Mechanisms of renal injury and repair: role of stem cells, chemokines and the nodosome
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Chemokine expression in renal ischemia/reperfusion injury is most profound during the reparative phase

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Chemokine expression in renal I/R injury

Abstract

Chemokines are important players in the migration of leukocytes to sites of injury and are also involved in angiogenesis, development, and wound healing. In this study we performed microarray analyses to identify chemokines that play a role during the inflammatory and repair phase after renal ischemia/reperfusion (I/R) injury, and investigated the temporal relationship between chemokine expression, leukocyte accumulation, and renal damage/repair.

C57Bl/6 mice were subjected to unilateral ischemia for 45min and sacrificed 3h, 1d and 7d after reperfusion. From ischemic and contralateral kidney RNA was isolated and hybridized to a microarray. Microarray results were validated with quantitative real-time RT-PCR (QRT-PCR) on RNA from an independent experiment. (Immuno)histochemical analyses were performed to determine renal damage/repair and influx of leukocytes.

Twenty out of 114 genes were upregulated at one or more reperfusion periods. All these genes were upregulated 7d after I/R. Upregulated genes included CC chemokines MCP-1 and TARC, CXC chemokines KC and MIP-2α, chemokine receptors Ccr1 and Cx3cr1, and related genes like MMPs. Microarray data of 1d and 7d was confirmed for 17 upregulated genes by QRT-PCR. (Immuno)histochemical analysis showed that the inflammatory and repair phase after renal I/R injury take place after respectively 1 and 7 days. Interestingly, chemokine expression was highest during the repair phase. In addition, expression profiles showed a biphasic expression of all upregulated CXC chemokines coinciding with the early inflammatory and late repair phase.

In conclusion, we propose that temporal expression of chemokines is a crucial factor in the regulation of renal I/R injury and repair.
Chemokine expression in renal I/R injury

Introduction

Renal ischemia/reperfusion (I/R) injury is a major cause of acute\(^1\) and chronic\(^2\) renal failure. Ischemia is caused by a sudden transient drop in blood flow, frequently occurring in shock, sepsis and during transplantation. Despite the progresses made in health care, there are still only supportive therapies available for this major clinical problem. Therefore, more insight into the mechanisms that regulate ischemic injury and post-ischemic repair are needed.

Chemokines are chemotactic cytokines that are well-known for their ability to direct the migration and activation of inflammatory cells. Chemokines can be divided into four families based on their amino acid sequence in relation to their cysteine moieties/differences in structure: CC, CXC, CX3C and XC (reviewed in\(^3\)). Within these chemokine families functional homology exists; the CXC chemokines attract mainly polymorphonuclear leukocytes to sites of acute inflammation and the CC chemokines attract mainly mononuclear cells to sites of chronic inflammation\(^3\).

Originally studied for their role in inflammation, it has now become clear that chemokines are also involved in other processes including angiogenesis, homeostasis, development, migration of stem cells and wound healing\(^4,5\). During renal I/R injury, infiltrated leukocytes\(^6-8\) as well as all types of renal cells including the tubular epithelial cells (TEC)\(^9\) start to produce chemokines. In different experimental models of renal injury the functional role of several of these chemokines has already been investigated (reviewed by Anders \(et\) \(al\).\(^10\)). In lupus nephritis for example, blocking the interaction between Ccl2/MCP-1 and Ccr2\(^11-13\) or neutralizing Cx3cr1\(^14\) ameliorated the initiation and progression of renal damage. In experimental diabetic nephropathy, Ccl2/MCP-1 deficiency\(^15,16\) or neutralizing Cxcl10/IP-10\(^17\) decreased renal damage by reducing the accumulation of macrophages or T cells, respectively. In ischemic renal injury a protective role of inhibiting Ccl2/MCP-1 signaling\(^18,19\), neutralizing Cxcl1/KC\(^20\) or Cxcl2/MIP-2\(^20\), and blocking the chemokine receptor Cx3cr1\(^21,22\) during the inflammatory response has been reported.

