T2* evaluation of iron overload at 3T and comparison with 1.5 T

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Introduction: To date the gradient echo multiecho T2* MRI technique is the most robust method for the sensitive, fast, and reproducible quantification of iron overload in transfusion dependent patients [1]. The 1.5T MRI scanner is generally used in the clinical arena. However, given that 3T scanners are becoming largely widespread, there is a growing need to assess the practicality of evaluating iron burden at 3T. The goal of this study was to establish the relationship between T2* values at 3T and 1.5T over the range of clinical interest of tissue iron concentrations.

Materials and methods: 20 borosilicate test-tube phantoms, 2.4 cm in diameter, that contained increasing concentrations of Fe(III)Cl3 (0.1, 0.15, 0.2, 0.25, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5 mM) in 0.1N standard solution of HCl (Iron standard solution, Fluka 03376; Hydrochloric acid solution 0.1N Sigma 2104) were scanned at 1.5T and 3T using a GRE multiecho sequence [2]. TEs ranged from 2 to 20.9 ms (1.5T) and 1.57 to 16.2 ms (3T) with an increment of 2.1 ms. Prior and after each scan, the phantom was monitored with a temperature probe with an accuracy of 0.1°C to avoid modification of T2* values due to temperature change [3]. The phantoms T2* values were calculated fitting the signal within a circular region of interest (ROI) to the decay model $S=S_0 \exp(-TE/T2^*) +C$. Moreover, 23 transfusion-dependent patients enrolled in the MIOT (Myocardial Iron Overload in Thalassemia) network [4] were scanned at 1.5T and 3T, with an intervening break of less than 20 minutes. A single transverse slice through the liver was acquired. The T2* value was determined over a large ROI of standard dimension, chosen in a homogeneous area. Three parallel short-axis views of the left ventricle were obtained using T2* GRE multislice multiecho sequence. The left ventricle was segmented into a 16-segments standardized model [5] and the T2* value on each segment was calculated as well as the global value and the mid-ventricular septum T2* value. MRI image analysis was performed using a custom-written, previously validated software (HIPPO MIOT®, IFC-CNR) [2].

Results: Figure 1a shows the T2* values at 3T and at 1.5T for the phantom experiment. The line of best fit had a slope of 0.61 and an intercept of 0.23. The R-squared value for the fit was 1.0, indicating that relationship between the phantoms T2* values at 3T and at 1.5T is strongly described by a linear model. Figure 1b shows the liver T2* values at 3T and at 1.5T for the patients. The line of best fit for the patients had a slope of 0.60 and an intercept of -0.03. The R-squared value for the fit was 0.90, suggesting that relationship between the liver T2* values at 3T and at 1.5T is appropriately described by a linear model. Figure 1c shows the global heart T2* values at 3T and at 1.5T for the patients. The line of best fit for the patients had a slope of 0.45 and an intercept of 10.45. The R-squared value for the fit was 0.29. Considering the mid ventricular septum, the line of best fit for the patients had a slope of 0.48 and an intercept of 12.27. The R-squared value for the fit was 0.31.

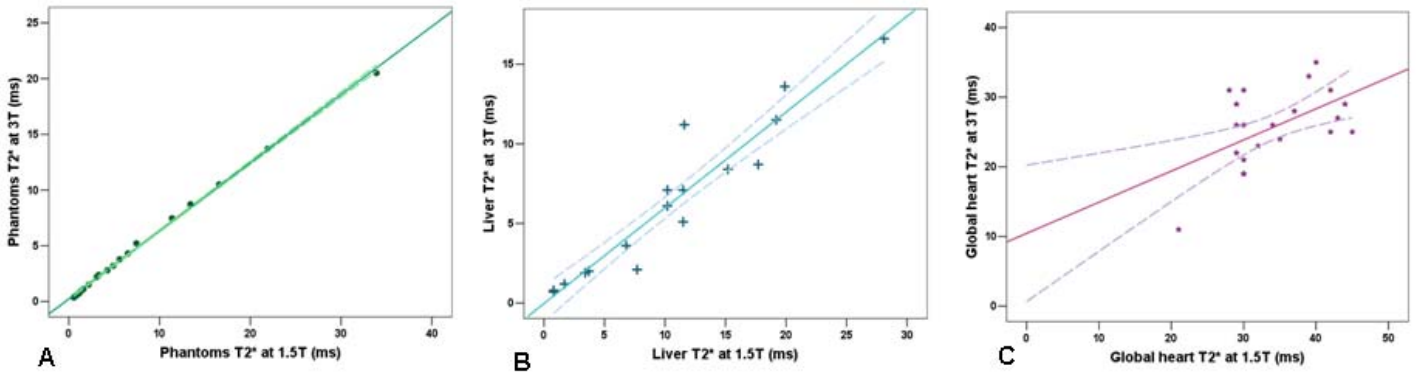

Figure 1: 3T vs. 1.5T values of T2 in the phantoms (A) in the liver (B) and in the heart (C) of transfusion dependent patients. In each graph, the line the line of best fit and the curves indicating 95% confidence interval (CI) are indicated.*

Discussion and Conclusions: A strongly significant linear relationship between T2* values at 1.5T and at 3T was found for both liver and phantoms data. The slope was about 0.6, with a negligible intercept. This result confirm the findings of Guo et al in heart T2* measurements (0.61 slope, 0.03 intercept, r=0.95) [6]. The patient population involved in this study had a mean global heart T2* value at 1.5T of 34.2±6.6 ms, well out of the clinical relevant range. This fact did not allow a reliable assessment of the relationship between T2* values at 1.5T and at 3T in heart, due to the small range of T2* covered (21-45 ms). Moreover, T2* measurement errors were relevant at high T2* values due to technical constraints in sequence design and presence of susceptibility artefacts [1,2].

References: [1] Wood JC Hemoglobin;32:85-96 [2] Positano V et al. NMR Biomed 2007;20:578-90 [3] He T JCMR 2009;11:P147 [4] Ramazzotti A et al. JMRI 2009 ;30(1) :62-68 [5] Cerqueira MD et al. Circulation 2002 ;105:539-542 [6] Guo H et al. JMRI 2009;30:394-400