Rapid QSM Acquisition with Wave-CAIPI

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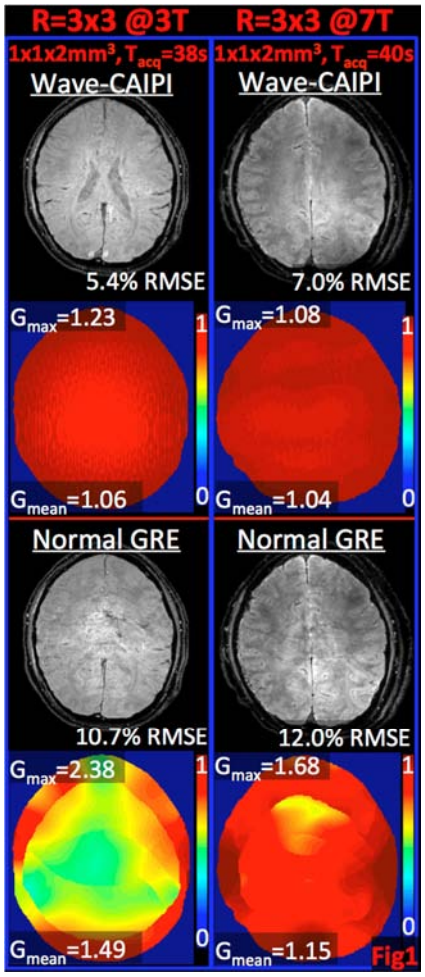
TARGET AUDIENCE: Scientists interested in highly accelerated parallel imaging acquisition and rapid Quantitative Susceptibility Mapping (QSM).

PURPOSE: Wave-CAIPI acquisition [1] enables highly accelerated parallel imaging with low g-factor penalty in a 3D gradient echo (GRE) scan by using i) 2D CAIPIRINHA controlled aliasing [2] and ii) additional sinusoidal G_y and G_z encoding gradients during the readout of each phase encoding line. In this work, we improved the robustness and reconstruction efficiency of Wave-CAIPI and applied it to challenging applications in phase imaging and QSM [3,4], which can be sensitive to phase error from imperfect parallel imaging reconstruction. Herein, data acquisition and reconstruction time of QSM are dramatically reduced by the combination of Wave-CAIPI acquisition and fast phase processing and QSM algorithms. For Wave-CAIPI reconstruction, we extend the initial proposal in [1] by i) reducing the Wave reconstruction time 25× (from 360 min to 14 min), ii) estimating accurate point spread functions (PSFs) from a fast prior training acquisition, and iii) increasing the resolution 4-fold. This enables high quality whole-brain 7T QSM at 1×1×2 mm^3 voxel size in **40 seconds**. For phase processing, Laplacian unwrapping [3] and SHARP filtering [4] comprise a fast pipeline (6 seconds) to produce the tissue field map. Dipole inversion with magnitude-weighted gradient regularization is performed with a fast solver (10 seconds) that employs preconditioned conjugate gradient (PCG) [5].