Although several studies have identified chemokines as participants in renal diseases, there is little information regarding their temporal expression. As tissue damage and repair is dependent on a timely induction and suppression of chemokines, and is modulated by the influx of leukocytes it is important to identify alterations in chemokine expression during renal ischemic injury. Therefore our aim was to determine the expression of chemokines and their receptors in a self-healing \textit{in vivo} model of I/R injury during different phases of I/R injury and to investigate the temporal relationship between the altered chemokine expression with renal damage/repair and influx of leukocytes.
Methods

Mice
Seven-week old male C57Bl/6 mice were purchased from Charles River (Maastricht, the Netherlands) and housed under SPF (Specific Pathogen Free) conditions receiving food and water ad libitum. All experimental procedures were approved by the local Animal Care and Use Committee of the University of Amsterdam, the Netherlands.

Renal I/R Injury Model
Unilateral and bilateral renal I/R injury was induced by clamping, respectively, the right or both renal arteries for 45 minutes under general anesthesia (0.07 mg/10 g mouse of fentanyl citrate fluanisone midazolam mixture, containing 1.25 mg/ml midazolam [Roche, Mijdrecht, the Netherlands], 0.08 mg/ml fentanyl-citrate, and 2.5 mg/ml fluanisone [Janssen Pharmaceuticals, Beerse, Belgium]). The contralateral (left) or sham-operated kidney was used as control when appropriate. After removal of the clamp, the kidneys were inspected for restoration of blood flow. For analgesic purposes, mice received a subcutaneous injection of 50 µg/kg buprenorphin (Temgesic; Schering-Plough, Brussels, Belgium) after closing the abdomen. Mice were sacrificed several time points after surgery. Kidneys were harvested and of each kidney one half was fixed in formalin and embedded in paraffin, and the other half was snap frozen in N2(l) and stored at -80°C until further use.

(Immunohistochemistry and antibodies
For (immuno)histological examination, 4µm paraffin sections were cut. Tubular injury was determined on sections stained with periodic acid Schiff after diastase (PasD). Immunohistochemical stainings to detect macrophages, neutrophils, T cells, apoptosis and proliferation were performed using rat-anti-mouse F4/80 (Serotec, Oxford, UK), FITC-labeled anti-mouse Ly-6G (BD Biosciences), rabbit-anti-human CD3 (clone Sp7; Lab Vision Corp., Fremont, CA, USA), rabbit-anti-mouse active caspase 3 (Cell Signaling Technology, Beverly, MA, USA) and rabbit-anti-human Ki67 (clone Sp6; Lab Vision Corp.) respectively. Macrophages, neutrophils, T cells, and apoptotic and proliferating TEC were counted in the cortico-medullar region in 10 randomly chosen, non-overlapping high power fields (hpf; 40x magnification).

RNA Isolation and Quality Control
Total RNA was isolated from a ¼ snap frozen kidney using the TRizol® reagent (Invitrogen, Breda, the Netherlands) method. The isolated RNA solution was treated with DNAsel (Qiagen, Venlo, the Netherlands) to remove any residual DNA. Subsequently a RNA cleanup kit (RNeasy; Qiagen) was used to obtain highly purified and concentrated RNA samples.
Chemokine expression in renal I/R injury

As high quality RNA is essential for acquiring good microarray results, the concentration and purity of the RNA was determined with a NanoDrop spectrophotometer ND-1000 (NanoDrop Technologies, Wilmington, DE, USA) and the ribosomal RNA band integrity was determined on an Agilent 2001 BioAnalyzer® (Agilent Technologies, Amstelveen, the Netherlands). RNA samples used for microarray experiments met all of the following criteria: A260/A280 ratio greater than 2.0, A260/A230 ratio greater than 1.7, and a sharp distinction at the small site of both the 18S and 28S ribosomal RNA bands/peaks.

Synthesis, Labeling and Amplification of cRNA
The TrueLabeling-AMP™ 2.0 kit (SuperArray, Frederick, MD, USA) was used to amplify and label cRNA according to the manufacturer’s protocol. In short, from 10µg of starting material (total RNA) cDNA was synthesized. Thereafter cRNA was synthesized and labeled with biotinylated-UTP (Roche) during an incubation of 4 hours to yield enough material for 1 microarray per sample. The obtained cRNA was purified using the ArrayGrade cRNA Cleanup Kit (SuperArray) and the concentration was determined with a NanoDrop.

