Imaging of Creatine Kinase Reaction Rate by MR Fingerprinting

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Introduction

Creatine kinase (CK) plays an important role in tissue metabolism by maintaining a stable ATP concentration. ^{31}P MRS provides the opportunity for noninvasive assessment of the CK reaction rate (k_f^{CK}) in vivo. However, imaging of k_f^{CK} remains challenging due to the inherently low sensitivity of ^{31}P MRS. In this study, we developed an MRF-based method for in vivo mapping of k_f^{CK} in rat hindlimb.

Methods

The MRF sequence is shown in Fig. 1. The sequence comprised of alternating acquisition of PCr and γATP with varied flip angles[1]. The acquisition blocks were interlaced with γATP saturation for enhanced encoding of magnetization transfer via CK. Spatial encoding was achieved by a single-shot spiral-in and spiral-out readout trajectory with 4x4 cm^2 FOV and 16x16 matrix size, leading to an in-plane resolution of 2.5x2.5 mm^2. Slice selection was achieved by outer volume suppression with 1-cm slice thickness. Total acquisition time for one signal average was 20 s. A dictionary was constructed by solving the modified Bloch-McConnell equation. Five parameters were matched, including k_f^{CK}, $\mathrm{PCr/ATP}$, $\mathrm{T_1^{PCr}}$, $\mathrm{T_1^{ATP}}$, and δ^{PCr}. Fingerprint matching used SVD-compressed dictionary to improve the matching efficiency[2]. Animal studies were performed on 4 Sprague-Dawley rats at 9.4T. MRF acquisition comprised of a total of 480 signal averages (160 min acquisition). k_f^{CK} in the anterior, center, and posterior regions of the hindlimb were compared.

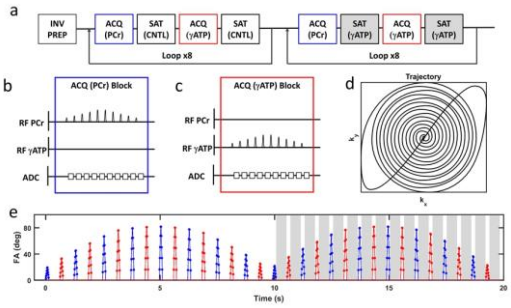

Fig. 1. **a**. Schematics of the pulse sequence. ACQ (PCr) and ACQ (γATP) are acquisition blocks for PCr and γATP. SAT (CNTL) and SAT (γATP) are contralateral and γATP saturation blocks. **b&c**. Sequence diagrams for one block of ACQ (PCr) and ACQ (γATP). **d**. Spiral trajectory used for spatial encoding. **e**. Timing and flip angles of all excitation pulses. Blue and red indicate PCr and γATP excitations. Shaded areas indicate γATP saturation.

Results

Using the first 20 singular values, SVD-compressed dictionary used only 6.25% of memory required by the full-size dictionary. Compressed matching also reduced matching time by up to 80% without sacrificing the accuracy. Fig. 2a shows a representative fingerprint from a pixel with its corresponding dictionary match, and Fig. 2b shows interpolated maps of k_f^{CK} and $\mathrm{PCr/ATP}$ from one rat. Results of ROI analysis are summarized in Table 1. Significant differences were found in k_f^{CK} between the anterior vs the center, as well as the posterior vs the center regions ($p<0.05$). $\mathrm{PCr/ATP}$ also differed between the center and the posterior regions ($p<0.05$).

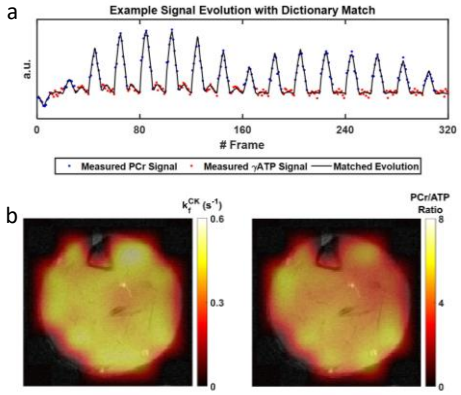

Fig. 2. **a**. A representative ^{31}P fingerprint and its corresponding dictionary match. **b**. Interpolated maps of k_f^{CK} and $\mathrm{PCr/ATP}$.

Table 1. Summary of matched k_f^{CK} and $\mathrm{PCr/ATP}$ in different ROIs.

ROI	k_f^{CK} (s^{-1})	$\mathrm{PCr/ATP}$
Anterior	0.40±0.05	4.51±0.33
Center	0.34±0.02	4.43±0.23
Posterior	0.38±0.03	5.01±0.31

Discussion/Conclusion

^{31}P MRF shows promising potential to perform localized metabolic mapping of CK reaction rate. Due to the small size of rat hindlimb, high spatial resolution (62.5 μL voxel volume) was necessary in the current study. This resulted in the relatively long acquisition time (160 min). The current method was able to detect differences in CK metabolism between different muscle regions. The MRF method enables further investigation of the physiological implications of such differences.

References

1. Wang CY et al, NMR Biomed. 2017; 30:e3786. 2. McGivney DF et al, IEEE Med Img. 2014; 33:2311.

Acknowledgements

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