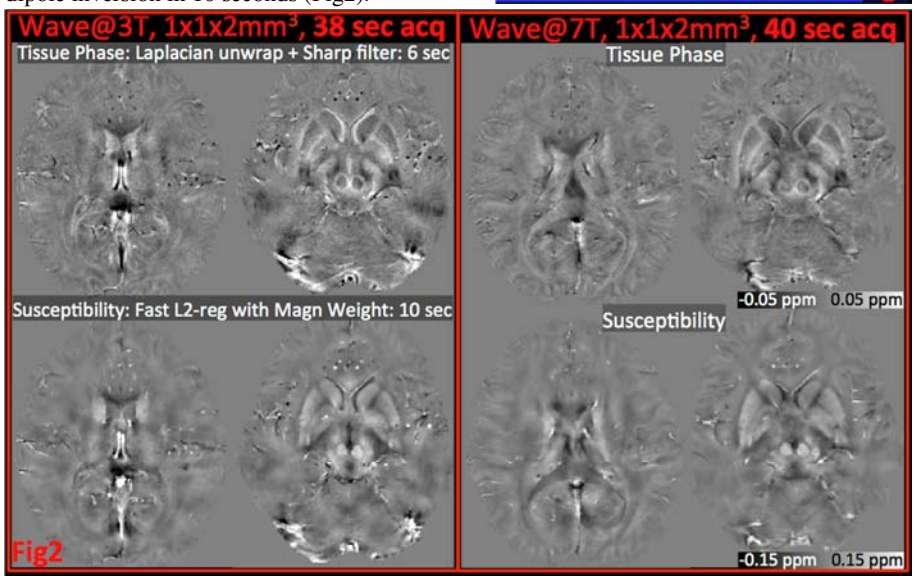


METHODS: **Image Encoding:** The voxel spreading effect of the Wave-CAIPI gradients along the readout can be expressed as a convolution in image space due to $psf(:,y,z)*img(:,y,z)$, where $img(:,y,z)$ is one row of a coil image at position (y,z), and $psf(:,y,z)$ is the point spread at this location. In the presence of R-fold undersampling along k_y-k_z, R image rows will collapse to yield a linear system that can be solved with the aid coil of sensitivities. The large forward model of the 3D data is separable into sub-systems [1], each representing a coupled forward model of R image rows that can be solved separately. We iteratively solve each of these sub-systems using the LSQR algorithm without explicitly forming the large encoding matrix. This leads to computational savings as PSF convolutions are efficiently performed via FFTs.

PSF Estimation: Gradient imperfections and eddy currents from G_y and G_z waves can cause the physical PSF to differ from the theoretical one, leading to poor reconstruction. To mitigate this, we estimate the physical PSF by: performing a simple and fast calibration acquisition with and without Wave gradients, computing the phase differences and performing linear regression of phase along y and z directions.

Phase Processing: Following masking with BET [6], raw phase images produced by Wave reconstruction is processed by Laplacian unwrapping [3] and SHARP filtering [4]. **QSM:** Dipole inversion with magnitude-weighted regularization [7] minimizes $\|\mathbf{D}\chi-\phi\|_2^2+\lambda\|\mathbf{MG}\chi\|_2^2$, where $\mathbf{D}$ is the dipole kernel, ϕ is the tissue field map, $\mathbf{M}$ is a binary mask derived from the gradient of the magnitude image, $\mathbf{G}$ is the gradient operator, χ is the susceptibility distribution and λ is a regularization parameter. The optimizer is found by solving $(\mathbf{D}^2+\lambda\mathbf{G}^T\mathbf{MG})\chi=\mathbf{D}^T\phi$. Without magnitude weighting ($\mathbf{M}=\mathbf{I}$), the system $(\mathbf{D}^2+\lambda\mathbf{G}^2)^{-1}$ is invertible in closed-form [5]. We utilize this as preconditioner to solve the magnitude-weighted problem efficiently. **Data Acquisition:** A healthy volunteer was scanned on Siemens scanners at 3T and 7T equipped with 32-chan array coils to acquire Wave-CAIPI data (1×1×2mm^3 res, FOV=224×224×120, max Wave gradient amp=6mT/m, slew=50mT/m/ms, 7 sinusoidal cycles/readout, **3T:** TR/TE=26/13.3ms BW=70Hz/px, T_{acq}=38s, **7T:** TR/TE=27/10.9ms, BW=80Hz/px, T_{acq}=40s). Normal GRE was also acquired for comparison.

RESULTS: **3T:** At R=3×3 acceleration, Wave reconstruction yielded 5.4% normalized root mean square error (RMSE) relative to the fully-sampled data, whereas the error was 10.7% for normal GRE (Fig1 left). From g-factor analysis, g_{max} and g_{mean} for Wave vs. Conventional GRE were found to be 1.23 vs. 2.38 and 1.06 vs. 1.49, respectively. **7T:** At R=3×3 acceleration, Wave reconstruction vs. Conventional GRE RMSEs were 7.0% and 12.0% (Fig1 right). g_{max} and g_{mean} for Wave vs. Conventional GRE were 1.08 vs. 1.68 and 1.04 vs. 1.15, respectively. Processing the phase with Laplacian unwrapping and SHARP filtering took 6 seconds and susceptibility maps were computed with PCG dipole inversion in 10 seconds (Fig2).



DISCUSSION: At R=3×3, Wave-CAIPI reduces the RMSE and the max g-factor 1.9 times relative to normal GRE at 3T and 1.6 times at 7T by increasing the average distance between aliasing pixels. This allows maximal utilization of the sensitivity profiles and reduces aliasing artifacts. Since the Wave g-factor approaches unity especially at ultra-high field, acceleration beyond R=9 is warranted. Here, we used a relatively short TE to target iron-rich deep gray matter structures, however to enhance cortical contrast, a longer TE would be required.

CONCLUSION: Wave-CAIPI imaging enables 9-fold accelerated parallel imaging acquisition with low artifact and SNR penalties. This allows high-resolution whole-brain GRE acquisition in 40 seconds. When combined with fast phase and susceptibility processing, this efficient acquisition-reconstruction method may facilitate clinical application of QSM.

REFERENCES: [1] Setsompop K et al. ISMRM'11; [2] Breuer FA et al. MRM'06; [3] Li W et al. NIMG'11; [4] Schweser F et al. NIMG'11; [5] Bilgic B et al. MRM'13; [6] Smith SM HBM'02; [7] Liu T et al. MRM'11.