Hybridization, Detection and Data Analysis of Microarrays
Mouse Chemokines & Receptors Pathway-specific Oligo GEArray® microarrays from SuperArray were used. The array membranes were pre-hybridized as described by the manufacturer. Overnight the membranes were hybridized with 4µg biotinylated-cRNA at 60°C with continuous but slow agitation. After washing, the Chemiluminescent Detection Kit from SuperArray was used to visualize the biotinylated-cRNA on the membranes. The chemiluminescent array image was captured with a CCD camera (LAS-3000; Fujifilm, Düsseldorf, Germany) and analyzed with the web-based GEArray Expression Analysis Suite (SuperArray). The expression of genes was normalized towards a set of housekeeping genes (Ppia, B2m, and Hspcb) present on the microarrays. The data are presented as fold increase in ischemic kidney compared with the contralateral kidney. The expression was considered to be upregulated when the fold increase was ≥2 and statistical significant.

Quantitative Real-Time RT-PCR (QRT-PCR) Analysis
The genes up-regulated 1 and/or 7 days after I/R injury were selected to confirm their upregulation by quantitative real-time PCR on an independent data set obtained from mice subjected to bilateral renal I/R injury or sham surgery. Primer sequences were designed based on Primer3 software and obtained from the Universal ProbeLibrary Assay Design Center (Roche). All primers (table 1) were synthesized by Sigma (Zwijndrecht, the Netherlands).
Table 1. Primers used for real-time RT-PCR quantification

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<td>NM_011333</td>
<td>Ccl6</td>
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</table>

Complementary DNA (cDNA) was synthesized using the M-MLV RT enzyme kit (Invitrogen), oligo dT primers (Sigma) and RNase inhibitor (Applied Biosystem, Nieuwerkerk a/d IJssel, The Netherlands) according to the manufacturer’s protocol. Quantitative real-time RT-PCR was performed on a LightCycler® 480 System (Roche) using LightCycler® 480 SYBR Green I Master mix (Roche). Forty-five cycles were carried out at an annealing temperature of 56-58°C. The starting concentrations of mRNAs were calculated by the LinRegPCR program (version 9.30 beta) as described previously²⁴. The expression of genes was normalized towards a set of housekeeping genes (Ppia, B2m, and Hspcb). The data are presented as fold increase.
in ischemic kidney compared with sham kidney. The expression was considered to be upregulated when the fold increase was ≥2 and statistical significant.

**Chemokine ELISA**

Kidneys obtained from mice subjected to bilateral renal I/R injury were homogenized in PBS containing 1% Triton X-100, 4mM EDTA and 1% protease inhibitor cocktail (P8340, Sigma). Concentrations of the chemokines Ccl2/MCP-1 and Cxcl1/KC were measured in renal homogenates by specific ELISA according to the manufacturer’s instructions (R&D, Minneapolis, MN, USA). Chemokine levels were corrected for the amount of protein present using the BioRad protein assay (BioRad Laboratories, Veenendaal, The Netherlands) with IgG as standard.

**Statistical analysis**

Results are expressed as mean ± standard error of the mean (SEM), unless mentioned otherwise. Data were analyzed by Mann-Whitney U test or unpaired Student’s t test when appropriate. Values of $P \leq 0.05$ were considered statistically significant. All statistical analyses were performed using GraphPad Prism4 (GraphPad Software, San Diego, California, USA).

