transcription 3 (STAT3), EGRF and JNK/Notch2 signaling pathways, which promote the excessive deposition of ECM components such as collagen [9]. Other types of cells including tubular epithelial cells, hematopoietic cells, and endothelial cells are also involved in the production of collagen [10]. Antifibrotic drugs focus on gene expression regulation have been developed, but the clinic outcomes were unsatisfactory.

Increasing evidence elucidates that epigenetic mechanisms, such as histone acetylation modifications, play an important role in interstitial fibrosis process [11, 12]. Acetylation of core histones is governed by opposing actions of a variety of histone acetyltransferases (HATs) and histone deacetylases (HDACs) [13]. HATs catalyze the transfer of acetyl groups from acetyl-CoA to the lysine  $\epsilon$ -amino groups on the N-terminal tails of histones, which weakens the interaction of the histone tail and DNA, promoting transcriptional activation. In contrast, HDACs remove the acetyl groups from acetylated histones, increase chromatin condensation, and suppress gene transcription [14]. Aberrant expressions of HDACs and subsequent epigenetic modifications have been extensively observed in various animal models of interstitial fibrosis, and inhibitory effects against tissue fibrosis by HDACs inhibitors have also been demonstrated in multiple organs, such as heart [15, 16], liver [17, 18], and kidney [19, 20], which presents the possibility of using HDACs as targets in the treatment of chronic fibrotic diseases. In this minireview, we will discuss HDACs inhibitors' application and molecular mechanism in renal interstitial fibrosis.

### HDACs in Mammalian Cell

The biochemical function of HATs is to catalyze the acetylation of histones, which results in an open structure of the DNA. Hyperacetylation of core histone facilitates the binding of transcription factors and promotes gene expression. On the contrary, HDACs remove acetyl groups from hyperacetylated histones and counteract with HATs. HATs and HDACs are recruited to gene promoters by DNA-binding proteins that recognize given DNA sequences and provide specific modulation on gene expression.

There are 18 characterized members of HDACs in human, which can be grouped into 4 classes based on biological function and DNA sequence similarity [21]. The class I and II HDACs are considered as the "classical" HDACs, whose activities are inhibited by small chemicals such as trichostatin A (TSA). Class III HDACs represent the silent information regulator 2 family of nicotinamide adenine dinucleotide-dependent HDACs (SIRT1–7), which share structural and functional similarities with the yeast silent information regulator 2 protein [22]. Finally, class IV HDAC is the newly discovered HDAC11. HDAC11 is most closely related to class I HDACs, but since the overall sequence similarities are very low, it can-

not be grouped into any of the other existing classes. In mammalian cells, different tissue distribution and its cellular location of each member is summarized in Table 1.

At present, the expression profiles and distribution of HDACs in the kidney have not been completely clarified. By using specific inhibitors, HDACs have been shown to be involved in a variety of important cellular processes such as cell proliferation, survival, differentiation, and cell apoptosis. Class I HDACs are expressed ubiquitously, localized to the nucleus, and interact with co-repressor complexes to exert their function. In the kidney, its expression was found in renal fibroblasts and renal tubular cells [23]. Class II HDACs are thought to have tissue-specific roles and are expressed in the renal tubules [24]. Class III HDACs are members of the sirtuin family and are characterized by a sirtuin core domain. Cellular distribution of this Class HDACs includes nucleus (SIRT1, SIRT6, and SIRT7), mitochondria (SIRT3, SIRT4, and SIRT5), and cytoplasm (SIRT2). SIRT1 and SIRT2 are found expressed in renal fibroblasts and tubular cell, while cellular distribution of other members in this sub-family is not clear. Studies have demonstrated the role of class III HDACs in tissue fibrosis, but results regarding SIRT1 in renal fibrosis are controversial, as both activation and inhibition of SIRT1 can attenuate renal fibrosis [25–29]. HDAC 11 is the sole member of class IV and is localized to the nucleus and may be involved in regulating the expression of interleukin 10. Expression of HDAC11 was found in renal tubules, where it negatively regulated PAI-1 expression and might be a novel target in ischemia and reperfusion injury [30]. However, the relationship between HDAC11 and renal fibrosis is unclear.

