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Mitophagy Dependent Macrophage Reprogramming Protects against Kidney Fibrosis

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Abstract

Mitophagy, by maintaining mitochondrial quality control, plays a key role in maintaining kidney function and is impaired in pathologic states. Macrophages are well-known for their pathogenic role in kidney fibrosis. Here, we report that PINK1/Parkin-mediated mitophagy in macrophages is compromised in experimental and human kidney fibrosis. We demonstrate downregulation of mitophagy regulators, mitofusin-2 (MFN2) and Parkin, downstream of PINK1 in kidney fibrosis. Loss of either Pink1 or Prkn promoted renal extracellular matrix accumulation and frequency of profibrotic/M2 macrophages. Pink1\(^{-/-}\) or Prkn\(^{-/-}\) bone-marrow-derived macrophages (BMDMs) showed enhanced expression of rictor. Mitochondria from TGF-β1-treated Pink1\(^{-/-}\) BMDMs exhibited increased superoxide levels, and reduced respiration and ATP production. In addition, mitophagy in macrophages involves PINK1-mediated phosphorylation of downstream MFN2 and MFN2-facilitated recruitment of Parkin to damaged mitochondria, and macrophage-specific deletion of Mfn2 aggravates kidney fibrosis. Moreover, mitophagy regulators were downregulated in human CKD kidney and TGF-β1-treated human renal macrophages, whereas Mdivi1 treatment suppressed mitophagy mediators and promoted fibrotic response. Taken together, our study is the first to demonstrate that macrophage mitophagy plays a protective role against kidney fibrosis via regulating PINK1/MFN2/Parkin-mediated pathway.
Introduction

Macrophages play an integral role in inflammation, and subsequent progression of kidney fibrosis, a common manifestation of chronic kidney disease (CKD) (1). Macrophage depletion in experimental models of kidney fibrosis such as unilateral ureteral obstruction (UUO) results in dramatically reduced interstitial fibrosis (2). Following kidney injury, tubular cell-derived chemokines including C-C motif chemokine ligand 2 (CCL2) promote the infiltration of C-C chemokine receptor type 2 (CCR2) expressing Ly6C\textsuperscript{high}/pro-inflammatory monocytes that express markers of M1/classically-activated macrophages into the kidney (3, 4). The inflammatory renal microenvironment favors the switch-over of Ly6C\textsuperscript{high}/pro-inflammatory or M1 population to Ly6C\textsuperscript{low}/anti-inflammatory phenotype, which exhibits a profibrotic transcriptional profile and may contribute to M2 macrophages (5, 6). Persistent kidney injury and inflammation result in the failure of tissue repair, mitochondrial dysfunction, and tubular apoptosis (1, 6, 7). Chronic unresolved inflammation also promotes switch-over of proinflammatory macrophages into anti-inflammatory or M2 phenotype (7), that results in increased transforming growth factor-beta 1 (TGF-\beta1) production (8). TGF-\beta1, a pluripotent multifunctional and a key profibrogenic cytokine favors the transdifferentiation of M2 macrophages into myofibroblasts (7, 8). Monocyte/Macrophage-specific deletion of TGF-\beta receptor II has been shown to significantly reduce the infiltration of macrophages and tubulointerstitial fibrosis (9). However, macrophage-specific TGF-\beta1 deletion failed to prevent kidney fibrosis (10, 11). Despite the increasing attention on the role of macrophages in kidney
fibrosis, the mechanism of macrophage-induced extracellular matrix (ECM) remodeling is poorly understood.

Mitochondrial dysfunction has emerged as a critical contributor to various diseases, including metabolic, cardiovascular, neurodegenerative, and neuromuscular diseases (12). The kidney has the highest number of mitochondria (13) second to the heart, to fulfill its energy demands for efficient electrolyte reabsorption, active transport, and removal of metabolic wastes (14). Therefore, the mitochondrial quality control through the removal of dysfunctional mitochondria is essential for cellular homeostasis and maintaining kidney function (13). The failure of elimination of damaged or superfluous mitochondria contributes to increased oxidative stress (12, 13). Mitophagy is the selective mitochondrial autophagy, which is triggered by excessive oxidative stress due to increased mitochondrial-derived reactive oxygen species (mROS) levels and plays a critical role in the recycling of damaged mitochondria (15).

The initiation of mitophagy involves tagging and fragmentation of dysfunctional mitochondria for sequestration in the mitophagosome that is chiefly controlled by two regulatory proteins: phosphatase and tensin homolog-induced kinase1 (PINK1; a serine/threonine kinase) and Parkin (E3 ubiquitin ligase, encoded by Prkn). Mitochondrial damage favors the accumulation of PINK1 on depolarized mitochondria (16). PINK1 promotes the recruitment of the cytosolic Parkin to the affected mitochondria (17, 18). Subsequent ubiquitination of outer mitochondrial membrane (OMM) proteins by E3 ligase activity of Parkin tags damaged mitochondria for degradation via recruitment of the autophagy adaptor p62/sequestosome 1 (p62/SQSTM1) and microtubule-associated protein light chain 3 (LC3), that results in an eventual turnover of dysfunctional
mitochondria (17-19). In the case of cardiomyocytes, mitophagy involves PINK1-mediated phosphorylation of mitofusin-2 (MFN2), an OMM protein that functions as a mitochondrial receptor for Parkin and promotes mitophagy by facilitating the recruitment of Parkin to the impaired mitochondria (20). Deletion of MFN1 and MFN2 suppressed mitophagy in mouse embryonic fibroblasts and cardiomyocytes (20, 21). Parkin, by ubiquitination of several OMM proteins including MFN1 and MFN2 (18, 19), plays a critical role in the regulation of mitophagy (15-17).

The underlying molecular mechanism of mitophagy in macrophages and its role during progressive kidney diseases remain poorly understood. Tang et al. recently reported findings of increased renal tubular damage in single and double Pink1 and Prkn knockout mice in a model of ischemic acute kidney injury (22). However, the functional role of macrophage mitophagy in the pathogenesis of kidney fibrosis, the common pathway in CKD, has not been previously investigated. Using two independent experimental mouse models of kidney fibrosis, and primary mouse and human renal macrophages, we uncovered a cytoprotective role of PINK1/MFN2/Parkin-dependent mitophagy against macrophage-induced fibrotic response during the progression of kidney fibrosis. Moreover, mitophagy regulators were downregulated in the human CKD kidney. We further demonstrate that the deficiency of mitophagy regulators results in macrophage reprogramming towards a profibrotic/M2 phenotype and promotes kidney fibrosis.
Results:

**Mitophagy regulators, Parkin and mitofusin-2 (MFN2), downstream of PINK1 are downregulated in kidney fibrosis.** To investigate the role of PINK1/Parkin mediated mitophagy during kidney fibrosis, we utilized a well-established murine model of kidney fibrosis induced by UUO. The expression of MFN2 (84 kDa) and Parkin (52 kDa), which are downstream regulators of PINK1-mediated mitophagy (15), was decreased in the kidneys of wild type mice 7 days after UUO compared to sham surgery (Figure 1A). The expression of LC3-II, a lipidated form of LC3 that wraps around the mitochondria and promotes mitophagosome formation (15-17), was also decreased after UUO (Figure 1A).

We employed an alternative model of kidney fibrosis induced by adenine diet (AD) and confirmed similarly reduced expression of MFN2, Parkin and LC3-II in the kidneys from mice fed with AD compared to control diet (Ctl) for 14 days (Supplemental Figure 1A). These findings in both experimental models indicate that the expression of downstream regulators of PINK1-mediated mitophagy decreased during kidney fibrosis.

**Loss of PINK1 or Parkin aggravates macrophage-derived fibrotic response and kidney fibrosis.** To understand the functional role of PINK1/Parkin-mediated mitophagy in kidney fibrosis, we compared the fibrotic response in the kidneys between PINK1-deficient (Pink1−/−), Parkin-deficient (Prkn−/−) mice and their corresponding littermate wild type (Pink1+/+ and Prkn+/+) mice 7 days after UUO or sham surgery. We found that the Pink1−/− and Prkn−/− mice both displayed higher collagen deposition in the obstructed kidneys compared to wild type mice, as assessed by Masson’s trichrome staining (Figure 1B). Moreover, kidneys from Pink1−/− and Prkn−/− mice showed higher protein expression of profibrotic markers, fibronectin (FN, 220 kDa), TGF-β1 (cleaved: 12.5 kDa) and
M2/profibrotic macrophage marker, arginase I (Arg-I, 35 kDa) after UUO than Pink1+/+ (Figure 1C) and Prkn+/+ (Figure 1D) mice.

