In Vivo Brain Sodium T2* Mapping with a Multiple-echo Flexible TPI Sequence

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INTRODUCTION

Regulation of sodium homeostasis through counterbalancing low intracellular and high extracellular concentrations with potassium ions is of vital importance for cellular function. The sodium MR signal is affected by the local electrical field gradient and exhibits bi-exponential relaxation behavior in brain tissues. The relaxation times not only are critical parameters for optimizing the sequences for quantifying tissue sodium concentration (TSC), but also convey information on the local environment of sodium ion. However, due to the low detection sensitivity of sodium, mapping the sodium relaxation times of in biological tissues *in vivo* is challenging. We demonstrate here that with an efficient multiple-echo flexible twisted projection imaging sequence (ME-flexTPI) (1,2) high quality T2* maps of the sodium MR signal in the entire human brain can be achieved within a reasonable scan time at 3T.

MATERIALS AND METHODS

Representative gradient waveforms of the ME-flexTPI sequence and the k-space sampling strategy of TPI-based sequences are shown in Fig. 1. A 500 us hard RF pulse was used for excitation, followed by multiple echoes were acquired with flexTPI readout trajectories.

Imaging was performed on a 3.0 Tesla clinical scanner (HDx Signa, GE Healthcare, Waukasha, WI) with multinuclear capabilities and a maximum slew rate of 15000 G/cm/s using a single-tuned transmit/receive (T/R) birdcage coil. Healthy adult human volunteers were recruited under an IRB approved protocol. Eight echoes were collected after each excitation with the ME-flexTPI sequence. Acquisition parameters include TR/FOV/flip angle/resolution =160 ms/22 cm/90° /5 mm isotropic. A radial fraction of 0.5 was used together with a maximum readout gradient strength of 0.6 G/cm to achieve a 2 ms readout duration for each echo. The TE interval between two adjacent echoes in each echo train was 3.45 ms. The long TR used decreased the data acquisition SNR efficiency for T2 mapping, but was used so that the same data could be quantified into TSC maps with the two calibration vials (NaCl conctration: 60 mM and 90 mM) placed on each side of the head. The scan time for each ME-flexTPI acquisition was ~18 minutes. The sequence was repeated three times with the TEs of the 1st echoes in each echo train being 0.2 ms, 0.7 ms and 1.2 ms, respectively. The total acquisition time for T2 mapping was ~60 minutes. A nonlinear fit algorithm was then applied to the 24 images using a bi-exponential decay model.

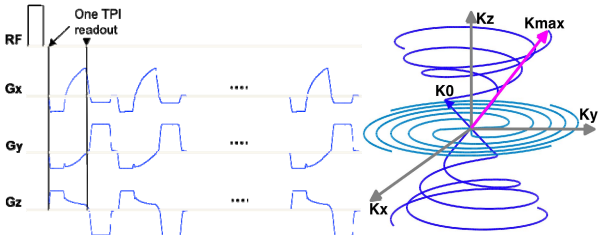

Fig.1 (a) Diagram of the ME-flexTPI sequence. (b) Illustration of k-space sampling strategy of flexTPI in which each trajectory has a radial component extending to K_0 along a cone of angle θ, and then twisting along the surface of the cone to K_{max}.

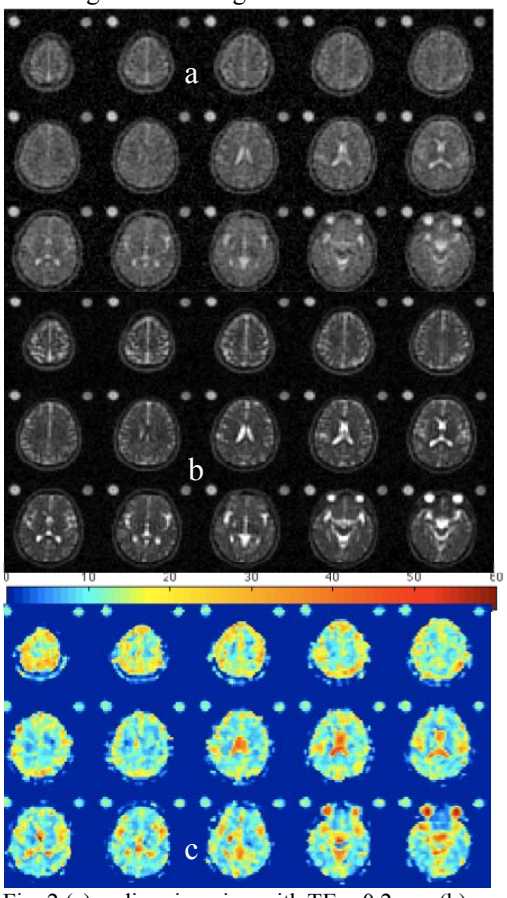

Fig. 2 (a) sodium imaging with TE = 0.2 ms, (b) magnitude sum of all echoes. (c) long T2* maps.

RESULTS AND DISCUSSION

Fig. 2a shows representative images from one subject collected with a TE of 0.2 ms. Signal loss due to T2 decay is minimal owing to the short TE and readout duration used. Fig. 2b shows the magnitude sum images of all 24 echoes. The contrast between brain parenchyma and CSF is significantly increased due to the long sodium T2 in CSF. There is nearly no distortion due to susceptibility in the calibration vials or the eyeball, which allows for obtaining reliable calibration curves from the vials. Fig. 2c shows the T2* maps of the long T2 component in the brain with high SNR and spatial resolution. The long T2* values in gray matter (GM) and white matter (WM) are ~14 ms and ~10 ms respectively. T2* values of the short T2-component range from 0.2-3 ms (not shown). The T2* in the CSF and vitreous humor was ~55 ms. These values are in agreement with literature T2 values obtained in tissue samples (3). The T2* maps therefore provide approximations of the T2s in the human brain, which reflect the sodium ion environment.

CONCLUSIONS

High quality T2* maps were achieved on a clinical 3T scanner with the ME-flexTPI sequence. With the availability of ultra-high field magnets such as 9.4T, sodium T2* maps can potentially be obtained in a clinically acceptable time.

REFERENCES

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