

## Whole-body T2\* mapping

C. Rossi<sup>1</sup>, A. Boss<sup>1,2</sup>, M. Haap<sup>3</sup>, P. Martirosian<sup>1</sup>, C. D. Claussen<sup>2</sup>, and F. Schick<sup>1</sup>

<sup>1</sup>Section of Experimental Radiology, Eberhard Karls University of Tuebingen, Tuebingen, Germany, <sup>2</sup>Department of Diagnostic Radiology, Eberhard Karls University of Tuebingen, Tuebingen, Germany, <sup>3</sup>Department of Endocrinology, Metabolism and Pathobiochemistry, Eberhard Karls University of Tuebingen, Tuebingen, Germany

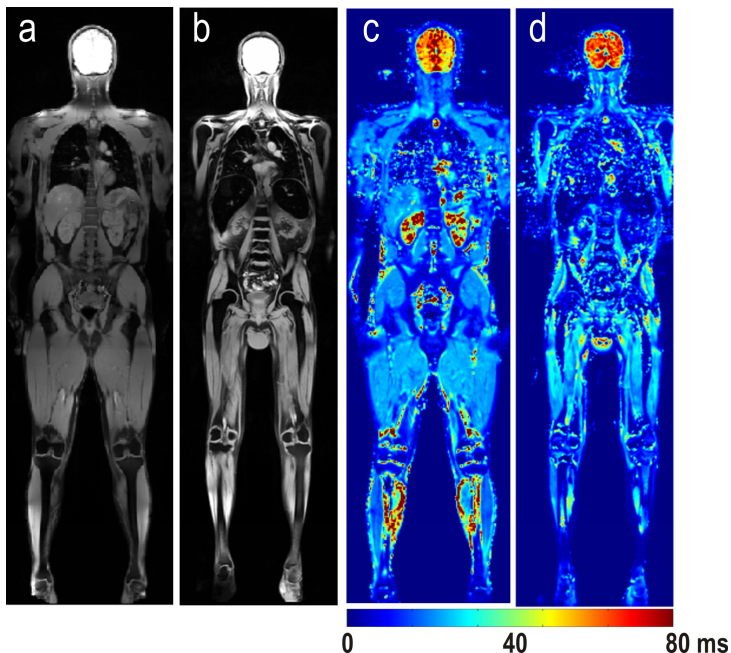
**Introduction:** Whole-body MRI allows for comprehensive tissue examinations especially useful in the detection and follow-up of malignant diseases<sup>1,2</sup>. In this study, we investigated the feasibility of an MRI protocol able to provide high quality T<sub>2</sub>\* relaxation maps of the entire body at 1.5T. Clinical applicability of the protocol was tested in one patient suffering from iron overload due to repeated blood transfusion treatments.

**Purpose:** To investigate the feasibility of a whole-body MRI protocol providing T<sub>2</sub>\* parametrical maps of the entire body at 1.5 Tesla.

**Material and Methods:** Seven healthy volunteers (mean age=30.1±3.7, 3 women and 4 men), and one patient (male, 53 years-old) with diagnosis of myelodysplastic syndrome, participated in the study. Images of five subsequent body levels were acquired using a fat-suppressed multi-echo (12 echo times were selected in the range between 4.8 and 76.3 ms) 2D gradient-echo sequence and afterwards composed. Parametrical T<sub>2</sub>\* maps of the whole-body were computed on a pixel-by-pixel basis. Local T<sub>2</sub>\* values were evaluated in the cerebral white and gray matter, liver, spleen, kidney, and skeletal muscles.

**Results and Discussions:** Good quality T<sub>2</sub>\* maps of the entire body were obtained without spatial distortions or significant artifacts (**Fig. 1**). In healthy volunteers, the computed T<sub>2</sub>\* values amounted to: 58.5±4.2 ms for white matter, 81.4±5.5 ms for gray matter, 63.5±3.3 ms for spleen, 65±10 ms for kidney, 34.3±7.0 ms for liver, and approx. 30 ms for skeletal muscle (e.g. vastus lateralis muscle =30.0±2.8 ms). The patient affected by myelodysplastic syndrome (serum ferritin concentration = 927 µg/dl) showed shortened T<sub>2</sub>\* values in liver (3.6±5.5 ms), spleen (3.1±4.8 ms), kidney (11.1±7.1 ms), and muscles (e.g. vastus lateralis muscle =25.1±3.4 ms) (**Table 1**). This study showed the feasibility of high quality T<sub>2</sub>\* whole-body mapping at 1.5 T. Preliminary results suggest that whole-body T<sub>2</sub>\* mapping may be used for the assessment of iron load in the entire body. This new modality may become a helpful tool for the comprehensive monitoring of iron balance in the body in patients treated with repeated blood transfusion.

**References:** <sup>1</sup>Schlemmer HP, et al. Invest Radiol 2005; 40: 64-71; <sup>2</sup>Boss A, et al. J Magn Reson Imaging 2006; 24: 1183-1187.



**Table 1** Local T<sub>2</sub>\* values (in units of ms) computed in the healthy group of volunteers and in the patient.

	Healthy volunteers	Patient
<b>White matter</b>	<b>58.5 ± 4.2</b>	<b>58.3 ± 6.0</b>
<b>Gray matter</b>	<b>81.4 ± 5.5</b>	<b>85.1 ± 7.2</b>
<b>Liver</b>	<b>34.3 ± 7.0</b>	<b>3.6 ± 5.5</b>
<b>Spleen</b>	<b>63.5 ± 3.3</b>	<b>3.1 ± 4.8</b>
<b>Muscle</b>	<b>30.0 ± 2.8</b>	<b>25.1 ± 3.4</b>
<b>Kidney</b>	<b>65.4 ± 10.3</b>	<b>11.1 ± 7.1</b>

**Fig. 1** The anatomical references (a,b) acquired using a FLASH sequence (TR/TE=200ms/4.8ms, flip angle=40°) are compared with the corresponding T<sub>2</sub>\* maps (c,d). Significant differences in the T<sub>2</sub>\* values computed in the healthy volunteers (a,c) and the patient (b,d) were found in liver, spleen, kidney, and muscles.