Using AD model of kidney fibrosis, we confirmed that Pink1−/− mice fed with AD (28 days) compared to Pink1+/+ AD fed mice displayed higher kidney collagen content, as confirmed by quantitation of hydroxyproline content (Supplemental Figure 1B), and lower kidney weight (Supplemental Figure 1C) suggesting higher renal damage, as the kidney weight negatively correlates with the degree of kidney damage (23). Circulating levels of CCL2 (also known as monocyte chemoattractant protein-1 (MCP-1)) are directly related to the monocyte infiltration, inflammation, and tubulointerstitial fibrosis (24), and AD fed Pink1−/− mice displayed higher plasma levels of CCL2 than AD fed Pink1+/+ mice (Supplemental Figure 1D), suggesting higher monocyte recruitment into the damaged kidney. Further, we observed that the kidneys from AD fed Prkn−/− mice also displayed higher expression of FN, collagen-I (Col-I, 115 kDa), and profibrotic macrophage markers CD206 (190 kDa) and galectin-3 (Gal-3) compared to AD fed Prkn+/+ mice (Supplemental Figure 1E). In addition, we demonstrated that the counts of Gal-3+ F4/80+ renal macrophages and TGF-β1+ F4/80+ renal macrophages were increased in the kidneys of mice fed with AD (28 days) compared to Ctl diet, as assessed by flow cytometry analysis of renal single-cell suspensions and gated on CD45+ SSC low mononuclear cells (Supplemental Figure 1, F and G). We further confirmed that the Gal-3+ F4/80+ renal macrophages were higher in the AD fed Pink1−/− or Prkn−/− mice compared to the AD fed Pink1+/+ or Prkn+/+ mice, respectively.

Taken together, the above findings from two independent experimental models of CKD suggest that PINK1 and Parkin exert protective functions against kidney fibrosis.
**PINK1 or Parkin deficiency amplifies frequency of renal profibrotic macrophages.**

To further investigate the involvement of PINK1 in modulating macrophage-derived fibrotic response during kidney fibrosis, we first determined the frequency of circulating and renal monocyte/macrophage populations after UUO. We compared the numbers of total mononuclear (CD45+ SSC low) and phagocytic (F4/80+ CD45+) populations and found similar increases in the absolute counts of both total mononuclear (Supplemental Figure 2A) and mononuclear phagocytic (Supplemental Figure 2B) cells in the obstructed kidneys from Pink1+/+ and Pink1−/− mice after UUO. The absolute numbers of profibrotic/M2 macrophages were determined by gating on CD206+ F4/80+ cells. The profibrotic/M2 macrophages in the kidneys also increased after UUO, however, the obstructed kidneys from Pink1−/− mice had significantly higher numbers of profibrotic/M2 macrophages than Pink1+/+ mice (Figure 2A).

The differential expression of Ly6C is related to specific monocyte phenotype (5, 25-27). Based on its differential expression, we gated three populations of CD11b expressing Ly6C\text{high}, Ly6C\text{int} and Ly6C\text{low} monocytes. The counts of pro-inflammatory (Ly6C\text{high} CD11b+) monocytes in the kidneys after UUO increased in the Pink1+/+ mice (Figure 2B). However, compared to Pink1+/+ mice, Pink1−/− mice exhibited a lower frequency of the pro-inflammatory monocytes in the kidney. The frequency of Ly6C\text{int} CD11b+ population, which is known to play reparative functions after kidney injury (25), was lower in the kidneys of Pink1−/− than Pink1+/+ mice. Moreover, the obstructed kidneys from Pink1−/− mice also had higher numbers of the Ly6C\text{low} CD11b+ monocytes compared to Pink1+/+ mice (Figure 2B). Lower frequency of Ly6C\text{high} and higher numbers of Ly6C\text{low} phenotype in the obstructed kidneys from Pink1−/− mice suggest a potential switch-over of Ly6C\text{high} to
Ly6C\textsuperscript{low} phenotype. There was no difference in the frequency of circulating pro-inflammatory (Ly6C\textsuperscript{high}, CD11b+) monocytes between Pink1\textsuperscript{+/+} and Pink1\textsuperscript{−/−} mice after UUO (Supplemental Figure 2C). However, the numbers of circulating Ly6C\textsuperscript{low}, CD11b+ monocytes after UUO were higher in Pink1\textsuperscript{−/−} mice (Supplemental Figure 2D). The Ly6C\textsuperscript{low} CD11b+ monocytes exhibit profibrotic transcriptional profile and favor the progression of kidney fibrosis through paracrine signaling (25-27), which could at least in part account for the higher numbers of the profibrotic/M2 macrophages in the fibrotic kidney of Pink1\textsuperscript{−/−} mice.

We next sorted the renal macrophages after sham or UUO surgery. The Pink1\textsuperscript{−/−} renal macrophages after UUO showed significantly higher expression of FN, indicating higher profibrotic macrophage expression in case of PINK1 deficiency (Figure 2C).

We further examined whether genetic deficiency of Pink1 could exaggerate TGF-β1-induced fibrotic response by macrophages. In response to TGF-β1 treatment, Pink1\textsuperscript{−/−} BMDMs displayed higher expression of profibrotic markers, including FN, Arg-I, and Gal-3 (26 kDa) (Figure 2D). These observations confirm that PINK1 suppresses the macrophage-induced fibrotic response.

We next investigated the effect of loss of Parkin on the expression of profibrotic/M2 macrophages and Ly6C monocyte populations after UUO. Consistent with the findings in Pink1\textsuperscript{−/−} mice, the increase in the absolute counts of profibrotic/M2 macrophages in the kidney 7 days after UUO was higher in Prkn\textsuperscript{−/−} mice than Prkn\textsuperscript{+/+} mice (Figure 3A). The obstructed kidneys from Prkn\textsuperscript{−/−} mice showed lower frequencies of both Ly6C\textsuperscript{high} CD11b+ and Ly6C\textsuperscript{int} CD11b+ populations than Prkn\textsuperscript{+/+} mice (Figure 3B). There were no differences in the UUO-induced increase in the numbers of total mononuclear
(Supplemental Figure 3A) and mononuclear phagocytic (Supplemental Figure 3B) populations in the kidney and circulating Ly6C\textsuperscript{high} (Supplemental Figure 3C) monocytes between \textit{Prkn}\textsuperscript{+/+} and \textit{Prkn}\textsuperscript{−/−} mice. While the frequencies of Ly6C\textsuperscript{low} CD11b\textsuperscript{+} monocytes in the kidney (Figure 3B) and circulating Ly6C\textsuperscript{low} monocytes (Supplemental Figure 3D) in the blood after 7 days of UUO were higher in \textit{Prkn}\textsuperscript{−/−} mice compared to \textit{Prkn}\textsuperscript{+/+} mice. These results provide evidence that Parkin, downstream of PINK1, also prevents macrophage-derived fibrotic response in the kidney.

To understand the role of PINK1/Parkin-mediated mitophagy in macrophage polarization, we further induced the differentiation of BMDMs towards M0, M1 or M2 phenotypes in the presence of their respective inducers. Both \textit{Pink1}\textsuperscript{−/−} and \textit{Prkn}\textsuperscript{−/−} BMDMs displayed greater ability to polarize towards the profibrotic/M2 phenotype (Figure 3C), as confirmed by higher expression of Arg-I and rictor (200 kDa). In addition, both \textit{Pink1}\textsuperscript{−/−} and \textit{Prkn}\textsuperscript{−/−} CD11b\textsuperscript{+} monocytes and F4/80\textsuperscript{+} macrophages isolated from peritoneal cavity also showed higher expression of rictor (Figure 3D). The increase in the expression of rictor is known to play a critical role in the differentiation of M2 macrophages (28, 29). In contrast, loss of either PINK1 or Parkin did not affect the expression of iNOS (130 kDa) expressing M1 macrophages. These findings indicate that the deficiency of either PINK1 or Parkin favors reprogramming of macrophages towards profibrotic/M2 phenotype.

\textbf{Myeloid-specific deletion of Mfn2 exaggerates kidney fibrosis.} To elucidate the macrophage-specific role of mitophagy in the progression of kidney fibrosis, we used \textit{LysM-Cre}\textsuperscript{+/-}\textit{Mfn2}\textsuperscript{fl/fl} mice, in which Cre recombinase activity was induced under myeloid-specific promoter lysozyme M (LysM). We observed that the kidneys from AD fed \textit{LysM-Cre}\textsuperscript{+/-}\textit{Mfn2}\textsuperscript{fl/fl} mice displayed higher expression of FN, CD206, TGF-β1, and Gal-3
compared to their respective control (LysM-Cre\(^{-/-}\)Mfn2\(^{fl/fl}\)) mice (Figure 4A). Even the basal level of FN expression in the kidney was higher in LysM-Cre\(^{-/-}\)Mfn2\(^{fl/fl}\) mice. AD fed LysM-Cre\(^{+/+-}\)Mfn2\(^{fl/fl}\) mice also displayed higher collagen deposition and frequency of the Ly6C\(^{low}\) CD11b\(^{+}\) monocytes in the kidneys compared to LysM-Cre\(^{-/-}\)Mfn2\(^{fl/fl}\) mice, as assessed by Masson’s Trichrome staining (Figure 4B) and flow cytometry (Figure 4C) respectively. These findings indicate that macrophage-specific deletion of mitophagy regulator Mfn2 aggravates kidney fibrosis and suggest a critical role of macrophage mitophagy in protection against kidney fibrosis.

