Fast whole brain susceptibility imaging using 3D spiral

B. Wu[1], W. Li[1], A. Avram[1], A. Guidon[1], and C. Liu[1]
[1]Brain imaging and analysis center, Duke University, Durham, NC, United States

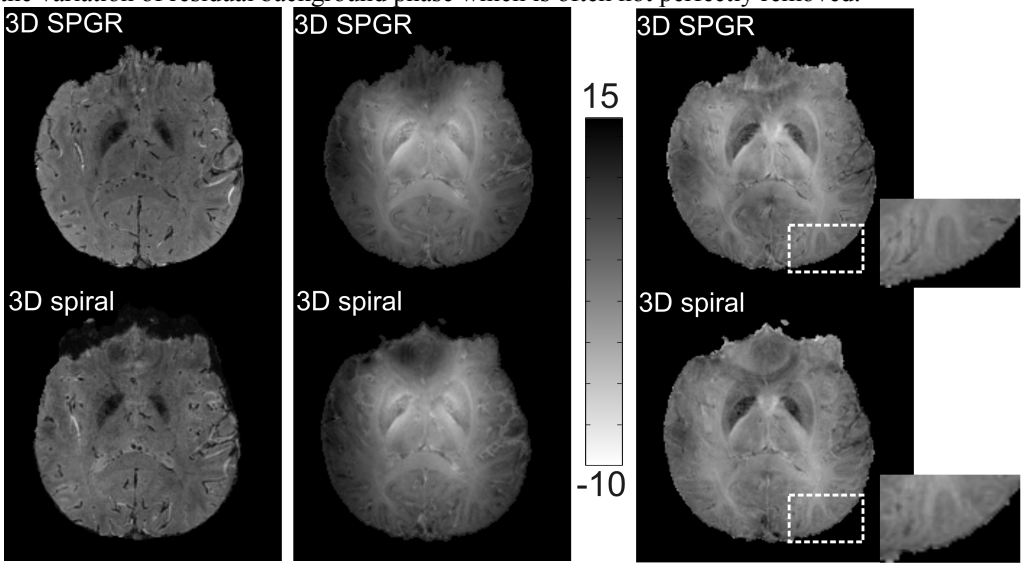
Introduction Quantitative susceptibility mapping potentially allows the in vivo tissue composition to be quantitatively assessed. Conventionally, susceptibility maps are calculated using the phase information obtained using 3D gradient echo sequence with a Cartesian sampling, i.e. 3D SPGR. Due to the long echo time used and the line-by-line data acquisition nature, data acquisition covering a sufficiently large brain volume is a considerably long process, which could take up to an hour for 1mm resolution whole brain coverage. Comparing to Cartesian sampling, spiral trajectory allows much more efficient use of the field gradient capability and hence achieve fast k-space coverage. In this work, we utilize 3D stack-of-spiral sequence (1) for the acquisition of image phase and hence the derivation of susceptibility map. We compare the susceptibility map obtained using 3D spiral and standard 3D SPGR, both qualitatively and quantitatively, given that a scan time reduction factor of 13 is achieved by using the 3D spiral sequence.

Method In vivo brain imaging of a healthy adult volunteer was performed with a GE scanner equipped with a 8 channel head coil. A 3D stack-of-spiral with 14 in plane interleaves was used in data acquisition. The following parameters were used: TE/TR = 40/65ms. Flip angle = 20, FOV = 19.2, matrix size = 192x192x120 to give a 1 mm isotropic resolution covering the whole brain region apart from the cerebellum. Another scan using a standard GE 3D SPGR sequence with identical parameters as above was also performed. The scan time for using the 3D SPGR sequence and the 3D spiral sequence was respectively 26 minutes and 2 minutes.

Complex data sets are reconstructed using the acquired data. Phase images were first extracted from each coil and individually performed phase unwrapping and background phase removal using the method proposed in (2). The processed phase maps from different coils are then averaged to give the final phase map. Susceptibility map were then calculated from the phase maps using pre-conditioned iterative method as described in (3).

Results An axial plane slice of reconstructed magnitude, phase image and the calculated susceptibility map using 3D spiral and 3D SPGR are shown in Fig.1. All three types of images from the two sequences are seen to be visually similar. A close look at the calculated susceptibility maps reveals that the susceptibility map obtained using 3D spiral sequence has slightly blurred edges where the susceptibility variation is low.

Quantitative susceptibilities values are calculated for iron-rich regions including GP, PU, SN and RN and shown in Table 1. The susceptibility values are obtained by taking the susceptibility difference between the selected regions and that of the CSF region. Very similar susceptibility values are resulted from the two sequences in the regions tested. The difference may be attributed to noise and the variation of residual background phase which is often not perfectly removed.



(a) Magnitude (b) Phase (c) Susceptibility

Figure 1 Comparison of an axial slice of the images obtained using 3D SPGR and spiral

	3D SPGR	3D spiral
GP	5.4	5.2
PU	2.1	2.3
RN	8.1	8.1
SN	7.0	7.3

x 0.01 ppm

Table 1 Calculated susceptibility values of different iron rich regions

Conclusion We show that the 3D stack-of-spiral sequence may be a good substitute to 3D SPGR for the obtaining the image phase information and hence derivation of susceptibility maps. In the experiment conducted, the susceptibility maps obtained from the two sequences are seen to be similar both qualitatively and quantitatively, despite the fact that the spiral sequence features a 13 times shorter scan time. Hence the spiral sequence could be very useful in case of high resolution and/or multi-orientation susceptibility imaging (4). The slight blurring observed in the susceptibility map obtained from the spiral sequence is a result of insufficient sampling at k-space peripheral region, and may be improved by employing a larger number of spiral interleaves.

Reference (1) Hu, et al., MRM 2007 (2) Schweser, et al., Neuroimage 2010
(3) Rochefort, et al., MRM 2010 (4) Wharton, et al., Neuroimage 2010