### Aberrant Expressions of HDACs in Renal Interstitial Fibrosis

The molecular process of renal interstitial fibrosis is accompanied by aberrant gene expression that confers proliferation and activation of interstitial cells. As the fundamental biochemical function of HDACs is to remove acetyl group from hyperacetylated histones, the gene expression of HDACs is thought to be associated with renal interstitial fibrosis. Moreover, the aberrant gene expression of HDACs in interstitial cells can provide an interpretation of deregulated gene expression of interstitial cells.

Many studies indicate that aberrant expression of HDACs was found in various models of renal interstitial fibrosis. The most popular model of renal interstitial fi-

**Table 1.** Classification of HDACs and its expression in kidney

Group	Member	Cellular distribution	Renal location	Aberration	Reference
Class I	HDAC1	Nucleus	Renal fibroblasts and tubular cell	Up	[36–39]
	HDAC2			Up	[36–39]
	HDAC3			Down/up	[37, 40]
	HDAC8			Down/up	[38, 43]
Class II	HDAC4	Nucleus/cytoplasm	Renal tubules	Up	[39]
	HDAC5			Up	[38]
	HDAC6			Up	[38, 41]
	HDAC7			Up	[36]
	HDAC9			ND	
	HDAC10			Up	[38]
Class III	Sirt1	Cytoplasm/nucleus/ mitochondria	Renal tubules and fibroblasts	Down	[23]
	Sirt2			Up	[25]
	Sirt3			Down	[27]
	Sirt4			ND	
	Sirt5			ND	
	Sirt6			ND	
	Sirt7			ND	
Class IV	HDAC11	Mainly nucleus	Renal tubule	ND	

HDACs, histone deacetylases.

brosis is unilateral ureteral obstruction (UUO) and diabetic nephropathy [31, 32]. Relative fewer studies focus on drug-induced or IRI-induced renal damage-associated fibrosis [33, 34]. In UUO mice, increased gene expression of HDAC-1, -2, and -7 was found both at transcriptional and translational levels [35]. Increase of HDAC-1 and -2 was also confirmed by other studies [36, 37]. In a mouse model of diabetic kidneys diseases (DKD), the activity of HDAC-1, -2, and -4 was found to be elevated in STZ-induced renal cortex, while the activity of HDAC-3, -5, and -8 was not significantly changed [38]. In the kidneys of adenine-fed CKD mice, HDAC3 was found to be upregulated, and selective HDAC3 inhibition effectively alleviated kidney injury [39]. In angiotensin II-infused mice, hypertensive stimuli enhanced the expression of HDAC6, and the inhibition of HDAC6 prevented fibrosis and inflammation [40]. Similarly, downregulation of SIRT3 was found in angiotensin II-infused mice, while overexpression of SIRT3 repressed the excessive production of mitochondrial superoxide [41]. All these studies show that members of HDACs are aberrantly expressed in different animal models, although not all the members of HDACs are fully investigated (Table 1).

The changes in HDAC expression are thought to be involved in transmission of signals under the condition

of renal interstitial fibrosis. The induction of HDACs likely contributes to the reduced level of histone acetylation and altered gene expression in the injured kidney. This forms the molecular basis to treat renal interstitial fibrosis with HDAC inhibitors (HDACi).

### Classification of HDACi

The development of HDACi has a long history, and a number of structurally diverse HDACi have been identified. Many HDACi are currently being evaluated in clinical trials, especially for cancer therapy [42]. In 2003, Mishra et al. [43] found that TSA treatment could significantly decrease the urine-protein excretion and the proliferative hallmarks of glomerulonephritis associated with systemic lupus erythematosus-induced lupus in mice for the first time. Thereafter, various HDACi have been investigated for their antifibrotic and anti-inflammatory effects in renal disease. The body of HDACi still gets growing, with many new chemicals derived from natural product are found to be potential HDACi. Based on their chemical structure, HDACi can be classified into the following categories [44]: hydroxamic acids (such as TSA and suberoylanilide hydroxamic acid); cy-

