Clinically-Constrained Resolution-Optimized flexTPI Acquisition Parameters for the Tissue Sodium Concentration Bioscale

I. C. Atkinson[1], A. Lu[1], and K. R. Thulborn[1]
[1]Center for Magnetic Resonance Research, University of Illinois at Chicago, Chicago, IL, United States

Purpose: The rapid transverse relaxation of the sodium magnetic resonance (MR) signal during signal acquisition causes a loss of spatial resolution, so called T_2-blurring. Conventional wisdom suggests that minimizing T_2-blurring by keeping the readout duration as short as possible will maximize spatial resolution. However, when the total acquisition time is limited to a clinically practical duration (e.g., 8-10 minutes), the parameters that maximize the spatial resolution of a flexible twisted projection imaging (flexTPI) acquisition do not correspond to the shortest possible readout [1]. This fact dictates how quantitative sodium imaging should be performed in order to measure the tissue sodium concentration (TSC) bioscale at a resolution matched to the tissue dimensions of human brain in order to address issues about regional brain health. Resolution optimized acquisition parameters for quantitative sodium imaging of brain parenchyma and cerebrospinal fluid are presented for the human brain and demonstrated at 9.4T and 3T.

Materials and Methods: Flexible TPI samples k-space with 3-D slew-rate limited projections that twist on a set of nested cones that lie within a sphere of radius K_{MAX} [2]. Signal decay during readout and sampling a sphere of k-space rather than the circumscribed cube limit the full-width at half-max (FWHM) resolution that can be achieved within a total acquisition time (T_{TOTAL}). The parameters optimizing the FWHM resolution of brain parenchyma were found by simulating the point-spread function of a source with relaxation times matching parenchyma (60% $T_{2,short}$=2.5 ms and 40% $T_{2,long}$=14 ms) or CSF (T_2=55 ms) for all possible flexTPI acquisition parameter sets that could be completed for T_{TOTAL}=10 min and T_{TOTAL}=4 min. For each parameter set, the relative signal-to-noise ratio was computed for a homogenous region by comparing the average simulated signal from a 10x10x10 cm^3 cube to a simulated noise-only acquisition. All simulations used T_R=160 ms, FOV=22 cm, a maximum readout duration of 42.5 ms, and the slew rate constrained gradient amplitude.

Quantitative sodium MR imaging was performed at 9.4 Tesla and 3.0 T with the resolution optimized (B and D) and minimum readout duration (A and C) parameters on a human volunteer providing informed consent, as shown in Table 1.

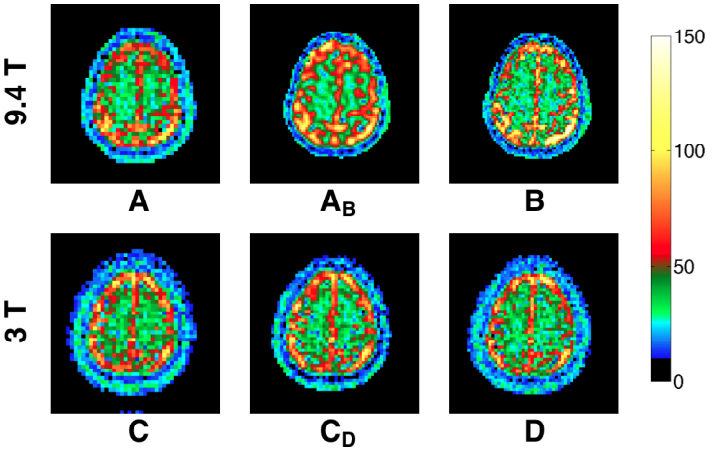

Figure 1: Representative slices from TSC bioscales in mM acquired at 9.4T (top) and 3T (bottom) on the same subject using the acquisition parameter sets shown in Table 1. Images A, B, C, and D were reconstructed at voxel sizes equal to their nominal resolutions shown in Table 1. Images A_B (C_D) are the result of reconstructing acquisition A (C) at the same voxel size as acquisition B (D).

Results and Conclusion: Figure 1 shows representative slices from the TSC bioscales. Although both A and B have identical acquisition times of 10 minutes, acquisition B has significantly improved resolution despite the longer readout duration. This matches the FWHM resolution expected in CSF and brain parenchyma (see Table 1) determined from the PSF simulation. Likewise, both C and D have identical acquisition times of 8 minutes (two averages of a 4-minute acquisition). Acquisition C theoretically has slightly improved resolution in brain parenchyma, although the difference is difficult to appreciate visually. Higher resolution quantitative 23-sodium imaging could not be performed at 3T because of the associated SNR penalty that would result in inaccurate and imprecise quantification. This means that in order to achieve a true resolution of less than 6 mm isotropic within a reasonable total acquisition time and with an SNR sufficient for robust quantification, imaging sodium imaging must be performed at ultra-high field.

	B_0 (T)	T_{TOTAL} (min)	Matrix	F_R	T_{ADC} (ms)	Nominal Res (mm)	FWHM Res CSF (mm)	FWHM Res Parenchyma (mm)	Relative[1] SNR CSF	Relative[1] SNR Parenchyma
A	9.4	10	44	0.60	2.3	5.00	7.69	7.92	0.64	0.58
B	9.4	10	76	0.20	27.3	2.89	4.69	5.69	0.50	0.46
C	3.0	2 x 4	44	0.24	10.5	5.00	7.77	8.68	1.41	1.41
D	3.0	2 x 4	56	0.15	34.4	3.93	6.35	8.03	1.24	1.13

Table 1: Acquisition parameters. [1]SNR of acquisition relative same signal type, does not include influence of B_0

References:
[1] Atkinson IC, et al. Proceedings of ISMRM, 2010, Abstract #7248.
[2] A Lu, et al. MRM, 2010; 63:1583-1593.

The authors gratefully acknowledge financial support from the PHS RO1 CA CA1295531. This work was funded in part by the Chicago Biomedical Consortium with support from The Searle Funds at The Chicago Community Trust.