Supplementary data

Imaging protocol

**Acquisition**

MRI scans were performed on a 1.5 tesla Philips Achieva scanner (Philips Healthcare, Best, Netherlands) with a 16-channel phase array surface coil. T₁-weighted images were obtained to map anatomy. ASL data were then acquired using the STAR method: pre- and post-labelling saturation pulses were used to reduce unwanted magnetisation of renal tissue (14). 20 label/control image pairs, repetition time (TR) = 4000 ms, flip angle = 90° and echo time (TE) = 3.4 ms, inversion times (TI) of 300, 600, 900, 1200, 1500, 1800, 2500 and 3400 ms were acquired. A sagittal 180 degree labelling pulse was applied along the descending aorta. A single coronal-oblique imaging slice was aligned on the long axis of the kidneys avoiding the renal pelvis and major blood vessels but allowing both kidneys to be measured simultaneously. Diffusion weighted measurements for DTI were then made using respiratory triggering on exhale with EPI readout, 32 gradient directions, b = 0 s mm⁻² image. 

**Parameter model**

Parameter model including bolus arrival time (BAT), the time for the labelled blood to reach the cortex and medulla, with units s; and bolus end time (BET), the time for the end of the magnetisation label to reach the renal tissue, with units s. DTI analysis was undertaken using in house software written in MATLAB and C++ to generate fractional anisotropy (FA) and apparent diffusion coefficient (ADC, units 10⁻³ mm² s⁻¹) maps for each kidney. Cortex and medulla were separated using the FA maps (threshold 0.3).

**Time from biopsy to MRI scan**

- **Patient 1**
  - Time: 12 weeks

- **Patient 3**
  - Time: 7 weeks

- **Patient 4**
  - Time: 15 weeks

- **Patient 5**
  - Time: 132 weeks

- **Patient 6**
  - Time: 100 weeks

**Table 1.**  Description of histology findings and disease activity and treatment (at the time of assessment) in the lupus nephritis patients. ASL data available where.*

<table>
<thead>
<tr>
<th>Patient</th>
<th>Class</th>
<th>Therapy</th>
<th>SLEDAI-2000 score</th>
<th>Time from biopsy to MRI scan</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>IV (segmental) nephritis</td>
<td>Mycophenolate mofetil, Prednisolone 20mg</td>
<td>6</td>
<td>12 weeks</td>
</tr>
<tr>
<td>2</td>
<td>IV (global)/V nephritis</td>
<td>Mycophenolate mofetil, Prednisolone 40mg</td>
<td>10</td>
<td>7 weeks</td>
</tr>
<tr>
<td>3</td>
<td>IV (segmental) nephritis</td>
<td>Mycophenolate mofetil, Prednisolone 30mg</td>
<td>8</td>
<td>7 weeks</td>
</tr>
<tr>
<td>4*</td>
<td>IV (segmental) nephritis</td>
<td>Mycophenolate mofetil, Prednisolone 30mg (previous Myocphenolate Mofetil)</td>
<td>12</td>
<td>15 weeks</td>
</tr>
<tr>
<td>5*</td>
<td>V nephritis</td>
<td>Prednisolone 6mg</td>
<td>4</td>
<td>132 weeks</td>
</tr>
<tr>
<td>6*</td>
<td>V nephritis</td>
<td>Mycophenolate Mofetil, Prednisolone 12.5mg</td>
<td>0</td>
<td>100 weeks</td>
</tr>
</tbody>
</table>

**Image analysis and quantification**

ASL images were analysed using software written in this laboratory in C++. Firstly T₁ maps were constructed using images acquired at different TI. These were then used to enable cortex and medulla segmentation using a threshold in T₁ of 1.2 s. ASL values were generated voxelwise using a three parameter model including bolus arrival and end times (13). Parameters measured included blood flow with units ml.(100 ml)⁻¹ min⁻¹; the bolus arrival time (BAT), the time for the labelled blood to reach the cortex and medulla, with units s; and bolus end time (BET), the time for the end of the magnetisation label to reach the renal tissue, with units s. Differentiation of cortex and medulla was not possible for the T₂* images (units s) thus values were calculated for each kidney as a whole.
Fig. 1. Correlation of ASL parameters with GFR and uPCR

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Fig. 2. Correlation DTI parameters with GFR and uPCR.

Fig. 3. Correlation of $T_2^*$ with GFR and uPCR.
Fig. 4. Differences in ASL parameters between groups (lupus nephritis patients are colour coded for comparison).

Fig. 5. Differences in DTI parameters between the groups.

Fig. 7. Differences in $T_2^*$ signal between the groups.