**PINK1-mediated mitophagy is suppressed in renal macrophages after UUO and in TGF-\(\beta\)1-treated macrophages.** To investigate the role of the mitophagy in macrophages, we first determined the effect of TGF-\(\beta\)1 treatment on PINK1 expression in THP-1 derived human macrophages. In our earlier studies, the detection of PINK1 expression in murine cells and tissues was limited due to lack of a reliable commercially available mouse specific anti-PINK1 antibody. Using THP-1 derived human macrophages, we confirmed that PINK1 expression significantly decreased after TGF-\(\beta\)1 treatment (Figure 5A). We next sorted the renal macrophages from wild type mice after sham or UUO surgery (Supplemental Figure 4A) and determined that the expression of MFN2 and Parkin was significantly reduced in the macrophages isolated from the fibrotic kidney after UUO (Figure 5B).

We next determined the effect of TGF-\(\beta\)1 on the recruitment of the mitophagy regulatory proteins to the mitochondria of macrophages. We isolated the mitochondrial fractions from the BMDMs cultured in the presence or absence of TGF-\(\beta\)1 for 48 hours. TIM23 (a mitochondrial protein) and \(\beta\)-actin (a cytosolic marker) were used to confirm the purity of
mitochondrial fractions. The expression of MFN2 and Parkin was significantly reduced in the mitochondrial lysates after TGF-β1 treatment (Figure 5C). Furthermore, confocal microscopy revealed that the colocalization of MitoTracker red dye stained mitochondria with autophagosome-specific marker LC3 was decreased in BMDMs after TGF-β1 treatment (Figure 5, D and E). *Pink1*−/− BMDMs displayed lower mitochondrial colocalization with LC3 than *Pink1*+/+ BMDMs. We further performed the quantitative analysis of mitophagy via flow cytometry using renal single-cell suspensions isolated from kidneys of *Pink1*+/+ and *Pink1*−/− mice fed with Ctl or AD diet for 28 days. The mitophagy in macrophages was assessed by flow cytometry staining and determining the median fluorescence intensity (MFI) of MitoTracker and LysoTracker dyes on F4/80+ cells. The mitophagy as assessed by MFI was lower in F4/80+ *Pink1*+/+ renal macrophages after AD diet and in F4/80+ *Pink1*−/− renal macrophages (Figure 5F). These data indicate that macrophage mitophagy is reduced in AD diet-induced kidney fibrosis and in *Pink1* deficient renal macrophages. We observed similar results in *Pink1*−/− BMDMs. The mitophagy in BMDMs was detected by quantifying double positive signals confirming the fusion and colocalization of Mtphagy dye-labeled mitochondria with Lyso-dye stained lysosome. The mitophagy in BMDMs was reduced after TGF-β1 treatment, and compared to *Pink1*+/+ BMDMs, *Pink1*−/− BMDMs displayed significantly reduced mitophagy (Figure 5, G and H) at the basal level. The above findings indicate that the mitophagy in macrophages is impaired under fibrotic conditions.

**MFN2 is phosphorylated by PINK1 and promotes Parkin recruitment to mitochondria in macrophage mitophagy.** PINK1 is a mitochondrial serine/threonine kinase capable of phosphorylating specific mitochondrial proteins, including MFN2 (20).
We observed that knockdown of PINK1 expression in THP-1-derived human macrophages using PINK1-specific siRNA resulted in decreased expression of phosphorylated MFN2 at serine-442 (Ser-442, 86 kDa), relative to non-targeting control siRNA transfected macrophages (Figure 6A). TGF-β1 treatment also reduced the expression of PINK1 (precursor or full length, 64 kDa) in THP-1-derived human macrophages. These findings suggest that MFN2 is a downstream mitochondrial protein target substrate of PINK1 in macrophages.

We further observed that the LysM-Cre+/− Mfn2fl/fl BMDMs from myeloid Mfn2 conditional knock out mice displayed significantly lower mitophagy with or without TGF-β1 treatment, compared to the corresponding control LysM-Cre−/− Mfn2fl/fl BMDMs (Figure 6, B and C). These results indicate that MFN2 plays critical functions in the regulation of mitophagy in macrophages.

PINK1-dependent recruitment of Parkin to mitochondria has been shown to promote mitophagy (30, 31). Thus, we investigated the role of MFN2 in the recruitment of Parkin to the mitochondria of macrophages. We isolated the mitochondrial fractions from the peritoneal macrophages cultured in the presence of DMSO (vehicle control) or FCCP (5 µM/ml) for 2 hours and analyzed for expression of Parkin and mitochondrial marker TOM20. Mitochondrial uncoupler FCCP induced recruitment of Parkin to the depolarized mitochondria as confirmed in LysM-Cre−/− Mfn2fl/fl macrophages (Figure 6D). However, in LysM-Cre+/− Mfn2fl/fl macrophages the FCCP-induced recruitment of Parkin to the mitochondria was considerably lower compared to LysM-Cre−/− Mfn2fl/fl macrophages. These findings suggest that MFN2 may function upstream of Parkin, and following PINK1-dependent activation of mitophagy, MFN2 promotes the recruitment of Parkin to the
mitochondria in macrophages.

**PINK1 deficiency impairs macrophage mitochondrial homeostasis during kidney fibrosis.** To further examine the role of TGF-β1-mediated suppression of the expression of mitophagy regulators in macrophages, we studied the effects of TGF-β1 on macrophage mitochondrial respiration as assessed by Mito Stress test. We show that the macrophage mitochondrial respiration was decreased after treatment with TGF-β1. Pink1<sup>-/-</sup> BMDMs after TGF-β1 treatment displayed significantly lower mitochondrial oxygen consumption rate (OCR), ATP production, spare respiratory capacity, and maximal respiration than Pink1<sup>+/+</sup> BMDMs (Figure 7A). There were no differences in the rate of non-mitochondrial respiration between Pink1<sup>+/+</sup> and Pink1<sup>-/-</sup> BMDMs. TGF-β1-treated Pink1<sup>-/-</sup> BMDMs exhibited higher production of mitochondrial-derived superoxide ions as measured by MitoSox staining (Figure 7B). These data suggest that TGF-β1 negatively affects macrophage mitochondrial homeostasis, and PINK1 deficiency further impairs the macrophage mitochondrial metabolic health.

We next studied the impact of the loss of PINK1-dependent mitophagy on the renal macrophage mitochondrial injury in experimental kidney fibrosis. We used transmission electron microscopy to analyze the ultrastructure of the renal macrophage mitochondria in the kidneys from Pink1<sup>+/+</sup> and Pink1<sup>-/-</sup> mice after 28 days of AD or control diet. Evidence of mitochondrial swelling in the renal macrophages was observed in Pink1<sup>+/+</sup> mice after AD-induced fibrosis. Renal macrophages from Pink1<sup>-/-</sup> mice fed with control diet displayed widening of the mitochondrial cristae. However, renal macrophages from AD fed Pink1<sup>-/-</sup> mice had higher numbers of abnormal mitochondria, with evidence of reduced density of matrix and disorganized cristae, compared to Pink1<sup>+/+</sup> AD fed mice (Figure 7C). These
data suggest that lack of PINK1-mediated mitophagy-dependent elimination of damaged mitochondria contributes to their accumulation. Collectively, the above findings provide evidence that PINK1 exerts a critical role in maintaining renal macrophage mitochondrial quality control, and its deficiency contributes to macrophage mitochondrial injury during kidney fibrosis.

**Mitophagy regulators, PINK1, MFN2, and Parkin are repressed in the kidney and in circulating mononuclear cells from patients with CKD.** Increased macrophage infiltration (32), and mitochondrial impairment (33) have been reported in patients with kidney diseases. Here, we explored the role of mitophagy in human kidney disease. Kidney allograft biopsy samples obtained from CKD patients with histological evidence of interstitial fibrosis and tubular atrophy (IFTA) (Table 1) displayed significantly lower mRNA expression of mitophagy regulators PINK1 (Figure 8A), MFN2 (Figure 8B), and PRKN (Figure 8C), compared to kidney biopsy samples from patients with no CKD (CKD-). Furthermore, circulating levels of chemokine CCL2 were higher in the plasma samples from CKD patients (Figure 8D). CCL2 acts as a ligand for CCR2 expressing macrophages, and increased levels are known to promote macrophage infiltration (34) and progressive tubulointerstitial kidney disease (35). Our findings suggest that in CKD, mitophagy is suppressed while increased circulating CCL2 induces macrophage infiltration to promote kidney fibrosis.

