

The Research Progress of TGF- β in Obstructive Renal Water

Xiaopeng Qin^{1,2}, Houjie Fu^{1,2}, Qun Huang^{2,*}

¹ Graduate School, Youjiang Medical University for Nationalities, Baise Guangxi, China

² Affiliated Hospital of Youjiang Medical University for Nationalities, Baise Guangxi, China

* Corresponding author: Qun Huang

Abstract: Transformation and growth factor β (TGF- β) is a newly discovered TGF- β super family that regulates cell growth and differentiation. Obstructive renal hydrophilic water causes the kidney unit to be damaged, and the renal function will also decrease. In the end, the kidneys are in a non-functional state, causing many harms to the physical and mental health of patients. Finders that can promote cell fibrosis, and play a key role in the pathological development of chronic kidney disease. TGF- β 1 participates in various processes, including promoting multi-energy stem cells into fibroblasts, stimulating kidney capillaries endothelial cells, polygonal shapes, polygonal shapes Cells and mesenchymal cells are converted into fibroblasts. Through the research on the TGF- β structure, type, synthesis, signal transition, and its relationship with renal fibrosis, it helps to reveal its role in renal fibrosis. This article will review the latest research progress of the pathogenesis of TGF- β in the pathogenesis of obstructive renal water hydrosis and treatment, in order to propose the latest research conclusions of obstructive kidney accumulation diagnosis and treatment, which provides theoretical guidance for the treatment of obstructive renal water.

Keywords: TGF- β 1; Obstructive Kidney Accumulation; Kidney Fibrosis.

1. Mechanism

Obstructive renal hydrophilic water is a common disease and multiple onsets of urology. It is mostly due to urinary tract stones, tumors (good, malignant), congenital malformations (such as the narrowing of children's congenital ureteral pelvis connection, fibrous beam compression, etc.), inflammation stimuli Inflammatory spots cause ureteral stenosis), bladder ureter reflection, etc., among which urinary tract stones and congenital deformities [1], of which the pelvic pelvic upjo obstruction is the primary cause of children's kidney water [2]. The cause of the accumulation of adult kidney water is first of the upper urinary tract stones. Different reasons cause a long period of obstruction of ureteral or pelvis exports, which will deepen the degree of water accumulation of pyelone, damage the kidney unit, thereby reducing renal function, eventually leading to the loss of renal function, and bringing many harms to the patient's physical and mental health. The long -term obstruction of the ureter or pelvic exports will deepen the degree of water accumulation. The pathogenesis of obstructive renal fibrosis is due to the increased pressure of the set system, which damage the skin cells on the renal tube [3, 4]. The inflammatory cells are infiltrated in the kidney quality in this process, releasing inflammatory medium, and activating fibroblasts. These processes cause the fibrosis of the kidney, which causes damage to the kidney structure and the overall function is damaged [5]. The etiology and pathogenesis of obstructive renal water water are not very clear. The TGF- β plays a vital role in the process of obstructive renal water. However, the detailed cause and pathogenesis need to be further studied. At present, the treatment of obstructive renal water water is mainly scientific theory of surgical intervention and no prevention and early intervention. Therefore, exploring the mechanism of TGF- β in obstructive renal hydrophilic and nephrotic fibrosis has important clinical significance for guiding how to protect kidney function.

2. Conversion Growth Factor β (TGF- β)

The transformation growth factor β (TGF- β) is a newly discovered group of super-family members who regulate cell growth and differentiation. The human TGF- β family consists of 33 genes. The protein encoded in this gene is secreted in the form of homologous di -gymnia or heterogeneity, and is synthesized by the immature preface. During the secretion process, these preparatory proteins were processed and cracking, and finally a mature di -polymer ligand connected by a sulfur bond. Based on the history of molecular identification, the TGF- β family has been given various names, including muscular protein, bone shape, protein (BMPS), growth differentiation factor (GDFS), Mulles channel inhibitory factor (MCIS), and TGF- β . 1.1TGF- β structure, type and synthesis.