**Table 2.** HDACi applied in animal models of renal fibrosis

HDACi	Specificity	Animal model	Reference
TSA	Class I/II	STZ-induced diabetic kidney UUO model Doxorubicin-induced nephropathy IRI-induced fibrosis Adenine CKD model	[39] [36, 39, 46, 55, 68] [35] [34] [35]
VPA	Class I	UUO model Doxorubicin-induced nephropathy STZ-induced diabetic kidneys	[38] [38] [39, 48]
MS-275	Class I	UUO model IRI-induced fibrosis	[37] [34]
NaB	Pan-HDACi	STZ-induced diabetic kidney	[32, 49]
SAHA	Class I/II	STZ-induced diabetic kidney	[33, 66]
SB939	Pan-HDACi	UUO model	[54]
Tubastatin A	HDAC6	Angiotensin II-infused mice	[41]

HDACs, histone deacetylases; TSA, trichostatin A; VPA, valproic acid; SAHA, suberoylanilide hydroxamic acid; HDACi, HDAC inhibitor; UUO, unilateral ureteral obstruction.

clic peptide (such as FK228); short-chain and aromatic fatty acids (such as butyrate); benzamides (such as MS-275), and miscellaneous compounds (such as depudecin). Many inhibitors are HDAC type specific, while some inhibitors are member specific. For example, valproic acid (VPA) exerts inhibition of both class I and II HDACs, with a high potency for class I HDACs, while Tubastatin A is a specific selective inhibitor of HDAC6. Still, some inhibitors can inhibit all HDAC isoforms nonspecifically (so-called pan-inhibitors). For example, SB939 (pracinostat) is a new orally active hydroxamate-based HDACi currently in phase II clinical trials, which can potently inhibit class I, II, and IV HDACs with excellent pharmacokinetic properties [45]. The often-used HDACi in renal interstitial fibrosis and their characters are listed in Table 2.

### Cellular and Molecular Mechanisms for HDACi in Kidney Fibrosis

As renal fibrosis is one of the typical complex diseases, many genes are involved in the fibrogenesis. Various molecular mechanisms are proposed to explain the renal interstitial fibrosis. Accordingly, the mechanisms of HDACi vary in different animal models (Fig. 1).

### Cellular Mechanisms of HDACi

#### *Inhibition of Fibroblast Activation and Proliferation*

Regardless of the initiating events, a feature common to renal fibrosis is the activation of ECM-producing myofibroblasts, which are derived from active fibroblast-type cells.  $\alpha$ -SMA is a representative marker of myofibroblast activation. In the kidney, the most abundant fibroblast-type cells are mesangial cells and fibroblasts. Another source of fibroblast-type cells is epithelial-mesenchymal transition (EMT) of tubular epithelial cells (also see below).

In animal models of renal fibrosis, fibroblast activation and proliferation can be represented by gene expression of  $\alpha$ -SMA, fibronectin, or collagens. These proteins are also taken as molecular markers of renal fibrosis. In other studies, connective tissue growth factor and PAI-1 are also taken as fibrosis markers. Connective tissue growth factor is a matricellular protein related to tissue and wound repair and fibrotic pathology, while PAI-1 protein can activate protease inhibitors to inhibit ECM degradation [46]. In all the animal studies, the tested HDACi can reverse the gene expression of fibrosis markers, indicating the inhibition of fibroblast activation and proliferation. Moreover, the reversed gene expression of fibrosis markers can be exerted by the direct regulation of histone acetylation of promoter regions in these genes [47]. In





confirmed by different groups [53, 54]. Thus, it is widely accepted that fibroblast-type cells derived from tubular epithelial cells play an important role in renal fibrosis.

The process of tubular EMT is defined as loss of the tubular epithelial phenotype and gain of mesenchymal features. At molecular level, EMT is characterized by a decrease in the expressions of E-cadherin and zonula occludens protein with an acquisition of de novo  $\alpha$ -SMA expression, as well as vimentin and fibronectin [55]. Moreover, morphologic and phenotypic evidence has also been noticed during the process of EMT. Active participation of EMT in CKD and acute kidney injury has also been reported in animal models and cell models. In our previous study, we found that treatment with high uric acid induced EMT of human tubular epithelial cells [56].