Similarly, peripheral blood mononuclear cells (PBMCs) from patients with severe CKD displayed lower expression of MFN2 (Figure 8E) and Parkin (Figure 8F), and higher mitochondrial-derived superoxide production (Figure 8G) than patients with mild or moderate CKD (Table 2). Higher mROS levels and lower expression of mitophagy...
regulatory proteins in patients with severe kidney disease provide evidence that mitophagy in mononuclear cells decreased with the progression of CKD.

**Mitophagy controls human primary renal macrophage-induced fibrotic response.**

We next isolated the macrophages from human kidney (Supplemental Figure 4B) and investigated the effects of TGF-β1 on the expression of mitophagy regulators. TGF-β1 treatment of human primary renal macrophages resulted in decreased expression of PINK1, MFN2, and Parkin, and increase in the fibrotic response as assessed by FN and CX3CR1 expression (Figure 8H). In line with our above findings, these data suggest that increased fibrotic response by renal macrophages is associated with decreased expression of mitophagy regulators.

We next determined the effect of mitochondrial division inhibitor 1 (Mdivi1), a mitophagy inhibitor that has also been shown to modulate mROS production through mitochondrial complex I (36). We observed that Mdivi1 treated human renal macrophages showed reduced expression of mitophagy mediators (PINK1, MFN2, and Parkin) (Figure 8I) and lower mitochondrial membrane potential than DMSO (vehicle) treated cells (Figure 8J). The decrease in the expression of mitophagy mediators was associated with increased expression of TGF-β1, CD206, CX3CR1, FN, and α-SMA (Figure 8I).
Discussion:
Mitophagy is found to be induced during acute kidney injury (14, 22, 37, 38) and compromised during CKD in animal models (39, 40). Mitochondrial dysfunction is also reported in human kidney disease (33). However, the role of macrophage mitophagy in the pathogenesis of kidney fibrosis in progressive CKD is largely unknown. Our findings utilizing two different models of kidney fibrosis indicate that the renal expression of mitophagy mediators is downregulated during kidney fibrosis and implicate the relevance in the development of kidney fibrosis. The present study provides the first demonstration that macrophage mitophagy is protective against kidney fibrosis via the PINK1/MFN2/Parkin-mediated pathway.

The paradigm that mitophagy protects against kidney fibrosis by modulating the macrophage-derived fibrotic response is in accordance with evidence provided by previous reports. For example, autophagy regulates the macrophage-derived mitochondrial-superoxide production, as both Beclin or LC3 deficient macrophages produce higher superoxide anion radicals (O$_2^-$) (41). Chemical inhibition of autophagy in macrophages using 3-methyladenine results in increased numbers of damaged mitochondria and the production of mROS (42). In addition, the increase in the ROS levels is associated with enhanced differentiation of alternatively-activated/M2 macrophages (43). In the mouse model of diabetic nephropathy, mitochondrial-targeted antioxidant (MitoQ), by scavenging mROS, has been shown to protect against high glucose-induced renal damage and mitochondrial dysfunction (40).

Our conclusion that PINK1-mediated mitophagy modulates macrophage-derived fibrotic response is supported by several compelling observations. First, we show that the renal
macrophages from fibrotic kidneys of both $\text{Pink1}^{-/-}$ or $\text{Prkn}^{-/-}$ mice display the amplified fibrotic response. Macrophage-specific deletion of $\text{Mfn2}$ aggravates kidney fibrosis. Second, the circulating and renal Ly6C$^{\text{low}}$ CD11b$^+$ monocytes and renal profibrotic/M2 macrophages are higher, while the Ly6C$^{\text{high}}$ proinflammatory and Ly6C$^{\text{int}}$ monocytes are lower during kidney fibrosis in $\text{Pink1}^{-/-}$ or $\text{Prkn}^{-/-}$ or $\text{LysM-Cre}^{+/-} \text{Mfn2}^{fl/fl}$ mice. Ly6C$^{\text{low}}$ monocytes and profibrotic macrophages contribute to advancing kidney fibrosis (4, 7, 25, 27) while Ly6C$^{\text{int}}$ population plays reparative functions during kidney injury (25). Third, both $\text{Pink1}^{-/-}$ or $\text{Prkn}^{-/-}$ renal macrophages show higher expression of Gal-3, a M2/profibrotic marker during kidney fibrosis. Fourth, both $\text{Pink1}^{-/-}$ or $\text{Prkn}^{-/-}$ BMDMs exhibit enhanced M-CSF and IL-4-induced polarization towards M2 phenotype and TGF-$\beta_1$-stimulated fibrotic response. The mechanism through which these mitophagy mediators regulate the macrophage-polarization towards M2 phenotype may be rictor-dependent. Loss of $\text{Pink1}$ in BMDMs results in greater mitochondrial-derived superoxide production after TGF-$\beta_1$ treatment. Previous studies have identified critical roles of rictor (28, 29, 44) and mitochondrial-derived ROS (43) in promoting macrophage differentiation towards M2 phenotype. Mitophagy is also demonstrated to regulate the expression of TGF-$\beta_1$ mRNA in alveolar macrophages (45). However, no study has investigated the role of PINK1-mediated mitophagy in macrophage reprogramming, particularly in the context of kidney fibrosis.

The reduced expression of mitophagy regulators in both the renal macrophages from the fibrotic kidney and the mitochondrial fractions from TGF-$\beta_1$ treated BMDMs suggest that macrophage mitophagy is compromised during kidney fibrosis. We, for the first time, demonstrate that the numbers of abnormal mitochondria in $\text{Pink1}^{-/-}$ renal macrophages
are increased in kidney fibrosis induced after 28 days of AD, suggesting the role of PINK1-mediated mitophagy in macrophage mitochondrial quality control. We show that after AD diet-induced kidney fibrosis and in response to TGF-β1, mitophagy in renal macrophages and BMDMs respectively decreases. The loss of Pink1 was associated with reduced mitophagy in macrophages. Our data also show that the expression of mitophagy regulatory proteins in the mitochondria of BMDMs decreases after TGF-β1 treatment. The decline in oxygen consumption rate (OCR), ATP production, and maximal respiration by BMDMs in response to TGF-β1 treatment further confirms that macrophage-mitochondrial respiration is impacted during fibrotic conditions. Our findings confirm that PINK1 exerts critical function in maintaining macrophage-mitochondrial homeostasis. Accordingly, TGF-β1-treated Pink1+/− BMDMs display lower mitochondrial respiration and higher mitochondrial-derived superoxide production. The mitophagy and mitochondrial respiration are highly interconnected processes. The damaged mitochondria with decreasing membrane potential are usually removed through mitophagy (15). Accumulation of dysfunctional mitochondria due to defective mitophagy in the absence of PINK1 exaggerates mitochondrial-derived oxidative stress that may negatively regulate mitochondrial respiration.

The understanding of the molecular regulation of mitophagy in macrophages is not well established. We show that PINK1 functions upstream of MFN2, as the phosphorylation of MFN2 at Ser-442 decreases after PINK1-knockdown in human macrophages. Our observations indicate that the MFN2 bridges between PINK1 and Parkin and facilitate the import of cytosolic Parkin to the depolarized mitochondria, as evidenced by LysM-Cre+/− Mfn2fl/fl BMDMs displaying significantly lower mitophagy with or without TGF-β1
Moreover, the FCCP-induced recruitment of Parkin on the depolarized mitochondria was lower in the absence of MFN2. These findings suggest that the mitophagy in macrophages involves MFN2-dependent recruitment of cytosolic Parkin to the damaged mitochondria. Our findings on the molecular regulation of mitophagy in macrophages support the published studies on the mechanism of mitophagy in other cells (20, 46). However, TGF-β1 induced decrease in the recruitment of mitophagy regulatory proteins on the mitochondria of macrophages is not described before, to our knowledge. Our findings in human primary renal macrophages and CKD patients strongly corroborate our experimental observations from animal models. Our studies confirm that the mitophagy in the kidney and mononuclear cells was impaired while the circulating levels of chemokine CCL2, which promotes macrophage recruitment into the kidney, was higher in patients with severe CKD. These findings on macrophages and mitophagy are in line with the earlier published studies performed in animal models (2, 4, 22, 39, 40) and collectively highlight the cytoprotective role of mitophagy against macrophage-derived progression of kidney fibrosis.