TGF- β is a protein with homologous di-gymnarian structure. It is connected by two sulfur bonds with similar or the same sub-bond, and its molecular weight is 1215kd. Among mammals, there are three types of homework types in TGF- β : β 1, β 2, and β 3, and each type of the same type is composed of 112 amino acids. These homologous bilaterals constitute TGF- β 1, TGF- β 2 and TGF- β 3, respectively, which have similar effects and high homogeneity in their biology. Like other secretion proteins, the biological synthesis process of TGF- β occurs in the late biological synthesis. It first moves steps such as folding, glycatyng, and processing from the ribosomes attached to most cells in the intravascular network of most cells, and then transferred from the internal quality mesh to the gogg. After removing the N-terminal SMS peptide, TGF- β was synthesized [6, 7]. During the processing of protein, the processing of the C -side area has caused it to transform into a long foreg just. Subsequently, the domain of the C -end area was further changed, and a shorter mature ligand finally formed. This process shows that unprocessed

ligands must go through dualization steps [6]. Through the binary reaction of the sulfur bond, the Flynn protease family members perform protein hydrolysis on these polypeptides, which generates the biocore extended by the N-terminal and the anterior peptide connected to it with the sulfur. LRP), as well as the di-polymer that is shortened by the C-side and a polypeptide connected by a sulfur (also known as the mature TGF- β) [6]. After the protein water disintegration, the two parts of TGF- β , that is, the TGF- β in the form of immature and mature forms, still maintains a state of combination, forming a so-called large lurking complex (LLC). In this latent state, there is no further processing, and they do not have direct biological activity. Only when the mature TGF- β is activated and released from its latent form, it can directly interact with the receptor on the cellular membrane, thereby triggering the signal transition-level reaction and enhanced the biological effects of target cells.

2.1. TGF- β Receptor Type and Signal Conduction.

The TGF- β 1 receptor belongs to the cross-diaphragmicine mixic/sourein kinase family, including three types: T type (T β Ri), T β Rii, and III (T β Riii). Among them, T β Ri and T β Rii are key elements that activate the TGF- β signaling pathway. TGF- β 1 is the most significant heterogeneous in the TGF- β super family, with powerful fibroblast factor characteristics [9]. It is not only an important induction factor for kidney fibrosis, but also one of the main activation factor of the TGF- β 1/SMAD2/3 signaling pathway [10]. Under the action of TGF- β 1, each unit is combined with a TGF- β II receptor (TGFB2) to form a composite ligand-receptor protein surface, which is then identified by type I receptor molecules (TGFB1) [11]. For BMP and activation, each monomer is combined with the corresponding I and II receptors [12]. Therefore, the binding of the ligand leads to the assembly of the heterogeneous tetraphoria receptor complex binding to the di agent ligand. Then, TGFB2 subtype phosphorylation is located in the Gly/SER region (GS region), rich in Gly/SER near the TGFB1 sub-kinase domain. Small protein FKBP12 is combined with the GS region in the TGFB of the no ligand to lock the kinase activity in a non-active state. Once the TGFB2 phosphorylation is phosphorylated, the GS region is considered to release FKBP12 and serves as the connection site of SMAD protein, and Smad protein is used as a substrate for TGFB1 kinase [13]. The core protein combined with TGF- β of the core protein (also known as the III TGF- β receptor) of the membrane anchoring protein, which is delivered to TGFB2. Other co-receptors are anchored to the cell surface through the tail of the glucocoplidsitol, including Cryptom and Cryptic, and exclusive guidance molecular (RGM) for the essential NODAL co-receptor as some BMP.

2.2. TGF- β and Obstructive Kidney Accumulated Water.

TGF- β is a type of fibrosis cytokine in the stagnant water accumulation, which can start and adjust a series of pathophysiological processes. TGF- β 1 participates in a variety of processes, including converting polyo-stem cells into fibrous maternal cells, stimulating kidney capillary endothelial cells, polygonal cells, and mesenchymal cells into fibroblasts [14-16]. Kuppe et al. [17] found that the single-cell transcription group found that the platelet derivative growth factor receptor receptor α -positive and β -positive

fibroblast/muscle fibroblasts are the main sources of human kidney fibrosis scar. TGF- β 1 can trigger renal fibrosis by activating typical SMAD or non-SMAD signals, leading to the activation of muscle fibroblasts, increasing the generation of ECM, and reducing ECM degradation [18]. LIU et al. [19] found that the HIF-1 α expression in the UUO model mice had a significant increase in HIF-1 α . At the time of hypoxia, HIF-1 α is raised to express P53 to inhibit the cell cycle process, resulting in G2/m cell blockage. In turn, this activates a fibrosis signal pathway mediated by the conversion growth factor- β (TGF- β) and connective tissue growth factor (CTGF), which ultimately promotes the production of extracellular matrix and promotes the development of renal fibrosis.