**Results**

**Microarray analysis of post-ischemic kidney**

Microarray experiments were performed to determine the temporal expression of several genes involved in renal I/R injury. The analysis was limited to genes that express chemokines and chemokine receptors, or related genes like growth factors and cytokines. Of the total of 114 genes present on the microarray, 20 were upregulated at one or more of the reperfusion periods. These transcripts were sorted according to the reperfusion time as illustrated in the Venn diagram (Figure 1). In table 2 the upregulated genes are expressed as a fold change compared with the contralateral kidney. The upregulated genes included CC chemokines (e.g. Ccl2/MCP-1 and Ccl17/TARC), CXC chemokines (e.g. Cxcl1/KC and Cxcl2/MIP-2α), chemokine receptors (Ccr1 and Cx3cr1), and other related genes like CSF1, matrix metalloproteinases (MMPs), TLR4 and the TLR adaptor molecule MyD88 gene. Interestingly, all these genes were upregulated 7 days after I/R injury. In addition, 6 of these genes were upregulated 1 day after ischemia and 2 genes (Cxcl2/MIP-2α and Cxcl10/IP-10) were upregulated at all reperfusion periods (i.e. 3 hours, 1 and 7 days). We could not detect any downregulated genes in the ischemic kidney.
Chemokine expression in renal I/R injury

Table 2. Upregulated genes 3 hours, 1 day or 7 days after renal I/R injury, expressed as a fold change compared with the contralateral kidney (n=4)

<table>
<thead>
<tr>
<th>Group</th>
<th>Symbol</th>
<th>Synonym</th>
<th>Time after I/R injury</th>
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<td></td>
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<td></td>
<td>3 hours</td>
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<td>CC chemokines</td>
<td>Ccl2</td>
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<tr>
<td></td>
<td>Cklfsf7</td>
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<td>Lymphotactin</td>
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<td>TLR4</td>
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Figure 1. Venn diagram
Venn diagram illustrating the number of genes that were up-regulated twofold or more at each of the three reperfusion periods examined.
Validation of microarray results by QRT-PCR

The microarray data of 1 day and 7 days after I/R injury was validated by means of QRT-PCR on mRNA obtained from an independent experiment. Although the extent of change in gene expression is not entirely the same, in general the gene expression levels determined by microarray analysis corresponded well with QRT-PCR data. Seventeen out of the 20 genes upregulated 7 days after ischemic injury could be confirmed (Figure 2). One day after ischemic injury we could validate 2 out of the 6 genes. Interestingly, also with QRT-PCR we observed the highest expression of the majority of upregulated genes 7 days after ischemic injury. These results confirmed the microarray data obtained in the present study.

Figure 2. Validation of the microarray results by quantitative real-time PCR (QRT-PCR). Expression of the upregulated CC chemokines, chemokine receptors, CXC chemokines, other chemokines and other genes 1 day (hatched bar) and 7 days (solid bar) after ischemic injury compared with sham (open bar). Seventeen out of the 20 genes had an increased expression 7 days after ischemic injury. Four of these genes were also upregulated 1 day after ischemic injury. MyD88 and TLR4 (other genes) had no altered expression after I/R injury, IL18 expression was downregulated 1 day after I/R injury. Data are expressed as mean ± SEM, n=7-8. *P≤0.05
Characterization of renal I/R injury