EMT under the condition of renal fibrosis can be reversed by HDACi treatment. In a cell model of HK-2 cells treated with TGF- $\beta$ , various HDACi including TSA, MS275, PCI34051, and LMK235 were applied to inhibit ECM proteins expression, while TGF- $\beta$ 1-induced E-cadherin downregulation was only observed in HK-2 cells treated with TSA or MS275 [57]. This work was coincident with a previous report in which TSA was applied to inhibit EMT induced by TGF- $\beta$  in HK-2 cells, and the acetylation level of EMT marker was significantly increased by TSA treatment [58]. Similarly, the inhibition of EMT induced by TGF- $\beta$  was also observed in SB939-treated HK-2 cells, which demonstrated the in vitro function of HDACi [59]. In STZ-induced diabetic kidneys, the nonselective HDACi TSA could efficiently inhibit EMT in vivo, as determined by Western blotting [38]. In the same animal model, the antifibrotic and renoprotective effects of VPA and NaB via inhibition of EMT were also detected [60, 61]. In UUO-induced renal fibrosis, the existence of EMT was demonstrated by the abundant cells coexpressing both  $\alpha$ -SMA and tubular marker, which indicated that these cells were at transitional stage between epithelia and mesenchyme [62]. However, the protein expression of EMT marker E-cadherin was controversial [37]. As EMT can happen in UUO-induced kidney, it can be speculated these HDACi have the ability to inhibit EMT in vivo, although the data in UUO model are not available at present. Briefly, tubular EMT plays an important role in the pathogenesis of renal interstitial fibrosis, inhibition of EMT by HDACi will undoubtedly alleviate renal fibrosis both in vitro and in vivo.

#### *Inhibition of Renal Inflammation and Immune Cells*

The relationship between interstitial inflammation and renal fibrosis is far from clear. Renal fibrosis is characterized by sustained inflammation, including inflammatory cell infiltration and secretion of cytokines. Besides immune factors, a wide range of nonimmune factors, including reactive oxygen species and advanced glycation end products, have been implicated in driving renal fibrosis via inflammation. Under the condition of renal damage, inflammation is precisely regulated by the immune system for tissue repairing, which seeks to eliminate the cause of injury. However, the sustained inflammatory response also can stimulate an inappropriate profibrotic response. Therefore, regulation of inflammatory response is a potential target for antifibrotic therapy.

Owing to the progresses in the past years, it is now clear that many elements of the innate and adaptive immune response participate in renal fibrosis. Once renal damages happen, acute inflammation and activation of innate immune mediators will be triggered. Subsequently, cytokines from renal intrinsic cells and innate immune cells will influence the activation of the adaptive immune response. Also, renal damages can directly activate the adaptive immune response. Inflammatory and immune mediators attempt to eliminate the inciting factors while activating the quiescent fibroblasts into myofibroblasts. Failure to eliminate the inciting factors can exacerbate the inflammatory response, which ultimately results in renal fibrosis.

In the classic UUO model of renal fibrosis, renal tubular cells can express several chemokines that induce the migration of inflammatory cells into the interstitium. This was observed in many studies. Although the role of macrophages in acute and chronic kidney injury is complex, For example, inflammatory M1 macrophages and anti-inflammatory M2 macrophages [63], the inhibition of initial macrophage influx by TSA treatment has been shown to attenuate tubulointerstitial injury in UUO model [35]. Many other HDACi also have the ability to inhibit macrophage infiltration. FR276457 is a hydroxamic acid derivative that inhibits both class I and II HDACs. Treatment with FR276457 after UUO resulted in decreased renal MCP-1 levels, a chemotactic cytokine that attracts macrophages to the kidney shortly after UUO [64]. In Ang II-induced hypertension mice, the HDAC6-selective inhibitor Tubastatin A reduced renal inflammation, as determined by qRT-PCR of MCP-1 and TNF- $\alpha$  [37]. Similarly, increased expression of inflammatory cytokines (TNF- $\alpha$  and IL-6) and profibrotic cytokines (TGF- $\beta$  and IL-13) in obstructed kidneys were signifi-

cantly reduced by SB939, a new orally active hydroxamate-based HDACi currently in phase II clinical trials [65]. Beside macrophages, other immune cells, which participate in renal fibrosis, can also be regulated by HDACi treatment. Like macrophages, T-cell infiltration is evident in most types of human and experimental CKD models [66]. In addition to produce chemokines and cytokines, T cells can participate in renal fibrosis by regulating the differentiation of fibrocytes. Moreover, T cells have also been proposed to promote renal fibrosis via EMT through the production of TGF- $\beta$ 1.