Chen et al. [20] found a group protein dehuminate 6 (HDAC6) inhibitors inhibited TGF- β 1 and epidermal growth factor receptor (EGFR) signal pathways in obstructive renal water water to delay the development of renal fibrosis. HDAC6 may become a potential target for the treatment of renal fibrosis. Kim et al. [21] studied the role of AKT1, one of the three sub-types of AKT, in obstructive renal water, and found that AKT1 mediated conversion growth factor 1 (TGF1)/transcription activation factor 3 (STAT3) channel promoting UUO mice Kidney fibrosis. YANG et al. [22] found that bone marrow-based macrophages β -catenin/foxo can not only suppress the renal fibrosis mediated by β -catenin/TCF, but also enhance its anti-inflammatory effect, thereby changing the bone marrow-based macrophage Transcription to reduce the inflammation and kidney fibrosis of UUO mice. Studies have found that among the NRK-52E cells of TGF- β 1 induced by TGF- β 1-induced NRK-52E cells in the UUO mouse kidneys and cultivation Increase. In addition, by activating a variety of signal pathways, LSD1 plays a key role in the adjustment of kidney EMT and fibrosis, so it can be used as a target for treating kidney fibrosis [23]. Gwon et al. [24] found that Apamin can inhibit UUO damage to mice's kidney inflammation response and ECM deposition, and in vivo and in vitro to inhibit the activation of fibroblasts in the body and body. Fibrosis has anti-kidney fibrosis. TGF- β 1 participates in the occurrence and development of obstructive kidney water. In-depth research on related factors can further clarify the mechanism of interstitial fiber in obstructive renal water.

3. Summary and Outlook

In short, the role of TGF- β in the course of obstructive renal water water is complicated, and the research of molecular levels is still the research direction of the next stage. In addition, the ultimate goal of our various research on TGF- β and obstructive kidney water water is to use these research results to solve the disease problems. However, many of our research results have not been converted into clinical clinical, so we have to continue to work hard. In order to better understand the various mechanisms of TGF- β and obstructive kidney water, and transform these mechanisms into clinical treatment, this will still be our future goal. This is still the focus of our future work. In short, TGF- β and obstructive renal water are a pathological process induced and developed by multiple factors. With the advancement of science and technology, the role of TGF- β in the pathogenesis of obstructive renal hydrophilic water pathogenesis will be clearer and more comprehensive, and medical treatment will also be widely used.