To correlate the chemokine expression with tubular damage and repair and the influx of different subsets of leukocytes, (immuno)histological stainings were performed. Tubular damage 3 hours, 1 day and 7 days after unilateral I/R injury was visualized with PasD staining (Figure 3). Hallmarks of tubular damage are dilation, loss of brush border, necrosis and cast deposition. Three hours after I/R there is dilation of the tubules and oedema in the interstitial space. After 1 day the tubular damage is increased, the tubules show extensive coagulative necrosis characterized by the presence of numerous ghost cells in the tubules, loss of nuclei and decrease of staining. Seven days after I/R injury tubules are still abnormal although coagulative necrosis is much less pronounced compared with day 1. Important is the chaotic arrangement of TEC which are dedifferentiated (absence of polarization, absence of brush border, high nuclear/cytoplasm ratio) and the presence of numerous
Figure 4. Quantification of infiltrating leukocytes and TEC apoptosis and proliferation in contralateral (open bars) and I/R (solid bars) kidneys. (a) Representative pictures of neutrophil (Ly6), macrophage (F4/80), T cell (CD3), apoptosis (active caspase-3) and proliferation (Ki67) immunostaining of contralateral kidney and kidneys 3 hours, 1 day and 7 days after I/R injury. Original magnification: 40x. (b) Neutrophils are increased at all three reperfusion periods, with the highest numbers 1 day after ischemic injury. (c) Macrophages are only increased 7 days after ischemic injury. (d) T cells are present in low amounts at all reperfusion periods, and only significantly increased 7 days after ischemic injury. (e) The number of apoptotic TEC is significantly increased at all three reperfusion periods and peaks 7 days after ischemic injury. (f) The number of proliferating TEC is only significantly increased 7 days after ischemic injury. Positive cells are given per high power field (hpf, 40x magnification). Data are expressed as mean ± SEM, n=4. *P≤0.05
mitotic figures, indicating high proliferation and hence reparative processes within the tubules. Indeed, proliferation of TEC was most abundant 7 days after I/R injury (Figure 4f) as determined by staining for Ki67 (Figure 4a). The number of apoptotic TEC was increased at all stages after I/R injury with the highest number of apoptotic TEC 7 days after I/R injury (Figure 4e) as shown by quantitative analysis of active caspase-3 immunostaining (Figure 4a). The influx of neutrophils, macrophages and T cells was determined by immunohistochemical staining (Figure 4a). Neutrophils were the first inflammatory cells after I/R injury with a peak after 1 day (Figure 4b). Macrophages were almost not detectable in the ischemic kidney until 7 days after I/R injury (Figure 4c). T cells could be detected at very low levels at all time points, but were only significantly increased 7 days after I/R injury (Figure 4d).

Biphasic expression of CXC chemokines and monophasic expression of CC chemokines after I/R injury
Chemokines are mainly known for their ability to attract inflammatory cells to sites of injury. Since we observed the highest levels of chemokine expression at the stage of active repair (i.e. 7 days after ischemic injury), we wanted to examine the temporal chemokines expression pattern in more detail. The expression of the CC and CXC chemokines at additional reperfusion periods after ischemic injury was evaluated to determine if there is a biphasic expression coinciding with the inflammatory and reparative response after ischemic injury.
In figure 5 the expression patterns of the upregulated CC and CXC chemokines after renal I/R injury is depicted. The 4 CC chemokines were expressed in a monophasic fashion with a clear peak 7 days after ischemic injury. In contrast, the CXC chemokines had a biphasic expression after ischemic injury with the first peak in the early (i.e. inflammatory) phase and the second peak during the reparative phase. The CXC chemokines Cxcl1/KC, Cxcl2/MIP-2α and Cxcl10/IP-10 had the highest expression during the inflammatory phase. The influx of neutrophils occurred along with the early peak of CXC chemokine mRNA expression. The kinetics of the CC chemokines mRNA expression paralleled those of the influx of macrophages into the interstitium.

Ccl2/MCP-1 and Cxcl1/KC protein levels
To further examine whether the expression patterns of selected chemokines identified by microarray and QRT-PCR studies correlated with protein levels, we next performed ELISA on total kidney homogenate. Since renal I/R injury is characterized by the early influx of neutrophils and a later monocyte influx, we determined protein levels of Cxcl1/KC and Ccl2/MCP-1 which are potent chemoattractants for neutrophils and monocytes, respectively. In accordance with our mRNA data, Ccl2/MCP-1 protein level is highest 7 days after renal ischemia (Figure 6a). Cxcl1/KC is significantly increased 1 and 7 days after renal ischemia compared with sham (Figure 6b). Furthermore, in line with our mRNA data Cxcl1/KC protein levels peak 1 day after renal I/R.
Chemokine expression in renal I/R injury

Figure 5. Expression profile of CC and CXC chemokines up to 14 days after renal ischemic injury.
To obtain an expression profile of the upregulated CC and CXC chemokines during the whole course of renal ischemic injury and post-ischemic repair, additional reperfusion periods (2 hours, 1, 3, 7 and 14 days) were analyzed by QRT-PCR. CC chemokine expression peaked only at 7 days after I/R injury. CXC chemokine expression was biphasic, with a peak during the early inflammatory response (2 hours and 1 day) and a second peak during the later repair phase (3 and 7 days). Data are expressed as mean ± SEM, n=6-8.