Our investigations using primary human renal macrophages also confirm that PINK1/Parkin-mediated mitophagy regulates macrophage-induced fibrotic response. This is based on our findings that i) the expression of downstream regulators of PINK1-dependent mitophagy decreases after TGF-β1-induced increase in the fibrotic response, and ii) the increase in the expression of fibrotic markers in Mdivi1-treated macrophages is associated with decrease in the expression of mitophagy regulators. However, further research is required to determine the PINK1/Parkin-dependent mechanism of regulation of macrophage polarization towards M2 phenotype through mROS or rictor.
In conclusion, our present studies provide a mechanistic understanding of the role of PINK1/MFN2/Parkin-mediated macrophage mitophagy and its role in the context of kidney fibrosis. Our findings indicate that the mitophagy regulators are downregulated in experimental animal models of kidney fibrosis, in renal macrophages from fibrotic kidney, in TGF-β1-treated primary mouse BMDMs and human renal macrophages, and in the human CKD kidney. The deficiency of mitophagy regulators contributes to mitochondrial dysfunction, impaired mitophagy, and elevated levels of mROS and rictor expression, both of which promote macrophage reprogramming towards profibrotic/M2 phenotype (Figure 9). Hence, it may be prudent to investigate the potential of therapeutically targeting the negative regulators of mitophagy to modulate the macrophage-derived progression of kidney fibrosis and protect against the advancement of CKD.
Methods:

**Mice.** *Pink1<sup>−/−</sup>* and *Prkn<sup>−/−</sup>* mice were provided by Dr. Jie Shen (Center for Neurologic Diseases, Brigham and Women’s Hospital, Harvard Medical School). C57BL/6 mice were purchased from the Jackson Laboratory. *Mfn2<sup>loxp/loxp</sup>* (stock 029902-UCD) mice were generated by Dr. David C. Chan and were purchased from Mutant Mouse Resource & Research Center. The myeloid-specific *Mfn2*-deficient strain was generated by crossing the *Mfn2<sup>loxp/loxp</sup>* (*Mfn2fl/fl*) line to a strain expressing Cre under the control of the endogenous promoter of lysozyme M (*LysM-Cre* strain; stock 004781, Jackson Laboratory). These myeloid-specific *Mfn2* deficient mice here referred as *LysM-Cre<sup>+/−</sup>Mfn2<sup>fl/fl</sup>*. The *LysM-Cre<sup>−/−</sup>Mfn2<sup>fl/fl</sup>* mice were used as corresponding controls.

**Unilateral Ureteral Obstruction (UUO) model of kidney fibrosis.** UUO surgery was performed as previously described (47). Briefly, mice (3 to 5 per group) were anesthetized, and ureteral obstruction surgery was carried out by double ligation of the left ureter using 4-0 silk suture via a left flank incision. Sham-operated mice had their ureters exposed but not ligated. The kidneys were harvested on day 7 for histology, western blotting, and flow cytometry. The blood was collected for flow cytometry.

**Adenine diet (AD)-induced model of kidney fibrosis.** Mice were fed with 0.2% of AD or control diet (Envigo; #TD150071) as previously described (48). The kidneys were collected at the end of the study on day 14 or day 28 for western blotting, hydroxyproline assay, and electron microscopy. Whole Blood samples were collected for chemokine analysis.

**Cell culture and transfection.** For the isolation of BMDMs, bone marrow cell suspension was prepared through flushing femurs and tibias, and cultured in the
presence of monocyte colony-stimulating factor (M-CSF; 10 ng/ml; Biolegend) for 7
days (49). The polarization of BMDMs towards M1 macrophages was performed using
recombinant interferon-gamma (rIFN-γ; 10 ng/ml, Biolegend), lipopolysaccharide
(LPS; 100 ng/ml, Invivogen), granulocyte monocyte colony-stimulating factor (GM-
CSF; 25 ng/ml; StemCell Technologies). For M2 macrophages, BMDMs were cultured
in presence of recombinant interleukin-4 (rIL-4; 10 ng/ml; Biolegend), M-CSF (25 ng/ml,
Biolegend) for 24 hours.
Peritoneal macrophages were isolated by recovering peritoneal lavage (49), allowed to
adhere to the sterile petri dishes for 3 hours, and subsequently subjected to treatment
with carbonyl cyanide 4-(trifluoromethoxy) phenylhydrazone (FCCP) (5 µM/ml; Abcam)
or DMSO (vehicle control) for 2 hours.
The macrophages from a human monocytic THP-1 cell line (ATCC #202) were derived
by incubating in the presence of phorbol 12-myristate 13-acetate (PMA; 10 ng/ml; Sigma)
for 3 days. Human SMARTpool on-target plus Pink1-specific (L-004030-00-0005) or non-
targeting (D-001810-10-05) siRNAs were purchased from Dharmacon (GE Healthcare).
THP-1 derived macrophages were transfected with a pool of either Pink1-specific or non-
targeting siRNAs using transfection reagent (Lipofectamine RNAimax; Thermo Fisher
Scientific) followed by treatment with TGF-β1 (5 ng/ml) for 24 hours.

**Isolation of Renal macrophages.** The macrophages from mouse and human kidneys
were isolated using Ficoll-Hypaque density gradient centrifugation followed by
magnetic-activated cell sorting (MACS) separation protocol (**Supplemental Figure 4**).
Kidney tissue was minced into 1 - 2 mm³ pieces and digested using collagenase type I
(2 mg/ml; Gibco). The single-cell suspensions obtained after digestion were
subsequently incubated with ACK lysing buffer (Gibco) for the lysis of red blood cells (RBCs), followed by isolation of renal mononuclear cells (RMNCs) by Ficoll-Hypaque (Gibco) density gradient centrifugation method (50). The macrophages from mouse RMNCs were sorted using anti-CD115 biotin-conjugated antibody and anti-Biotin microbeads (Miltenyi Biotec) using MACS cell separation protocol for CD115 positive selection (Supplemental Figure 4A) (28). The macrophages from human RMNCs, were sorted using PE-conjugated anti-CD68 antibody and anti-PE ultrapure microbeads (Miltenyi Biotec) using MACS positive cell selection protocol (Supplemental Figure 4B).

**Peripheral blood mononuclear cells (PBMCs) isolation.** PBMCs were isolated from whole blood using Ficoll-Paque density gradient centrifugation method as previously described (50). Blood samples were first diluted in PBS in 1:1 and layered on the surface of Ficoll-Paque (GE Healthcare) and centrifuged at 670 g for 20 minutes at 20°C with no breaks. The mononuclear cells were carefully harvested from the interface of diluted plasma and Ficoll. RBCs were lysed using ACK lysing buffer (Gibco). Cells were washed and stored in cryopreservation media (40% RPMI, 50% FBS, 10% DMSO) in -80°C until further use for flow cytometry staining.

**Flow cytometry.** The surface and intracellular staining were performed on renal single-cell suspensions, BMDMs, or peritoneal macrophages. The nonspecific sites were blocked by using anti CD16/32 antibody (BioLegend #101302) by incubating cells for 15 minutes at 4°C. The following antibodies were used for staining: anti-CD45 (Biolegend), anti-F4/80, anti-CD11b, anti-CD206, anti-Ly6C (Thermo Fisher Scientific, Waltham, MA), anti-Gal-3 (Biolegend, San Diego, CA), anti-latency associated peptide (LAP or TGF-β1) (Biolegend, San Diego, CA), anti-MFN2 (Abcam, Cambridge, MA)
and anti-Parkin (Cell Signaling Technology, Danvers, MA) antibodies. The fixation permeabilization treatment was performed before staining for an intracellular marker using fix/perm buffer (Thermo Fisher Scientific) for 15 minutes at 4°C. The secondary fluorochrome-conjugated antibodies used were anti-rabbit Alexa Fluor 488 and anti-mouse Alexa Fluor 647 (Thermo Fisher Scientific). The stained cells were washed twice with FACS buffer (PBS with 2% Fetal Bovine Serum) and fixed using 2% paraformaldehyde (Santa Cruz Biotechnology Inc.). The cells were captured using BD Accuri C6 flow cytometer, and the data were analyzed using C6 analysis (BD Biosciences) or FlowJo version 10.8 (Tree Star, Inc, Ashland, OR) software.

**Measurement of mitophagy, membrane potential and superoxide levels by Flow Cytometry.** The mitophagy in renal single-cell suspensions was determined through flow cytometry staining for MitoTracker and LysoTracker dyes and anti-F4/80 antibody (Thermo Fisher Scientific) as per the manufacturer’s protocol. The mitophagy in BMDMs was detected according to the assay protocol (mitophagy detection kit, Dojindo, Rockville, MD) using flow cytometry (51, 52). BMDMs were incubated with Mtphagy dye (100 nmol/l) at 37°C for 1 hour with 5% CO₂ and 95% humidity, followed by treatment with TGF-β1 (5 ng/ml) for 48 hours at 37°C in serum-free M-CSF conditioned media. The cells were then washed and incubated with lyso dye (1 μmol/l) for 1 hour. The mean fluorescence intensity (MFI) or the counts of the double positive signal for the Mtphagy dye labeled mitochondria colocalized with Lyso dye-labeled lysosomes were measured using flow cytometry (Accuri C6, BD Biosciences, San Jose, CA).