References

- [1] Chen Jie. The analysis of the influencing factors of the recovery of the recovery of the renal function after the destruction of the severe renal water obstruction [D]. Zunyi Medical University, 2022.
- [2] Bo S, Sedaghat F, Pavuluri K, et al. Dynamic Contrast Enhanced-MR CEST Urography: An Emerging Tool in the Diagnosis and Management of Upper Urinary Tract Obstruction[J]. *Tomography*, 2021,7(1):80-94.
- [3] Zhu Li, Ding Longhui, Shi Weifeng. GFR combined with serum CYS C, β_2 -Mg to varying degrees of diagnostic value for patients with water accumulation [J]. *Molecular diagnosis and treatment magazine*, 2023,15 (01): 157-160.
- [4] Hu Jian, Peng Qiang. Poor pelvic formation under the laparoscopic pelvic pelvis on severe congenital renal water surgical indicators, pain scores and prognosis [J]. *PLA pharmaceutical magazine*, 2021, 33 (03): 87 -90.
- [5] Jin B, Zhu J, Zhou Y, et al. Loss of MEN1 leads to renal fibrosis and decreases HGF-Adams5 pathway activity via an epigenetic mechanism[J]. *Clin Transl Med*, 2022,12(8): e982.
- [6] Ten D P, Arthur H M. Extracellular control of TGFbeta signalling in vascular development and disease[J]. *Nat Rev Mol Cell Biol*, 2007,8(11):857-869.
- [7] Robertson I B, Rifkin D B. Regulation of the Bioavailability of TGF- β and TGF- β -Related Proteins[J]. *Cold Spring Harb Perspect Biol*, 2016,8(6).
- [8] Miyazono K, Heldin C H. Role for carbohydrate structures in TGF-beta 1 latency[J]. *Nature*, 1989,338(6211):158-160.
- [9] Jung Y S, Kim Y H, Radhakrishnan K, et al. Orphan nuclear receptor ERR γ regulates hepatic TGF- β 2 expression and fibrogenic response in CCl(4)-induced acute liver injury[J]. *Arch Toxicol*, 2021,95(9):3071-3084.
- [10] Yuan Q, Tang B, Zhang C. Signaling pathways of chronic kidney diseases, implications for therapeutics[J]. *Signal Transduct Target Ther*, 2022,7(1):182.
- [11] Groppe J, Hinck C S, Samavarchi-Tehrani P, et al. Cooperative assembly of TGF-beta superfamily signaling complexes is mediated by two disparate mechanisms and distinct modes of receptor binding[J]. *Mol Cell*, 2008,29(2):157-168.
- [12] Gipson G R, Goebel E J, Hart K N, et al. Structural perspective of BMP ligands and signaling[J]. *Bone*, 2020,140:115549.
- [13] Huse M, Muir T W, Xu L, et al. The TGF beta receptor activation process: an inhibitor- to substrate-binding switch [J]. *Mol Cell*, 2001,8(3):671-682.
- [14] Ram C, Gairola S, Syed A M, et al. Biochanin A alleviates unilateral ureteral obstruction-induced renal interstitial fibrosis and inflammation by inhibiting the TGF- β 1/Smad2/3 and NF-kB/NLRP3 signaling axis in mice[J]. *Life Sci*, 2022,298: 120 527.
- [15] Jiang M, Bai M, Xu S, et al. Blocking AURKA with MK-5108 attenuates renal fibrosis in chronic kidney disease[J]. *Biochim Biophys Acta Mol Basis Dis*, 2021,1867(11):166227.
- [16] Ai K, Li X, Zhang P, et al. Genetic or siRNA inhibition of MBD2 attenuates the UUO- and I/R-induced renal fibrosis via downregulation of EGR1[J]. *Mol Ther Nucleic Acids*, 2022, 28:77-86.
- [17] Kuppe C, Ibrahim M M, Kranz J, et al. Decoding myofibroblast origins in human kidney fibrosis[J]. *Nature*, 2021,589 (7841): 281-286.
- [18] Yu X Y, Sun Q, Zhang Y M, et al. TGF- β /Smad Signaling Pathway in Tubulointerstitial Fibrosis[J]. *Front Pharmacol*, 2022,13:860588.
- [19] Liu L, Zhang P, Bai M, et al. p53 upregulated by HIF-1 α promotes hypoxia-induced G2/M arrest and renal fibrosis in vitro and in vivo[J]. *J Mol Cell Biol*, 2019,11(5):371-382.
- [20] Chen X, Yu C, Hou X, et al. Histone deacetylase 6 inhibition mitigates renal fibrosis by suppressing TGF- β and EGFR signaling pathways in obstructive nephropathy[J]. *Am J Physiol Renal Physiol*, 2020,319(6): F1003-F1014.
- [21] Kim I Y, Lee M Y, Park M W, et al. Deletion of Akt1 Promotes Kidney Fibrosis in a Murine Model of Unilateral Ureteral Obstruction[J]. *Biomed Res Int*, 2020,2020:6143542.
- [22] Yang Y, Feng X, Liu X, et al. Fate alteration of bone marrow-derived macrophages ameliorates kidney fibrosis in murine model of unilateral ureteral obstruction[J]. *Nephrol Dial Transplant*, 2019,34(10):1657-1668.
- [23] Zhang X, Li L X, Yu C, et al. Targeting lysine-specific demethylase 1A inhibits renal epithelial-mesenchymal transition and attenuates renal fibrosis[J]. *FASEB J*, 2022,36 (1):e22122.
- [24] Gwon M G, An H J, Gu H, et al. Apamin inhibits renal fibrosis via suppressing TGF- β 1 and STAT3 signaling in vivo and in vitro[J]. *J Mol Med (Berl)*, 2021,99(9):1265-1277.