Recently, the function of FOXP3<sup>+</sup>IL-17<sup>+</sup> T cells in UUO model was revealed by Wu et al. [67], whose results showed that the attenuation of renal fibrosis by TSA was associated with the plasticity of FOXP3<sup>+</sup>IL-17<sup>+</sup> T cells. This is a new mechanism to explain the biological effects of HDACi. On the other hand, the chemokines and cytokines produced by renal intrinsic cells contribute to renal fibrosis. It is hard to discriminate the cell source of the chemokines and cytokines from renal samples directly. However, the in vitro model can answer the question. Treatment with TNF- $\alpha$  in rat tubular epithelial cells (NRK 52E) led to upregulation of MCP-1 and CSF-1, a chemokine involved in the initiation of tubulointerstitial injury, while this upregulation was significantly reversed by TSA [35]. This in vitro data suggested that HDACi could inhibit the production of cytokine and chemokines in activated tubular cells. Recently, anti-inflammatory effect of TSA was demonstrated in a model of cisplatin nephrotoxicity, in which TSA upregulated a novel anti-inflammatory protein, and activated microglia/macrophage WAP domain protein in epithelial cells [68]. Thus, the gene expression of inflammatory cytokines and chemokines in renal intrinsic cells can be efficiently inhibited by treatment of HDACi, which can in turn ameliorate renal fibrosis.

## Molecular Mechanisms of HDACi

### *Inhibition of TGF- $\beta$ Signaling*

TGF- $\beta$  is a master regulator of renal fibrosis, as well as fibrosis in other organs [69]. Numerous studies have manifested that increased expression and activation of profibrotic TGF- $\beta$  is associated with renal interstitial fibrosis. TGF- $\beta$  is also taken as the predominant pathogenic factor that drives glomerular and interstitial fibrosis. The canonical TGF- $\beta$  signaling pathway involves the phosphorylation and activation of Smad2 and 3 through TGF- $\beta$  receptor 1. Subsequently, the Smad complex

translocates to the nucleus and activates the transcription of specific targets such as collagen, fibronectin, and  $\alpha$ -SMA. Alternatively, binding of TGF- $\beta$  with TGF $\beta$ R can also activate a wide variety of Smad-independent pathways (noncanonical signaling) to modify cell function [70, 71]. TGF- $\beta$  induces renal fibrosis through several ways, including direct acting on fibroblasts and other cell types to induce ECM synthesis and reduce ECM degradation, and inducing the transition of various cell types into fibroblast-type cells that are capable of depositing ECM in injured kidneys. Under the condition of UUO injury, the protein level of TGF- $\beta$  in sample from kidney tissues was much higher than that in control sample, as determined by ELISA [36]. Moreover, the mRNA expression of TGF- $\beta$  in UUO kidney was also upregulated as determined by real-time RT-PCR [72]. Although the cell type, in which TGF- $\beta$  expression is activated, is unclear, these studies undoubtedly showed the association of profibrotic TGF- $\beta$  with renal fibrosis. To inhibit the activation of TGF- $\beta$  signaling, various kinds of HDACi were applied in UUO-induced renal fibrosis. For example, Manson et al. [73] found that TSA inhibited the expression of TGF- $\beta$ -dependent profibrotic genes in a manner that depended on BMP receptor signaling.

Besides UUO model, activation of TGF- $\beta$  signaling was found in other animal models. In a hypertension-induced kidney fibrosis model, Ang II induced the gene expression of TGF- $\beta$  in the mouse kidney both at transcriptional and translational level. However, this induction was blunt by a specific HDAC6 inhibitor or Smad3 knockdown, which suggested the profibrotic TGF- $\beta$  signaling was Smad-dependent [74]. Also, in a cell model of human renal mesangial cells treated aggregated IgA1 from IgAN patients, the protein levels of fibrosis markers and pSmad2/3 were increased, while pretreatment with the HDACi TSA or VPA partially reversed biological effects of aggregated IgA1 [46]. All these studies suggested activation of TGF- $\beta$ /Smad signal pathway contributes to renal fibrosis, while treatment of HDACi can reverse the signal pathway.

