SODIUM T_2* MAPPING OF THE HUMAN KIDNEYS *IN VIVO* AT 7 TESLA

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TARGET AUDIENCE: Abdominal radiologists, physicists interested in sodium T_2* mapping and in developing sequences for fast relaxing tissues.

PURPOSE: *In vivo* sodium (^{23}Na) MRI of the kidneys is not only challenging because of its intrinsic low concentration, but also due to its very short biexponential transversal relaxation, consisting of a fast (~60% of signal) and slow component (~40% of signal). To date, ^{23}Na T_2* relaxation times in the kidneys have been measured solely in animals.[1-3] However, for absolute quantification of ^{23}Na content and for sequence optimization, it is essential to know the T_2* values in the human kidneys. Recent technical and methodological developments for 7T systems improved ^{23}Na MRI and enabled studies that were not possible previously. Thus the aim of this study was to measure the T_2* relaxation times of the human kidney *in-vivo* at 7.0T for the first time.

METHODS: Eight healthy volunteers (4 women, 4 men) with a mean age of 29.4±3.6 (mean±standard deviation) years (range: 24.5-33.5 years) and a mean body-mass-index of 21.7±2.6 kg/m^2 (range: 19.5-27.5 kg/m^2) were included in this prospective study. All volunteers were asked to avoid drinking of water within 60 minutes before the examination. There were no other restrictions of food and water intake. The local ethics commission approved this study and written informed consent was obtained from all volunteers before measurements. All measurements were performed on a 7T whole body system (Magnetom, Siemens Healthcare, Erlangen, Germany) with a six-channel ^{23}Na-only spine-array coil (Quality Electrodynamics, Mayfield Village, Ohio, USA). After a series of localizers, a multi-echo 3D gradient-echo sequence with a variable echo time scheme (vTE-GRE) [4] was applied to map T2* relaxation times in the kidneys. The echo times were sequentially shifted; during first TR all odd TEs and during second TR all even TEs were recorded. Measurement parameters for vTE-GRE were as follow: resolution= 4x4x15 mm^3; 12 slices; 10 echo times with TE=2.64, 4.93, 13.76, 19.18, 24.59, 30.01, 40.00, 45.42, 55.00, 60.42 ms; TR= 75 ms; BW= 60 Hz/pixel; 24 averages; measurement time= 46:50 min. The T_2* maps (Fig 1B) were calculated by fitting the ^{23}Na signal decay mono-exponentially on a pixel-by-pixel basis using a least squares fitting routine with three parameters written in IDL (RSI, Boulder, CO, USA) (Fig 2). To assess the fitting precision, a corresponding measure of goodness-of-fit (R^2) map (Fig 1C) was calculated for each T_2* map in IDL. Two coronal T_2* maps representing the center part of the kidneys were evaluated in each volunteer using OsiriX (OsiriX, Geneva, Switzerland), totaling to 32 measurements. The vTE-GRE images with the shortest TE (2.64 ms) (Fig 1A) were used to manually draw region-of-interest (ROI) around the visible renal cortex and the medulla. The partially seen calyceal systems of the kidneys were spared. The ROIs were subsequently copied from the vTE-GRE image to T_2* and R^2 maps and the mean values and corresponding standard deviations were obtained. All statistical analyses were performed using MedCalc (MedCalc, Mariakerke, Belgium). A Kolmogorov-Smirnov test verified normal distribution of the data (p= 0.659). A paired t-test was used to compare the T_2* values of the renal cortex and the medulla.

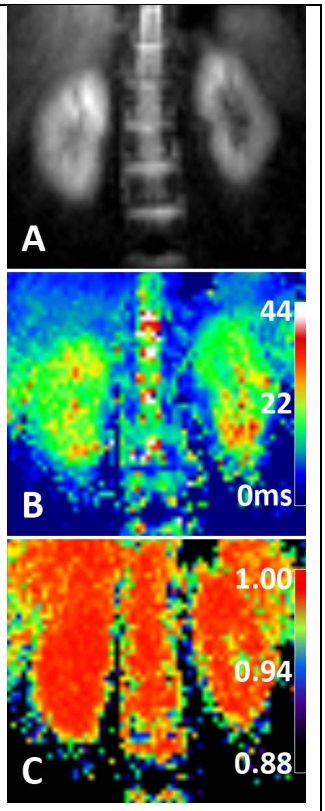

Fig.1: A. ^{23}Na vTE-GRE image of healthy volunteer acquired with TE= 2.64 ms, **B.** corresponding color-coded ^{23}Na T_2*map and **C.** corresponding color-coded R^2 map.

RESULTS: The mean ^{23}Na T_2* relaxation times of all volunteers were 17.9±1.2 ms (range: 16.5-19.1) in the renal cortex and 20.4±1.5 ms (range: 18.7-22.4) in the medulla. The mean R^2 were 0.987±0.008 in the renal cortex and 0.993±0.005 in the renal medulla A paired t-test revealed significantly lower T_2* values in the renal cortex when compared to the medulla (p< 0.001).

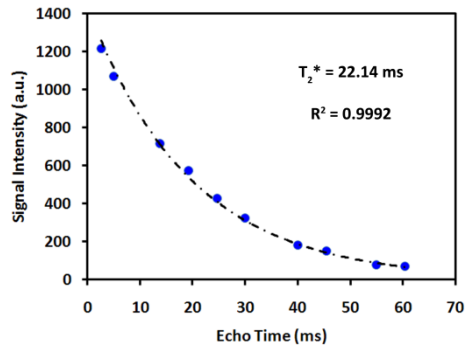

Fig .2: T2* fit from one pixel in renal medulla of a healthy volunteer. R^2 stands for the goodness-of-fit.

DISCUSSION: To the best of our knowledge, the literature reports only animal T_2* data from kidneys, and therefore this is the first report on *in vivo* human T_2* relaxation times in the kidneys. Due to the quite long first TE (2.64 ms), the contribution of the short component of the biexponential decay was minimal and our T_2* values represent mainly long T_2* component. Slightly different T_2* relaxation times were published from animal models. Maril et al. reported a short (2.2 ms) and a long T_2* component (20.4 ms) for intact rat kidneys at 4.7T.[1] For surgically exposed rabbit kidneys at 4.7T, Wolff et al. showed a long T_2* component of 20.1±2.0 ms in the cortex and 25.3±1.2 ms in the medulla.[2] Neuberger et al. calculated a long T_2* of 29.2±3.8 ms for the cortex, 36.1±2.8 ms for the medulla, and a fast T_2* component of 0.8±0.6 ms for the cortex and 1.0±0.6 ms for medulla the in mice kidneys at 17.6T.[3] Our T_2* results are in good agreement with the long T_2* components published by Maril et al.[1] and Wolff et al.[2] Moreover, similar to the results from animal studies, we observed shorter T_2* values in the renal cortex compared to the medulla.

CONCLUSION: The high SNR provided by 7T and multi-echo vTE-GRE sequence allowed the *in vivo* measurements of ^{23}Na T_2* relaxation times in human kidneys for the first time. This data may provide the basis for absolute quantification of ^{23}Na content in human kidneys.

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