

# An Investigation of the Accuracy of 3D $T_2^*$ Mapping of Ultra-Fast Relaxing Species with Conical-SPRITE

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## Introduction

Over the past few years SPRITE imaging techniques have been demonstrated to be ideal for non-biological imaging where the NMR signal is often short-lived (1). By sampling a single point, following each RF excitation, convolution of the point spread function with  $T_2^*$  decay is avoided and imaging of fast relaxing species is made feasible. Quadrupolar nuclei present in biological tissues ( $^{17}\text{O}$  and  $^{23}\text{Na}$ ) are characterized by bi-exponential relaxation with a rapidly-decaying component in restricted environments. Quantitative imaging of these fast relaxing nuclei demands the use of SPRITE-like sequences. Single point imaging techniques, although advantageous for imaging short  $T_2^*$  samples, are inefficient because only a single datum point is acquired following each excitation and therefore suffer from long acquisition times. Acquisition times can be dramatically reduced, and SNR increased, through the implementation of rapid centric order sampling schemes, such as the nested conical trajectories of Conical-SPRITE (2). Sampling inefficiency can be improved through the acquisition of multiple points after each RF excitation. Each of these multiple points, weighted by the  $T_2^*$  decay, can be reconstructed into different but complete k-spaces. However, each of these independent k-spaces will have a different step size and hence yield images with slightly different fields of view. The chirp-Z transform algorithm can be employed to reconstruct the multiple point images with a common FOV. These FOV corrected images can be combined for the purpose of  $T_2^*$  mapping. An evaluation of the quantitative  $T_2^*$  mapping capability of multiple point Conical-SPRITE is presented.

## Methods

The Conical-SPRITE sequence was implemented on a 4T Varian UnityInova system equipped with a 40mT/m whole-body gradient coil. For the purposes of evaluation of the methodology, an idealized quasi-spherical vessel of  $\text{H}_2\text{O}$ , doped with  $\text{MnSO}_4$  to reduce  $T_2^*$ , was imaged. The measured bulk relaxation parameters of the sample were:  $T_2^* = 1.12 \pm 0.01$  ms;  $T_1 = 23.2 \pm 0.2$  ms. Images were acquired with a matrix of  $64 \times 64 \times 64$ , TR = 8.0ms, flip angle = 7.2, FOV =  $128 \times 128 \times 128$  mm and 2 averages. Four consecutive scans with  $t_p = 0.3, 1.0, 3.0,$  and  $6.0$  ms and a corresponding dwell time of 11, 80, 250, 500  $\mu\text{s}$  were performed where each scan acquired 4 multiple points following each RF excitation. The total acquisition time was 68 minutes. The multiple points were used to reconstruct independent k-spaces each with a different  $T_2^*$  weighting and a slightly different FOV; the latter was corrected by use of the chirp-Z transform.  $T_2^*$  maps and spin density maps were created by fitting the data to a mono-exponential decay function.

## Results

Figure 1a shows a  $T_2^*$  map of the homogeneous phantom described above with the  $^1\text{H}$  spin density map shown in Figure 2a. The profile through the phantom in the  $T_2^*$  map (Figure 1b) is extremely uniform and yields a value of  $T_2^* = 1.11 \pm 0.02$  ms. The profile through the spin density map (Figure 2b) does not exhibit a 'flat top' but this is because of dielectric effects. In Figure 3a, the results of a single pulse bulk  $T_2^*$  measurement are shown yielding a  $T_2^*$  value of  $1.12 \pm 0.01$  ms. In contrast, Figure 3b shows the results of a single voxel fit yielding a  $T_2^*$  value of  $1.11 \pm 0.02$  ms; bulk and single voxel fits show excellent agreement.

## Discussion

The potential of SPRITE imaging of fast-relaxing nuclei is, ultimately, in the realisation of quantitative information. Here, we have investigated quantitatively the accuracy of the  $T_2^*$  fit that results from imaging a fast-relaxing system using SPRITE. Our results demonstrate that  $T_2^*$  mapping of a species which relaxes on the order of 1ms is feasible using Conical-SPRITE. Furthermore, the data acquisition time is commensurate with possible clinical application. Quantitative imaging of quadrupolar species such as  $^{23}\text{Na}$  or  $^{17}\text{O}$  is complicated because of bi-exponential relaxation behaviour. However, the results presented here indicate that bi-exponential fitting should be easily achievable as long as a reasonable SNR is ensured.

## References

- (1) B. J. Balcom, SPRITE Imaging of Short Relaxation Time Nuclei, in "Spatially Resolved Magnetic Resonance", pp. 75-86, Wiley-VCH, Toronto (1998)
- (2) Meghan Halse, David Goodyear, Bryce MacMillan, Pavol Szomolanyi, David Matheson and Bruce J. Balcom, JMR, *in press* (2003)

Figure 1a

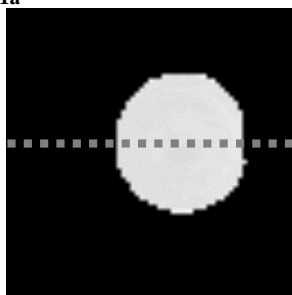


Figure 1b

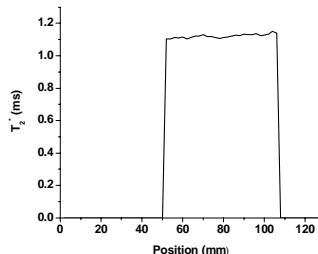


Figure 1 (a) Central 2D slice of the 3D  $T_2^*$  map. (b) Profile through the  $T_2^*$  map in (a) along the line shown.

Figure 2a

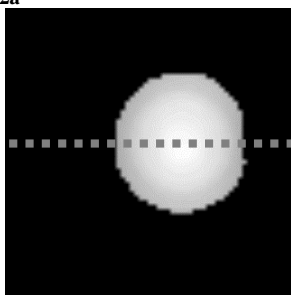


Figure 2b

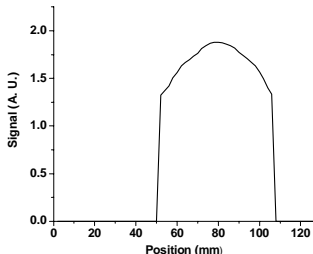


Figure 2 (a) Central 2D slice of the 3D density map. (b) Profile through the density map in (a) along the line shown.

Figure 3a

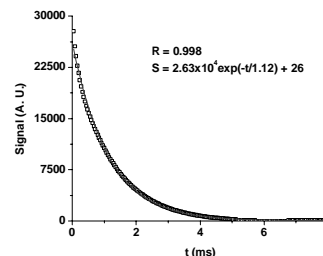


Figure 3b

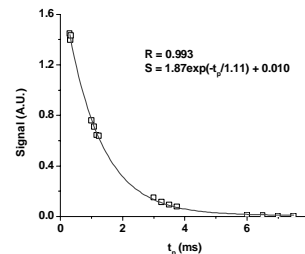


Figure 3 (a) Bulk  $T_2^*$  decay (b)  $T_2^*$  decay of a single voxel in the image reconstructed from four multiple point acquisitions.