The mitochondrial membrane potential was determined by calculating MFI or positive signal for MitoTracker Red dye (50 nM, Thermo Fisher Scientific) stained cells. The levels
of mitochondrial-derived superoxide or reactive oxygen species (mROS) were detected by MitoSox staining (5 μM; Thermo Fisher Scientific). The cells were captured using BD Accuri C6 flow cytometer.

**Measurement of oxygen consumption rate and ATP production.** Mitochondrial respiration was determined using Mito Stress test by Seahorse XF96 Extracellular Flux analyzer (Agilent Technologies, Billerica, MA) according to the manufacturer’s protocol. Briefly, 2.5 x 10⁴ BMDMs were counted using hemocytometer and seeded per well in 96-well Seahorse plate and incubated overnight in serum-free M-CSF conditioned media followed by treatment with TGF-β1 (5 ng/ml) for 24 hours at 37°C in the CO₂ incubator. One hour before the measurement of mitochondrial respiration, the BMDMs were washed, and the media was replaced with 175 μL of Seahorse XF RPMI media (without phenol red) supplemented with 1 mM of sodium pyruvate and 2 mM of glucose solution for 1 hour at 37°C in the CO₂ free incubator. The measurement for OCR on Seahorse analyzer was performed for each well, three measurements at the basal level, three after automated injection of Oligomycin (1 μM) FCCP (1 μM), and finally, three after injections of both rotenone (1 μM) and antimycin A (1 μM). The cell counts were confirmed using CyQUANT™ kit (Thermo Fisher Scientific). The results were analyzed using XF Wave software (Agilent Technologies).

**Enzyme-Linked Immunosorbent Assay (ELISA).** The levels of CCL2 in the mouse plasma (LS Bio; LS-F271-1) and human plasma (R&D Systems #DCP00) samples were quantitated using sandwich ELISA by following manufacturer’s instructions.
Transmission electron microscopy. Kidney tissues were fixed with 2.5% glutaraldehyde, 4% paraformaldehyde, and 0.02% picric acid in 0.1 M sodium cacodylate buffer at pH 7.2 for overnight at 4°C. Tissues were washed twice with 0.1 M sodium cacodylate buffer. Following a secondary fixation in 1% osmium tetroxide and 1.5% potassium ferrocyanide, the samples were dehydrated through a series of graded ethanol and embedded in an EPON analog resin. Ultrathin sections were cut using Accu-Edge high-profile blades (4685; Sakura) on a Microm HM 355S (Thermo Fisher Scientific). Sections were placed on the copper grids, contrasted with lead citrate, and captured on the electron microscope (JEM 1400, JEOL). Images were recorded with the associated digital camera (Veleta 2K, Olympus-SIS). The number of abnormal mitochondria in renal macrophages (3 and 10 cells for control and adenine diet respectively) were calculated using ImageJ software (NIH).

TaqMan quantitative PCR (qPCR). Total RNA was extracted from human kidney tissue using RNeasy mini kit (74104; Qiagen) according to the manufacturer’s instructions. The mRNA was converted into cDNA using SuperScript III reverse transcriptase kit (Life Technologies) and subjected to qPCR. The relative expression levels of PINK1 (Hs00260868), MFN2 (Hs00208382) and PRKN (Hs01038318) mRNA were determined using the quantitative TaqMan qPCR method. qPCR was performed in the ABI PRISM 7500 Real-Time PCR System (Applied Biosystems). The data were normalized to a housekeeping gene ACTB (Hs01060665). The gene expression assay reagents were procured from Thermo Fisher Scientific.

Western blot, immunohistochemistry (IHC) and immunofluorescence assay (IF). The mouse kidney tissue and BMDMs were harvested in tissue extraction (Thermo Fisher
Scientific #78510) and mammalian protein extraction (Thermo Fisher Scientific #78501) buffers, respectively containing protease inhibitor cocktail (Thermo Fisher Scientific #78441). Mitochondrial fractions were isolated using the mitochondrial isolation kit (Biovision #K265-25). Protein concentrations were determined using the BCA assay (Thermo Fisher Scientific #23225). The membranes were subjected to western blot analysis with the antibodies against fibronectin Abcam #2413), collagen I (Abcam #21286), TGF-β1 (Cell Signaling Technology #3711S), CD206 or Mannose receptor-1 (Abcam #64693), Arginase-I (Arg-I; Santa Cruz Biotechnology #271430), Galectin-3 (Santa Cruz Biotechnology #32790), MFN2 (Abcam #56889), phospho-MFN2 (Serine-442) (Millipore Sigma #ABC963), PINK1 (Santa Cruz Biotechnology #517353), Parkin (Cell Signaling Technology #2132S), LC3 (Sigma-Aldrich #L7543), TIM23 (BD Biosciences #611223) and human or mouse β-actin (Cell Signaling Technology #2132S). Chemiluminescent bands were visualized using enhanced chemiluminescence solution (Thermo Fisher Scientific). Quantification of Western blots was performed using ImageJ software version 1.46 (NIH).

For IHC, Kidney tissues from mice after UUO or Sham surgery or from the mice fed with AD or control diet were fixed overnight in 4% paraformaldehyde. Sections were dehydrated and embedded in paraffin blocks. Sections (4 μm) were collected on Superfrost Plus positively charged microscope slides (Thermo Fisher Scientific), deparaffinized, and stained with Masson’s trichrome.

Immunofluorescence staining for confocal microscopy on BMDMs was performed using anti-LC3 antibody (Sigma-Aldrich #L7543), and MitoTracker Deep Red (Invitrogen # M22426) and Hoechst blue (Thermo Scientific #62249) dyes. The images were captured
on Zeiss LSM 880 confocal microscope at x40 magnification with a zoom factor of 1.6. The colocalization of LC3 (green) on MitoTracker (red) dye was quantified using ImageJ software (NIH).

**Statistics.** The statistical analysis was performed on statistical software (GraphPad Prism version 5.0). Data were analyzed using one-way analysis of variance (ANOVA) followed by Bonferroni post-hoc or Newman-Keuls post-hoc test. To compare two groups, data were analyzed by Student's unpaired t-test or Mann-Whitney test.

**Study approvals.** All animal experiments were performed under protocols approved by the Institutional Animal Care and Use Committee (IACUC) of Weill Cornell Medicine. Human blood and kidney biopsy samples were obtained under the approved protocols by the Institutional Review Board (IRB) registry study at Weill Cornell Medicine. Human kidneys used for macrophage isolation were obtained from the New York organ procurement organization (OPO). These deidentified kidneys, from deceased organ donors, were rejected for clinical transplantation and are not considered as "human subject research" as per the standard NIH definition. Hence, no IRB approval of the protocol for the kidneys tissue used for the macrophage isolation was required.
Author contributions

DB and MEC designed the project. DB performed all experiments. KPC, KN, EP, MR, and LT contributed to the experimental plan. DB, AMKC, and MEC analyzed the data and wrote the manuscript. OA and TM contributed human clinical samples. MEC supervised the project.

Acknowledgments

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Disclosure Statement

The spouse of MEC is a cofounder and shareholder, and serves on the Scientific Advisory Board of Proterris, Inc. AMKC is a cofounder, stockholder and serves on the Scientific Advisory Board for Proterris, which develops therapeutic uses for carbon monoxide (CO). AMKC also has a use patent on CO.

Competing Interests

All authors declare no competing interests.
References:


49. Weng SY. et al. IL-4 Receptor Alpha Signaling through Macrophages Differentially Regulates Liver Fibrosis Progression and Reversal. *EBioMedicine.* 2018;29:92-103.


