

A bone-marrow-optimized quantitative MRI protocol: towards better patient follow-up.

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ABSTRACT

Introduction

Recent progresses on quantification of MRI vertebral bone marrow biomarkers (VBMBs), allow robust quantification method with spatially resolved sequences.

A comprehensive MRI tissue characterization of vertebral bone marrow includes the measurement of the following biomarkers: fat fraction (FF), T1 and T2* relaxation times of the water and fat components (T1W, T1F, T2*W, T2*F), IVIM (IntraVoxel Incoherent Motion) diffusion (D) and perfusion parameters (perfusion fraction f and pseudo-diffusion coefficient D*). In the current study, we sought to investigate the effect of spatial heterogeneity of bone marrow within a single vertebra on these seven VBMBs.

Material and Methods

Two regions-of-interest (ROIs), the anterior and posterior area of lumbar vertebrae, were chosen for investigation (Figure 1).

MRI experiments were carried out in 14 young healthy volunteers at 1.5 T. The RESOLVE diffusion-weighted sequence was used for the measurements of the IVIM parameters and the VIBE-Dixon sequence for the measurements of FF, T1W, T1F, T2*W and T2*F. The entire MRI protocol lasted less than 6 minutes and the protocol was repeated two times. ROI measurements in anterior region were compared to those in the posterior region, with the Wilcoxon signed-rank test.

Results

A significant difference in the values of FF, f, T1F, T2*W and D was observed between the anterior and posterior region (Table 1). The regional difference in FF, f and T2*W can be ascribed to the difference of tissue characteristics, such as the trabecular bone density and the vascular network, within vertebrae.

Discussion

The regional variation of VBMBs observed in the current study indicates that care should be taken in reproducing the same ROI location along a longitudinal study. Furthermore, the MRI protocol presented here allows for the measurement of seven VBMBs in less than 6 minutes. It could be of interest for longitudinal studies of bone marrow diseases, such as myeloma, during the patient treatment and follow up.