### *Inhibition of EGRF Signaling and STAT3 Pathway*

The epidermal growth factor receptor (EGFR) is a transmembrane glycoprotein that is a member of the protein kinase superfamily. Binding of the protein to a ligand induces receptor dimerization and tyrosine autophosphorylation. Besides EGF, other ligands such as heparin-binding EGF-like growth factor and TGF- $\alpha$  can activate EGFR, which leads to the activation of ERK and STAT3, and subsequently the induction of various cellular re-

sponses. Activation of EGRF signaling is involved in renal fibrosis. Either genetic or pharmacologic inhibition of EGFR significantly suppresses renal fibrosis in several animal models including Waved-2 mouse, UUO, Ang II-induced renal fibrosis, and hyperuricemic nephropathy [75–77]. Moreover, activation of the EGFR can induce Smad3 phosphorylation and fibrotic response via reactive oxygen species-dependent mechanisms [78].

Some HDACis were found to inhibit EGRF signaling. By using selective inhibitor of SIRT-1 and/or -2, renal fibrosis was significantly attenuated in obstructive nephropathy, which was accompanied by dephosphorylation of EGFR and STAT3 [48]. Similarly, MS-275, a selective class I HDACi, also has shown to ameliorate renal fibrosis in UUO mice by suppressing phosphorylation and expression of EGFR and its downstream signaling molecule STAT3 [36]. Suberoylanilide hydroxamic acid, a Class I/II HDACi approved by US FDA for CTCL, was also found to reduce EGFR protein and mRNA in cultured proximal tubule cells and in diabetic kidneys [79]. Moreover, activation of EGFR and STAT3 was required for the proliferation of renal proximal tubular cells, while blocking of class I HDAC activity with a highly selective inhibitor or small interfering RNA resulted in reduced proliferation and suppressed EGFR expression and phosphorylation [23]. In addition, inhibition of HDAC6 with TSA could downregulate the expression of EGFR in Pkd1 mutant renal epithelial cells by an accelerated trafficking of EGFR [80]. These studies demonstrate the role of EGRF signaling in renal fibrosis and its inhibition by HDACi is a key molecular mechanism.

#### *Inhibition of JNK/Notch2 Signaling*

Notch signaling has an important role in kidney development and is downregulated in the adult kidney [81]. However, this signal pathway can be reactivated after renal injury. Expression of Notch pathway proteins was found to be correlated with the severity of fibrosis and the decline of renal function [82]. Moreover, expression of Notch in renal tubular cells was found to be both necessary and sufficient for fibrosis development and genetic deletion of the Notch pathway reduced renal fibrosis in a mouse model of folic acid-induced nephropathy [83]. More recently, Tung et al. [84] reported that TGF- $\beta$ 1-stimulated expression of  $\alpha$ -SMA, fibronectin, phospho-JNK, and cleaved Notch-2 was significantly decreased by TSA treatment, while the levels of phospho-Smad2/3, phospho-p38, and phospho-ERK remained unchanged. They further demonstrated that administration of TSA or a  $\gamma$ -secretase inhibitor significantly ameliorated renal fi-

bro sis through suppression of the JNK/Notch-2 signaling activation in UUO mice. This work provided evidence that HDACi has the ability to inhibit JNK/Notch signaling and the crosstalk among different signaling pathways is involved in renal fibrosis.

## **Conclusions**

Increasing evidence has clearly indicated that aberrant expressions of HDACs and subsequent epigenetic modifications play a crucial role in the pathogenesis of renal fibrosis. Therefore, the inhibition of HDAC enzymes with specific inhibitors might become an important therapeutic approach for chronic fibrotic kidney diseases. The TGF- $\beta$  signaling pathway plays a central role in renal fibrosis, and numerous HDACis prevent renal fibrosis by directly inhibiting this pathway. With the progress made in discovering novel HDACi, more potential HDACi will be applied in antifibrotic researches. As clinical trials with HDACis have shown promising results in antifibrotic therapy, it is rational to anticipate that less toxic isoform-selective HDACis will improve clinical outcomes in the future.

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The authors declare that they have no potential conflicts of interest.

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## **Author Contributions**

J.Z. and L.N. conceived the idea. L.N. and Y.L. analyzed the data. J.Z., L.N., and B.Z. wrote the manuscript. All authors approved the final manuscript.



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