CONSISTENCY ASSESSMENT FOR R_2^* MEASUREMENTS OBTAINED WITH DIFFERENT TECHNIQUES AT 7 TESLA

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Introduction

R_2^* relaxometry has been established as an important technique in various quantitative MR approaches [1, 2]. In practice, transverse relaxation of ^1H nucleus usually deviates from the ideal mono-exponential decay due to the influences of various factors such as B_0 inhomogeneity [3] and slice profile imperfection [4]. Free induction decay (FID) distortion causes discrepancy between R_2^* values obtained with different measurement methods. This problem is becoming more and more important with the growing availability of high and ultra-high field scanners in recent years. In this study, we investigated the consistency between R_2^* values measured with three different methods in a group of volunteers at 7 Tesla.

Materials and Methods

Axial brain images of four healthy volunteers (3 male and 1 female, 38±15 years old) were acquired on an Achieva 7T whole body scanner (Philips, Cleveland, OH) with a 16-channel head coil (Nova, Wilmington, MA). High temporal resolution FID measurements were obtained with a multi-echo (ME) 2D gradient echo (GRE) sequence with the following scanning parameters: field-of-view (FOV) 220×180 mm^2, 20 slices with no gap, voxel size $0.86 \times 0.86 \times 3.00$ mm^3, TR/FA = 1988 ms/90°, 31 TE's ranging from 1.7 ms to 40.3 ms (ΔTE = 1.3 ms). Another data set with higher spatial resolution was also acquired with a 3D dual echo (DE) turbo field echo (TFE) sequence with the following scanning parameters: FOV 200×100 mm^2, 32 slices, no gap, voxel size $0.50 \times 0.50 \times 1.60$ mm^3, TR/FA/TE1/TE2 = 13.3 ms/8°/2.3 ms/10.5 ms.

For each volunteer, twenty cubic regions-of-interest (ROIs) were defined in low brain white matter by an experienced radiology reader. Each ROI covers $3 \times 3 \times 1$ voxels in the ME images and $5 \times 5 \times 2$ voxels in the DE images so that its size and volume were comparable between those data sets. ROI center positions were matched by rigid-body registration between the two data sets. The ROI's were picked to represent brain regions with different levels of cross-slice B_0-inhomogeneity (quantified by the maximum cross-slice difference in local resonance frequencies, $\gamma\Delta B_0/2\pi$). Eighty ROIs were thus grouped by heterogeneity level into three groups: low ($\gamma\Delta B_0/2\pi \leq 15$ Hz, 27 ROI's), moderate (15 Hz $< \gamma\Delta B_0/2\pi \leq 50$ Hz, 35 ROI's) and high ($\gamma\Delta B_0/2\pi > 50$ Hz, 18 ROI's), for better illustration and analysis of the comparison results.

Both the ME and DE data sets were fitted to the classical mono-exponential decay model. While R_2^* measurement with 2D GRE sequences is prone to FID distortion caused by cross-slice B_0 inhomogeneity, 3D sequences are less sensitive to B_0 variations along the slice selection direction. In order to take this factor into account, high temporal resolution FID curves in the 2D ME data set were also fitted to a model that corrects for the quadratic background field inhomogeneity effect [5]. The B_0 information used by the quadratic correction model was collected with a B_0 map sequence described in [5]. ROI-averaged R_2^* values obtained with the three measurement methods were compared using graphical and statistical techniques.

Results

R_2^* values obtained from the 3D DE sequence were plotted against mono-exponential (Fig. 1a) and quadratic correction (Fig. 1b) R_2^* values from the 2D ME sequence. The three groups of ROIs corresponding to low, moderate, and high levels of cross-slice B_0 inhomogeneity were represented by dots, crosses, and triangles, separately. It is clearly demonstrated that the mono-exponential 2D ME R_2^* values are systematically larger than the 3D DE R_2^* values in regions with moderate and high inhomogeneity (Fig. 1a). After quadratic correction for the cross-slice B_0 inhomogeneity, the 2D ME sequence can generate R_2^* values that are overall consistent with those from the 3D DE sequence in all three groups of ROIs (Fig. 1b). This observation is also supported by the paired student's t-test result, which shows that the mono-exponential 2D ME R_2^* values are significantly different from the 3D DE R_2^* values ($p < 0.01$), while the difference between 3D DE and quadratic correction 2D ME R_2^* values are not statistically significant ($p = 0.84$).

Moreover, there are several data points scattered far away from the line of unity in the data cloud in Fig. 1b. It suggests that the observed consistency is a population/group property. Substantial differences may exist in individual measurements of R_2^*.
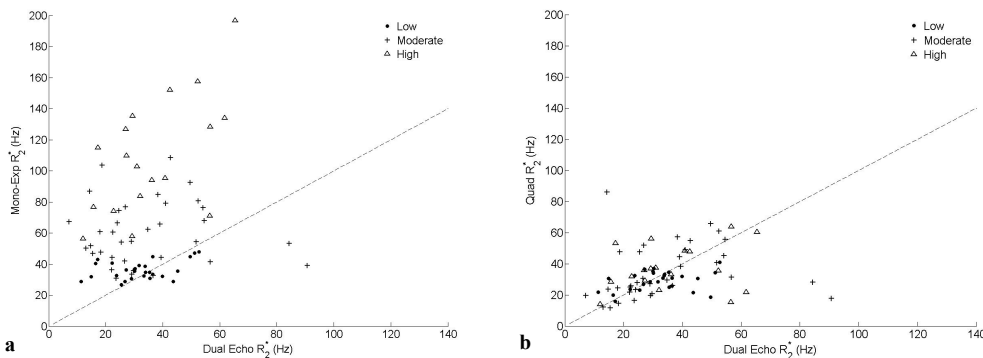
Fig. 1. 3D dual echo R_2^* values plotted against classical mono-exponential (a) and quadratic correction (b) R_2^* values from the 2D multi-echo sequence. Eighty data points from four healthy volunteers are grouped by cross-slice background field inhomogeneity into three groups: low (dots), moderate (crosses), and high (triangles). The dashed line marks out the line of unity.

Discussion and Conclusion

Our data demonstrate that at 7 Tesla, the influence of cross-slice B_0 variation must be corrected for the 2D imaging technique to generate R_2^* measurements that are consistent with those obtained using a 3D technique. Therefore, caution is needed for comparison between R_2^* measurements obtained in different studies. Only R_2^* values obtained from 2D techniques with appropriate correction for background field inhomogeneity effect and 3D techniques are comparable.

References

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