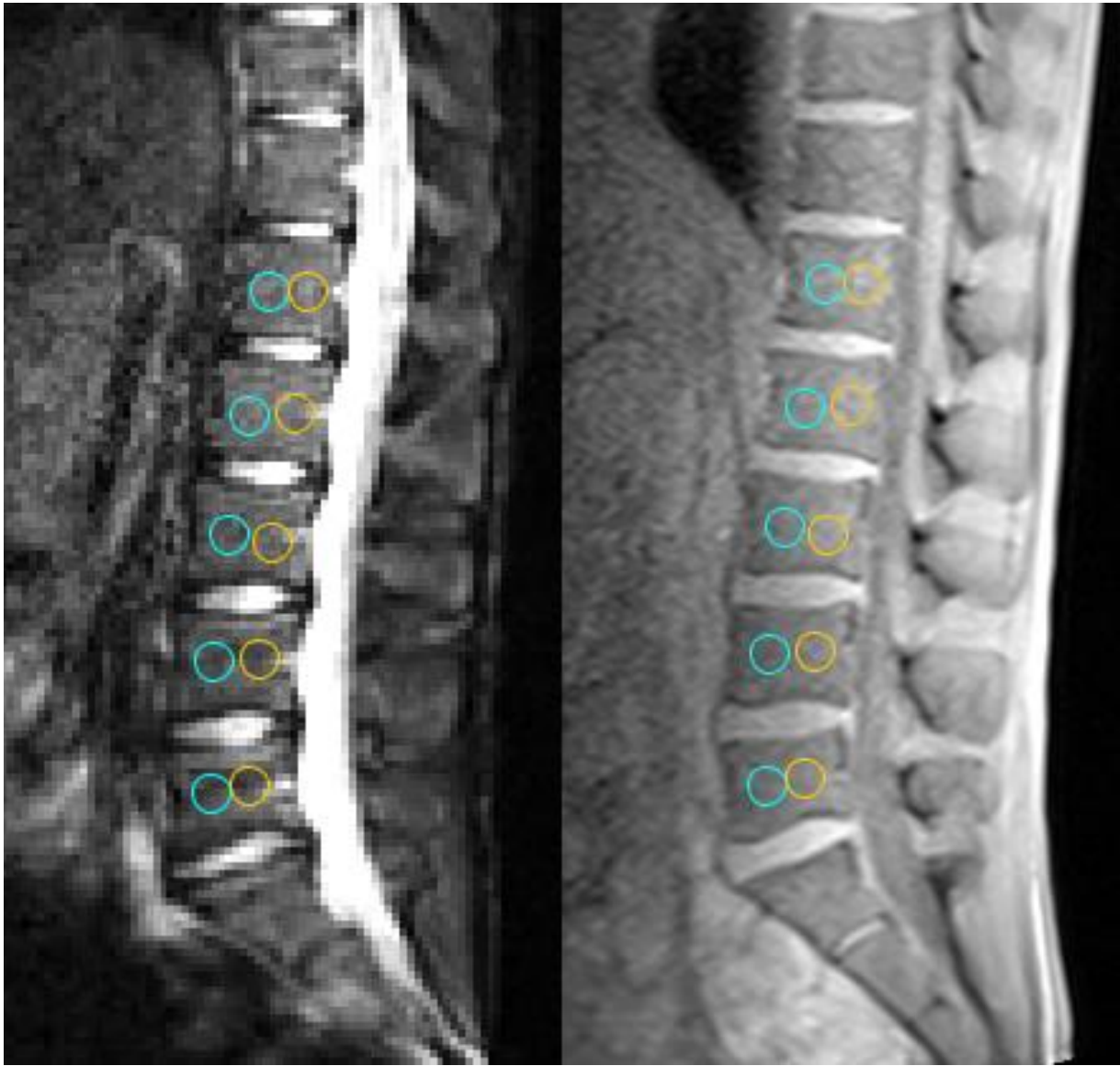


Figure 1 Sagittal MR Images of RESOLVE sequence (left), $b = 0 \text{ s/mm}^2$, and DIXON sequence (right), $TE = 1.23 \text{ ms}$ and $FA = 5^\circ$, of a healthy volunteer. ROIs are shown with cyan and orange circles for anterior and posterior regions, respectively.

	Anterior		Posterior		p-value	
	R ₁	R ₂	R ₁	R ₂	R ₁	R ₂
FF (%)	30 ± 10	30 ± 8	34 ± 10	34 ± 10	2.1 10⁻⁶ *	2.5 10⁻⁷ *
f (%)	14 ± 9	16 ± 10	22 ± 12	21 ± 10	3.2 10⁻⁸ *	6.7 10⁻⁴ *
T_{1W} (ms)	780 ± 190	785 ± 176	768 ± 189	761 ± 189	0.18	0.11
T_{1F} (ms)	295 ± 92	308 ± 87	336 ± 99	338 ± 86	2.9 10⁻⁴ *	3.8 10⁻³ *
T_{2*W} (ms)	13 ± 4	13 ± 4	12 ± 5	12 ± 4	4.0 10⁻³ *	8.5 10⁻⁷ *
T_{2*F} (ms)	13 ± 20	10 ± 5	11 ± 7	12 ± 7	0.51	0.13
D (×10⁻³ mm²/s)	0.39 ± 0.12	0.44 ± 0.26	0.42 ± 0.12	0.49 ± 0.20	2.7 10⁻³ *	6.7 10⁻⁵ *
D* (×10⁻³ mm²/s)	18 ± 12	18 ± 10	23 ± 15	26 ± 17	0.01	4.7 10⁻⁴ *

*Table 1 Numerical values of VBMBs, expressed as mean ± standard deviation, for both anterior and posterior region for the first and the second repetition (R1, R2 respectively). The p-value from the paired signed rank Wilcoxon test is given for each parameter. * : p-value < 0.01.*