Table 1. Clinical characteristics of adult patients with and without CKD

<table>
<thead>
<tr>
<th>Cohort characteristics</th>
<th>Non-CKD ((n = 9))</th>
<th>CKD ((n = 6))</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age, years</td>
<td>43.0 (38.5 to 58.0)</td>
<td>45.5 (43.3 to 54.5)</td>
<td>0.375</td>
</tr>
<tr>
<td>Sex, Male/Female</td>
<td>5/4</td>
<td>2/4</td>
<td>0.398*</td>
</tr>
<tr>
<td>GFR (mL/min/1.73 m²)</td>
<td>33.0 (27.5 to 42.0)</td>
<td>24.5 (16.8 to 33.0)</td>
<td>0.047</td>
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<tr>
<td>Urine ACR (mg/g)</td>
<td>50.4 (7.9 to 234.1)</td>
<td>762.8 (74.8 to 1413)</td>
<td>0.009</td>
</tr>
<tr>
<td>Serum Creatinine (mg/dL)</td>
<td>1.9 (1.6 to 2.5)</td>
<td>2.3 (1.9 to 3.6)</td>
<td>0.044</td>
</tr>
<tr>
<td>BUN (mg/dL)</td>
<td>26.0 (22.5 to 36.0)</td>
<td>49.0 (27.5 to 63.8)</td>
<td>0.009</td>
</tr>
<tr>
<td>Induction therapy</td>
<td>9/9</td>
<td>6/6</td>
<td>-</td>
</tr>
<tr>
<td><strong>Immunotherapies (at the time of transplantation)</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Basiliximab</td>
<td>2/9</td>
<td>1/6</td>
<td>0.810</td>
</tr>
<tr>
<td>ATG</td>
<td>7/9</td>
<td>5/6</td>
<td>0.810</td>
</tr>
<tr>
<td><strong>Maintenance Immunotherapies</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Tacrolimus</td>
<td>9/9</td>
<td>5/6</td>
<td>0.234</td>
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<tr>
<td>MMF</td>
<td>9/9</td>
<td>5/6</td>
<td>0.234</td>
</tr>
<tr>
<td>Cyclosporin A</td>
<td>0</td>
<td>1/6</td>
<td>0.234</td>
</tr>
<tr>
<td>Rapamycin</td>
<td>0</td>
<td>1/6</td>
<td>0.234</td>
</tr>
</tbody>
</table>

GFR, glomerular filtration rate; ACR, albumin/creatinine ratio; BUN, blood urea nitrogen, ATG: anti-thymocyte globulin, MMF: Mycophenolate mofetil. Continuous variables are presented as median (interquartile range) and analyzed using t-test. ^ Proportions analyzed using chi-square test.

Table 2. Clinical characteristics of pediatric patients with CKD

<table>
<thead>
<tr>
<th>Patient characteristics</th>
<th>Mild or Moderate CKD ([GFR \geq 30 \text{ ml/min/1.73m}^2]) ((n = 15))</th>
<th>Severe CKD ([GFR &lt;30 \text{ ml/min/1.73m}^2]) ((n = 8))</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age, years</td>
<td>14.0 (9.0 to 15.2)</td>
<td>15.9 (12.3 to 17.6)</td>
<td>0.088</td>
</tr>
<tr>
<td>Sex, Male/Female</td>
<td>10/5</td>
<td>2/6</td>
<td>0.057@</td>
</tr>
<tr>
<td>GFR (mL/min/1.73 m²)</td>
<td>48.8 (38.0 to 74.6)</td>
<td>13.9 (6.1 to 25.8)</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Urine ACR (mg/g)^</td>
<td>32 (5.2 to 97)</td>
<td>706.8 (58.0 to 6649.0)</td>
<td>0.026</td>
</tr>
<tr>
<td>Serum Creatinine (mg/dL)</td>
<td>1.3 (0.83 to 1.65)</td>
<td>4.4 (2.0 to 10.7)</td>
<td>0.001</td>
</tr>
<tr>
<td>BUN (mg/dL)</td>
<td>25.0 (18.0 to 30.0)</td>
<td>61.5 (53.5 to 78.5)</td>
<td>&lt;0.0001</td>
</tr>
</tbody>
</table>
GFR, glomerular filtration rate; ACR, microalbumin/creatinine ratio, ^ available on n = 11 (moderate or mild CKD) and n = 4 (severe CKD) patients; BUN, blood urea nitrogen. Values are expressed as median (interquartile range) and compared using t-test. Proportions analyzed by chi-square test.
Figure 1. Mitophagy-related proteins are downregulated in experimental kidney fibrosis and loss of PINK1 or Parkin promotes kidney fibrosis. A) Western blot and densitometry analysis for expression of Mitofusin 2 (MFN2), Parkin, and microtubule-associated protein light chain 3 (LC3) normalized to β-actin in kidney tissue lysates from wild type mice 7 days after sham or UUO surgery. Data are mean ± SEM representative of 3 independent experiments, (n = 3 per group), and analyzed by student's unpaired 2-tailed t-test.

B) Representative Masson’s trichrome-stained kidney tissue sections (40X magnification) from wild type, Pink1−/− and Prkn−/− mice 7 days after sham (n = 3 per group) or UUO (n = 5 per group) surgery. Ten areas from random fields per experimental group were analyzed and quantitated using ImageJ. Data are mean ± SEM, compared using one-way ANOVA. Scale bars: 200 μm.

C and D) Western blot and densitometry analysis for the expression of fibronectin (FN), TGF-β1, and arginase I (Arg-I) normalized to GAPDH in kidney tissue lysates from Pink1+/+, Pink1−/− (C), Prkn+/+, and Prkn−/− (D) mice 7 days after sham or UUO surgery. Data are mean ± SEM representative of 3 independent experiments, (n = 3 per group), and analyzed by one-way ANOVA. *P< 0.05 and **P<0.01, ***P<0.001.
Figure 2

**A** PINK1 deficient renal macrophages display higher profibrotic response. A) Representative flow cytometric plots and analysis showing the numbers of CD206+ F4/80+ cells in the kidney from Pink1+/+ and Pink1−/− mice 7 days after sham or UUO surgery (n = 5 per group).

**B** Representative flow cytometric data showing the counts of Ly6Chigh, Ly6Cint, and Ly6Clow CD11b+ populations in the kidney from Pink1+/+ (n = 4 per group) and Pink1−/− (n = 3 per group) mice 7 days after sham or UUO surgery.

**C** Densitometry analysis and western blot for fibronectin (FN) normalized to GAPDH in Pink1+/+ and Pink1−/− renal macrophages isolated 7 days after sham (n = 3 per group) or UUO (n = 5 per group) surgery.

**D** Western blot for fibronectin (FN), arginase (Arg-I), galectin-3 (Gal-3) and β-actin in Pink1+/+ or Pink1−/− bone-marrow-derived macrophages (BMDMs) cultured in the absence (-) or presence (+) of TGF-β1 (5 ng/ml) for 24 hours. The data are representative of three independent experiments. Data are mean ± SEM. *P< 0.05, **P<0.01 and ***P<0.001 analyzed by one-way ANOVA.
Figure 3. Loss of Parkin increases profibrotic macrophages during kidney fibrosis. A) Flow cytometric data showing the numbers of CD206+ F4/80+ cells in the kidney from Prkn+/+ and Prkn−/− mice 7 days after sham (n = 4 per group) or UUO surgery (n = 3 per group). B) Frequencies of Ly6C^{high}, Ly6C^{int}, and Ly6C^{low} CD11b+ populations in the kidney from Prkn+/+ and Prkn−/− mice 7 days after sham (n = 5 per group) or UUO (n = 5 per group) surgery analyzed by flow cytometry. C) Western blot for inducible nitric oxide synthase (iNOS), arginase (Arg-I), rictor, and GAPDH on M0, M1 or M2 wild type, Pink1−/− or Prkn−/− BMDMs. The data are representative of three independent experiments. D) Flow cytometry data showing the expression of rictor on CD11b+ (upper panels) or F4/80+ (lower panels) populations in the cells isolated from peritoneal cavity. The data are representative of three independent experiments and are mean ± SEM. *P < 0.05, **P < 0.01, and ***P < 0.001 analyzed by one-way ANOVA.
Figure 4. Myeloid-specific loss of MFN2 promotes kidney fibrosis. A) Western blot and densitometry analysis for the expression of fibronectin (FN), CD206, TGF-β1, galectin-3 (Gal-3), and GAPDH in kidney tissue lysates from Mfn2 fl/fl LysM Cre−/− and Mfn2 fl/fl LysM Cre+/− mice fed with control (Ctl) or adenine (AD) diet for 28 days. B) Representative Masson’s trichrome-stained kidney tissue sections (20X magnification) from Mfn2 fl/fl LysM Cre−/− and Mfn2 fl/fl LysM Cre+/− mice fed with Ctl or AD diet for 28 days. Scale bars: 200 μm. C) Representative flow cytometric data showing the counts of Ly6Chigh, Ly6Cint, and Ly6Clow CD11b+ populations in the kidney from Mfn2 fl/fl LysM Cre−/− and Mfn2 fl/fl LysM Cre+/− mice fed with Ctl or AD diet for 28 days. n = 2 (Ctl) or n = 3 (AD) samples per group.
Figure 5

A. Western blots showing PINK1 and β-actin normalized to GAPDH expression in sham and UUO kidneys. TGF-β- TGF-β+.

B. Western blots showing MFN2, Parkin, and TIM23 normalized to β-actin expression in sham and UUO kidneys. MFN2/GAPDH, Parkin/GAPDH.