Figure 6. Renal Ccl2/MCP-1 and Cxcl1/KC protein levels after ischemic injury.
(a) Renal Ccl2/MCP-1 protein levels were significantly upregulated 7 days after ischemic injury (solid bars) compared with sham (open bar) and 1 day post-ischemia (hatched bars) kidney. (b) Renal Cxcl1/KC protein levels were significantly upregulated 1 (hatched bar) and 7 (solid bar) days after renal ischemia compared with sham kidney (open bar). Data are expressed as mean ± SEM, n=4 (sham) and n=9 (1 and 7 days). *P≤0.05 compared with sham.
Chemokine expression in renal I/R injury

Discussion

In the present study, we identified chemokine, chemokine receptor and chemokine related genes whose expression is affected in renal I/R injury. Instead of using whole genome microarrays for which data analysis could be complicated, we conducted pathway-specific oligonucleotide arrays that contain 114 chemokines or related genes. Using QRT-PCR we validated the microarray results and finally obtained 18 genes with an altered expression 1 and/or 7 days after I/R injury, of which the majority of these genes were chemokines. Interestingly, all genes were significantly upregulated during the repair phase, suggesting that they play a major role in the resolution of ischemic injury.

Chemokines promote cell infiltration and activation observed in many disease states. In addition, chemokines are involved in other processes including angiogenesis, homeostasis, development, migration of stem cells and wound healing. Therefore, chemokines are important players in the initiation and progression of the inflammatory response and in addition might have a great impact in the reparative stage taking place after tissue injury. In the present study, we found a tight temporal relationship between chemokine expression and renal repair. Usually, chemokines are regarded as playing an essential role in mediating leukocyte recruitment and activation during initiation as well as progression of renal inflammation. The current study however demonstrates that both CC and CXC chemokines are mainly expressed during the reparative phase of renal I/R injury. Additionally, we found that the time of influx of the different types of leukocytes correlated with the upregulation of certain chemokines.

In general, at an inflammatory or diseased site neutrophils are the first leukocytes to be recruited. In line with previous studies by our group, we currently found that neutrophils are the first inflammatory cells infiltrating the damaged site in renal I/R injury. These recruited neutrophils can clear dead cells and debris but can also amplify renal tissue injury. The ELR+ CXC chemokines (possess the ELR amino acid motif) are the main neutrophil chemoattractants, and play an important role in regulating neutrophil chemotaxis and activation in ischemic tissue. Among them are Cxcl1/KC and Cxcl2/MIP-2α, which are upregulated early after ischemic injury. The early expression of Cxcl1/KC was already described in 1991 by Safirstein et al. Cxcl1/KC and Cxcl2/MIP-2α have already been described as being important in the onset of inflammatory response after renal I/R by regulating neutrophil influx. In addition, the chemokine receptor Ccr1 is of functional relevance for neutrophil recruitment during I/R.

Macrophages are believed to play a dual role in kidney injury. Although widely recognized as contributing to the pathogenesis of renal fibrosis, glomerular and interstitial macrophages may also play beneficial, reparative and matrix remodeling roles during tissue repair. Indeed, in this study we see significantly more macrophages in the repair phase (t=7d) of renal I/R. In addition, it has previously been shown...
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that adoptive macrophage transfer in the regenerative period not only leads to better tissue preservation, but also contributes to increased regeneration in renal I/R injury. However, decreasing Ccr2-positive macrophage by administering an antagonist for Ccl2/Mcp-1 early during renal I/R injury is proposed as a profitable therapy for I/R injury in the kidney. In addition, Ccr2-deficient mice had decreased F4/80-positive cell infiltration and were protected from acute tubular necrosis in renal I/R injury. The majority of the macrophages express the receptor Cx3cr1, suggesting that this receptor might mediate macrophage trafficking to the kidney. In our I/R model, Cx3cr1 expression is significantly increased 7 days after injury, the peak moment of macrophage influx. Furuichi et al. showed that Cx3cr1 is upregulated at later stages in renal I/R injury and that Cx3cr1 deficiency attenuates macrophage influx 7 days after renal I/R injury. In contrast, Oh et al. concluded that early ischemic ATN is partially a Cx3cr1-dependent process as serum creatinine, ATN score, and macrophage infiltration are reduced by Cx3cr1 inhibition at early stages of post-ischemic reperfusion. It is important to acknowledge the heterogeneity of macrophages; functionally distinct subpopulations may exist in the same tissue and play critical roles in both the initiation and recovery phases.

