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Super-fast assay of creatine kinase using ^{31}P-MT-MR fingerprinting at 7T in the human brain

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BACKGROUND

Energy buffering and transport via phosphocreatine (PCr)/creatine kinase (CK) shuttle play important roles in cellular energy metabolism to maintain neuronal activity and normal brain function. Non-invasive measurement of CK reaction rates has been possible using ^{31}P magnetic resonance spectroscopy (MRS) combined with magnetization transfer (MT). However, MT methods typically require long acquisition time, which limits their clinical applications.

METHODS

- Based on a b-SSFP-type sequence, with varying phase alternating flip angles [1,2]
- 20 mm slice in the occipital lobe was excited using a 1D slice selective RF pulse
- Excitation profile, dictionary creation and fitting process in Widmaier et al. [3]
- Approach is compared with the state-of-the-art EBIT MT approach [4]
- 38 averages and 1 dummy scan were acquired for MRF (scan time of 18.5 min)
- 16+1 scans for the EBIT (scan time of 18.5 min)
- In vivo data from 6 healthy subject
  (3 female; 3 males; age 18-30 years; written informed consent)
- Reproducibility with test-retest (15 min break)
- MR experiments were performed on a 7T/68cm MR scanner (Siemens Medical Solutions, Erlangen, Germany)
- ^{1}H quadrature surface coil and a single-loop ^{31}P coil for the occipital lobe.

CONCLUSION

- Feasibility of T_1^{PCr}, T_1^{ATP}, and k_{CK} estimates using MT-^{31}P-MRF at 7T in the human brain
- In good agreement with EBIT method and literature values [4-8]
- Test-retest reproducibility: coefficient of variations (CV) <10% in 4 min 15 s scan time → **4 times faster** than the EBIT method
- MT-^{31}P-MRF provides **fast** and **reproducible** approach for *in vivo* creatine kinase metabolic rate assay
- Potential for investigating energy metabolism in a clinical setting

AIMS

- Introduce SAR efficient ^{31}P-MT-MRF approach
- Accelerate in vivo assay of CK at 7T in the human brain
- Report estimations of T_1 relaxation times and creatine kinase rate (k_{CK})
- Evaluate their test-retest reproducibility vs EBIT

RESULTS

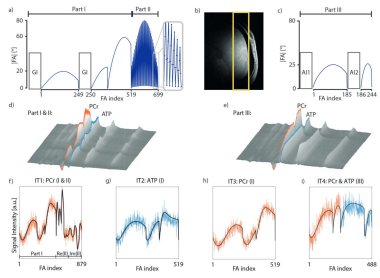

Figure 1: Sequence diagram with patterns (a,c) and resulting grouped average waterfall spectra (d,e) . (b) An exemplary 20 mm selected slice in the occipital lobe. (f-i) Example of the NIIM matching procedure. Solid black lines indicate the matched dictionary entry. PCr is marked in blue, and ATP is marked in orange.

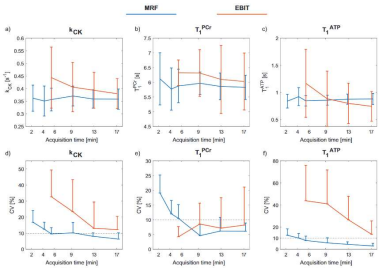

Figure 2: (a,b,c) Estimated parameters for MT-31P-MRF and the EBIT method over the acquisition time. (d,e,f) Coefficient of variation (CV) [%] of MT-^{31}P-MRF and the EBIT method over the acquisition time. All Values are shown in mean and STD.

	MT-^{31}P-MRF						EBIT
Averages	37	27	19	11	8	4	16
t_{acq} [min]	17:24	12:50	9:17	5:30	4:15	2:18	17:04
SNR_{PCr} [dB]	12.0	11.3	9.9	8.0	6.5	4.3	-
SNR_{ATP} [dB]	9.8	9.1	7.8	5.8	4.6	2.6	-
k_{CK} [s^{-1}]	0.36±0.04	0.36±0.04	0.37±0.04	0.36±0.06	0.35±0.07	0.34±0.08	0.38±0.06
T_1^{PCr} [s]	5.83±0.37	5.86±0.42	5.96±0.41	5.93±0.79	5.97±0.64	5.74±1.51	6.03±0.97
T_1^{ATP} [s]	0.88±0.10	0.87±0.09	0.86±0.10	0.87±0.14	0.89±0.14	0.90±0.18	0.85±0.27*
C_r	1.34±0.12	1.34±0.13	1.34±0.14	1.35±0.14	1.36±0.16	1.35±0.22	1.31±0.17

*Table 1: Estimated parameters (mean ± STD), SNR and acquisition time for different number of averages. (*n=5)*

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