C. Western blots showing MFN2/TIM23 and Parkin/TIM23 normalized to β-actin expression in sham and UUO kidneys. MFN2/TIM23, Parkin/TIM23.

D. MitoTracker, LC3, Merge, and Zoom images showing colocalization of MitoTracker and LC3 in TGF-β- and TGF-β+ conditions. Pink1+/+, Parkin+.

E. Graph showing LC3 MitoTracker colocalization (%) in TGF-β1- and TGF-β1+ conditions. Pink1+/+, Pink1−/−.

F. Bar graph showing Mitophagy of Renal Macrophages (MFI) in Ctrl AD and TGF-β1 conditions. Pink1+/+, Pink1−/−.

G. Bar graph showing Mitophagy of BMDMs (MFI) in TGF-β1 conditions. Pink1+/+, Pink1−/−.

H. Flow cytometry histograms showing Lyso dye and Mitophagy dye counts in TGF-β1- and TGF-β1+ conditions. Unstained control, Pink1+/+, Pink1−/−.
Figure 5. Macrophage PINK1-mediated mitophagy is suppressed during fibrotic conditions. A) Western blot and densitometry analysis for PINK1 expression normalized to β-actin in THP-1 derived human macrophages cultured in absence (-) or presence (+) of TGF-β1 (5 ng/ml) for 48 hours (n = 5 per group). B) Western blot and densitometry analysis for MFN2 and Parkin normalized to GAPDH in renal macrophages isolated from wild type mice 7 days after sham or UUO surgery (n = 3 per group). C) Western blot and densitometry analysis for MFN2 and Parkin normalized to TIM23 in mitochondrial lysates from BMDMs (n = 4 per group) cultured in the absence (-) or presence (+) of TGF-β1 (5 ng/ml) for 48 hours. β-actin (a cytosolic marker) was used to confirm the purity of mitochondrial fractions. D and E) Representative confocal microscopy images (D) and quantification of mitochondria colocalized with LC3 (E). Pink1+/+ and Pink1-/− BMDMs cultured in absence or presence of TGF-β1 were analyzed using MitoTracker (red) dye, anti-LC3 (green), and Hoechst blue dye. White arrows indicate colocalization of LC3 with mitochondria. Over 100 cells from 6 random fields per experimental group each in triplicates were analyzed using Imagej. Scale bar: 10 mm. F) Mitophagy assessment in Pink1+/+ and Pink1-/− F4/80+ renal macrophages from mice fed with control (Ctl, n = 5 per group) or adenine (AD, n = 7 per group) diet for 28 days and stained with MitoTracker and LysoTracker dyes using flow cytometry. G and H) Mitophagy assessment in Pink1+/+ and Pink1-/− BMDMs (n = 3 per group) cultured in the absence or presence of TGF-β1 (5 ng/ml) for 48 hours using flow cytometry (G). (H) Representative histograms for the detection of mitophagy showing the lyso stained positive lysosomes gated for Mtphagy dye bound mitochondria. Data are mean ± SEM representative of 3 independent experiments and analyzed by student’s unpaired 2-tailed t-test (A, B, C) or one-way ANOVA (E, F, G). *P< 0.05. **P<0.01, and ***P<0.001.
Figure 6. PINK1-mediated phosphorylation of MFN2 and MFN2-facilitates Parkin recruitment to the macrophage mitochondria. A) THP-1-derived human macrophages transfected with PINK1 siRNA or non-targeting (NT) control siRNA, cultured in the absence (-) or presence (+) of TGF-β1 (5 ng/ml) for 48 hours. Western blot for PINK1 (full length, 64 kDa; cleaved, 52 kDa) and phosphorylated (Serine-442)-MFN2 (86 kDa). B and C) Mitophagy measured in LysM-Cre−/− Mfn2fl/fl (n = 3 per group) and LysM-Cre+/- Mfn2fl/fl BMDMs (n = 5 per group) cultured in the absence (-) or presence (+) of TGF-β1 (5 ng/ml) for 48 hours (B). (C) Representative histograms for the assessment of mitophagy showing the lyso dye positive events, gated for Mitophagy dye stained population. The mean fluorescence intensity (MFI) of Mitophagy dye bound mitochondria colocalized with Lyso dye-labeled lysosomes measured using flow cytometry. D) Western blot for Parkin, and TOM20 in peritoneal macrophages isolated from LysM-Cre−/− Mfn2fl/fl and LysM-Cre+/- Mfn2fl/fl cultured in the presence of DMSO (vehicle control) or FCCP (5 µM/ml) for 2 hours. Data are mean ± SEM, and representative of 2 independent experiments. *P< 0.05 and ***P<0.001 analyzed by one-way ANOVA.
Figure 7

**A** PINK1 mediates macrophage mitochondrial respiration during kidney fibrosis. A) *Pink1*+/+ and *Pink1*-/- BMDMs were cultured in the absence (−, n = 5 per group) or presence (+, n = 5 per group) of TGF-β1 (5 ng/ml) for 24 hours. Box-and-whisker plots displaying the first and the third quartiles, with the line within the box indicating the median value (upper panel). Oxygen consumption rate (OCR) under basal conditions followed by the sequential measurements after addition of oligomycin, FCCP, rotenone or antimycin A were determined using Mito Stress test. Dot-plots show mean ± SEM. B) Frequency of mitochondrial-derived superoxide detected in *Pink1*+/+ and *Pink1*-/- TGF-β1-treated BMDMs (n = 3 per group) using MitoSox staining by flow cytometry. C) Representative transmission electron microscopy (TEM) images displaying renal macrophages (labeled as M; 12,000X magnification; Scale bars: 2 μm) and their mitochondria (pointed by arrow, 80,000X magnification; Scale bars: 200 nm) in *Pink1*+/+ and *Pink1*-/- mice after 28 days of control (Ctl) or adenine (AD) diet. Abnormal mitochondria counted from 4 (Ctl) or 7 (AD) renal macrophages from n = 3 mice per group. Data are mean ± SEM. *P < 0.05, **P < 0.01, and ***P < 0.001 analyzed by one-way ANOVA (A: upper panel and C) or student’s unpaired 2-tailed t-test (A: lower panels and B).
Figure 8. Mitophagy is compromised in patients with CKD and in TGF-β1 treated human renal macrophages. A - C) Relative mRNA expression levels of PINK1 (A), MFN2 (B), and PRKN (C) normalized with β-actin (ACTB) were determined by TaqMan qPCR in kidney biopsy from patients with CKD (CKD+, n = 6) and patients without CKD (CKD-, n = 9) and analyzed using Mann-Whitney test. D) Plasma CCL2 levels in patients with (CKD+, n = 6) or without CKD (CKD-, n = 9) were determined by ELISA and analyzed using Mann-Whitney test. E - G) Frequency of MFN2 (E) and Parkin (F) and median fluorescence intensity (MFI) of MitoSox dye (G) in peripheral blood mononuclear cells (PBMCs) from patients with severe-CKD (n = 8) vs. mild or moderate CKD (n = 15) were determined by flow cytometry and analyzed using student’s unpaired 2-tailed t-test. H) Western blot for the expression of PINK1, MFN2, Parkin, Fibronectin (FN), CX3CR1 and β-actin in human primary renal macrophages cultured in the absence (-) or presence (+) of TGF-β1 (5 ng/ml) for 24 hours and analyzed using student’s unpaired 2-tailed t-test. I) Western blot for the expression of PINK1, MFN2, Parkin, TGF-β1, CD206, CX3CR1, FN, α-SMA and β-actin in human primary renal macrophages cultured in the presence of DMSO (vehicle control) or Mdivi-1 (50 µM) for 3 hours. J) Mitochondrial membrane potential in human primary renal macrophages treated with DMSO (vehicle control) or Mdivi-1 (50 µM) for 3 hours detected by staining with MitoTracker dye through flow cytometry. The histogram was gated from FSC vs. SSC parent population. Data are mean ± SEM, *P<0.05, **P<0.01 and ***P<0.001.
Kidney injury by suppressing the expression of mitophagy regulators (PINK1, MFN2, and Parkin) contributes to mitochondrial dysfunction in renal macrophages. The deficiency of PINK1 causes a reduction in the mitofusin-2 (MFN2) phosphorylation at Serine-442. The loss of MFN2 results in lower recruitment of Parkin to the mitochondria and defective mitophagy in macrophages. The failure of mitophagy causes accumulation of abnormal mitochondria, increase in mROS production, and expression of rictor in macrophages. mROS and rictor, both promote the differentiation of macrophages towards profibrotic/M2 phenotype. The increase in the frequency of profibrotic/M2 macrophages results in higher extracellular matrix (ECM) production and progression of kidney fibrosis.