The numbers of T cells in the post-ischemic kidney are low, but they are significantly increased 7 days after renal I/R injury. This upregulation coincides with an increased expression of several chemokines (e.g. Cxcl10/IP-10 and Ccl17/TARC) involved in T cell chemotaxis. Direct evidence supporting a role of T cells as both mediators and protectors of I/R in rodent models is reviewed by Huang et al. Recently it has been shown that kidney ischemia induces long-term T cell infiltration. However, the role of chemokines in T cell influx in post-ischemic kidneys has not yet been studied in detail.

Our data suggest that chemokines are not solely linked to the acute inflammatory response and the infiltration of different subsets of leukocytes in the post-ischemic kidney. Especially the high expression of chemokines during the repair phase (t=7d) and the fact that all upregulated CXC chemokines had a biphasic expression coinciding with the acute and reparative phases after renal I/R injury, led us to propose a pleiotropic role of chemokines during the different phases after an ischemic insult in the kidney. For instance HGF-mediated Cxcl1/KC production has been shown to influence the normal effects of HGF on epithelial morphogenesis, suggesting that Cxcl1/KC can act in an autocrine fashion in these cells, thereby playing a beneficial role in the repair process as well. In addition to Cxcl1/KC, Cxcl2/MIP-2α has also been shown to stimulate proliferation of epithelial cells. Conversely, Furuichi et al. showed that the induction of Cxcl10/IP-10 in ischemic kidney inhibits tubular cell proliferation. This controversy can be explained by the presence or absence of the ELR motif in CXC chemokines. In general, ELR⁺ CXC chemokines (e.g. Cxcl1/KC and Cxcl2/MIP-2) have angiogenic properties while ELR⁻ CXC chemokines (e.g. Cxcl4/PF4 and Cxcl10/IP-10) behave as angiostatic. Besides, CXC chemokines influence proliferation in several cell types including hepatocytes, gastric epithelial
cells, and intestinal epithelial (crypt) cells. Apparently, chemokines integrate inflammatory responses and reparative processes that play crucial role in renal I/R injury. Interestingly, during the reparative phase there is presumably a tight balance between ELR+ and ELR- CXC chemokines to regulate epithelial cell proliferation. The chemokines Ccl6, Ccl8, Ccl12, Cxcl4, Cklfsf3, Cklfsf7 and Xcl1 are not discussed here. Their role in renal I/R injury and repair remains to be elucidated. Based on their expression profile we hypothesize that these chemokines are involved in the repair of the post-ischemic kidney. In addition some other genes were upregulated after renal I/R injury. Among them are MMP2 and MMP7. In general, MMPs degrade the extracellular matrix (ECM), however, recently new biological roles of MMPs by proteolytic action on a variety of non-ECM substrates have been described (reviewed in ). The increased expression of both MMPs during the reparative phase after renal I/R injury suggests a role in remodeling tubular structure. Functional studies in animal models of renal inflammatory diseases have generated conflicting results with regard to the role of chemokines (reviewed by Anders et al. KI 2003). Our data indicate that these contradictory results could merely reflect the time points at which the chemokines were targeted. The analysis of temporal and spatiotemporal chemokines expression will therefore be crucial for the design of effective therapies. In conclusion, our study shows the expression profile of chemokines and related genes after renal I/R injury. Interestingly, all these chemokines are significantly increased during the reparative phase. A biphasic expression, coinciding with the acute inflammatory and the later reparative phase, of the CXC chemokines was observed. This study provides an important resource for exploring new therapeutic targets for the treatment of ischemic kidney injury and indicates that effective therapeutic interventional strategies will strongly depend on the exact time point at which the intervention takes place.

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