# Fast Decomposition of Water and Lipid Using a GRASE Technique with the IDEAL Algorithm

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**Introduction**: Recently the IDEAL algorithm (Iterative Decomposition of water and fat with Echo Asymmetry and Least square estimation) has drawn significant attention [1]. Compared to conventional Dixon methods, the IDEAL algorithm produces robust lipid and water separation by iteratively searching the optimal field map. However, this technique requires a minimum of three acquisitions to collect data at different phase shifts, which leads to long scan time, such as its implementation with FSE [2]. To address this issue, we presented a method by combining the IDEAL algorithm with a radial GRASE (GRAdient and Spin-Echo) sequence, which provides fast and accurate separation of lipid and water as well as the capability to generate the $T_2$ and $T_2^+$ maps [3]. In this work, we propose a new technique by incorporating the IDEAL algorithm into the Cartesian GRASE method (IDEAL-GRASE) with an effective approach to correct the phase error in the source images, a problem inherent to GRASE methods due to the fast switching of the polarities of the readout gradient.

**Methods**: A diagram of the IDEAL-GRASE pulse sequence is shown in Fig. 1. Similar to [3], a 4-echo data acquisition scheme is used. This is possible because a 3-echo acquisition with the middle echo shifted relative to the SE point leaves extra space. This extra space is used for the acquisition of a 4$^{th}$ echo (as shown by the dashed-line rectangle in Fig. 1) to improve noise performance without penalty in scan time.

In IDEAL-GRASE, there is an additional SE period (referred to as calibration period) following the regular data acquisition period. Data acquired in this calibration period are used to correct phase error in the source images due to gradient delay and eddy current caused by fast switching of the readout gradients. As illustrated in Fig. 1, in odd TRs, the polarities of the readout gradients in the calibration period are the same as



Fig. 1 Schematic diagram of the IDEAL-GRASE sequence.

those in the regular data acquisition periods. In even TRs, the polarities of the readout gradients in the calibration period are all flipped. The phase encoding gradients are turned off during the calibration period to utilize the high SNR data at the center of *k*-space.

To estimate the phase error, Fourier transform (FT) is performed on all calibration data after the scan direction of the lines acquired with negative readout gradients is reversed. The FT of echo $E_n$ from an odd TR is divided by that of the same echo from the following even TR. The phase of the quotient is averaged over all odd-even TR pairs and fit to a polynomial. The polynomial is then halved and subtracted/added in the frequency direction from the phase of the source image obtained from the odd/even echo. This is equivalent to eliminating the phase error in data acquired with positive/negative polarity and making it consistent with data acquired with pseudo-neutral polarity. The above procedure is repeated for all echoes and all coils. Then the IDEAL algorithm is performed on the corrected source images to separate the lipid and water components.

The IDEAL-GRASE sequence was implemented on a 1.5T GE Signa NV-CV/i MRI scanner. To demonstrate this technique, in vivo pelvic data were acquired with echo shifts = ($-5\pi/6$, $-\pi/6$, $\pi/2$, $7\pi/6$), BW = $\pm125$ kHz, ETL = 10, NEX = 1, and matrix = $256\times240$ for each echo (excluding the calibration data), TR = 1 s. For comparison, pelvic data were also collected using IDEAL-FSE [2] with same imaging parameters. In vivo heart data were acquired with echo shifts = ($-3\pi/2$, $-\pi/2$, $\pi/2$, $3\pi/2$), BW = $\pm62.5$ kHz, ETL = 8, NEX = 1, and matrix = $256\times192$ for each echo, ECG triggering (TR = 1RR), and a double-inversion preparation period. Informed consent was obtained from volunteers prior to imaging. The IDEAL algorithm and the phase error correction method, implemented using MATLAB, were used to process the data to generate the water and lipid images as well as the phase map.

**Results:** The improvement with phase error correction in IDEAL-GRASE is illustrated in Fig. 2. In the figure we show the water images of the pelvis generated (a) without and (b) with the proposed phase error correction. Compared to the water image obtained without phase error correction, the lipid signal in the water image obtained with phase error correction is suppressed more completely and uniformly in



Fig. 2 Water images of the pelvis obtained with IDEAL-GRASE (a) without and (b) with phase error correction, and (c) using IDEAL-FSE.

the frequency (horizontal) direction. The performance of lipid/water separation of IDEAL-GRASE with phase error correction is comparable to that obtained with IDEAL-FSE (Fig. 2c), but the latter requires a longer scan time (~ 3 times longer).

Figure 3 shows examples of black-blood (a) water and (b) lipid images of the heart with phase error correction. These results demonstrate that excellent water and lipid separation throughout the entire field-of-view can be achieved by combining the IDEAL algorithm with the GRASE technique. The acquisition of IDEAL-GRASE data in heart is possible because of the short imaging time (i.e., a breath hold).



Fig. 3 (a) Water and (b) lipid images of the heart obtained using IDEAL-GRASE. Data acquired in a single breath hold.

**Conclusion**: In this work we demonstrated that robust and time-efficient water and lipid separation can be achieved by combining the IDEAL algorithm and the Cartesian GRASE method with a phase error correction approach. With this technique, one complete data set can be acquired in a single breath-hold period. This is particularly useful where fast imaging is desired.

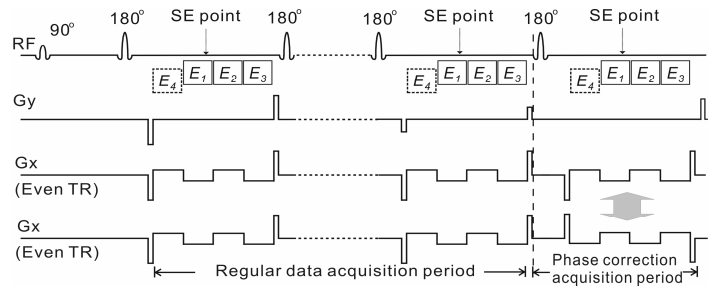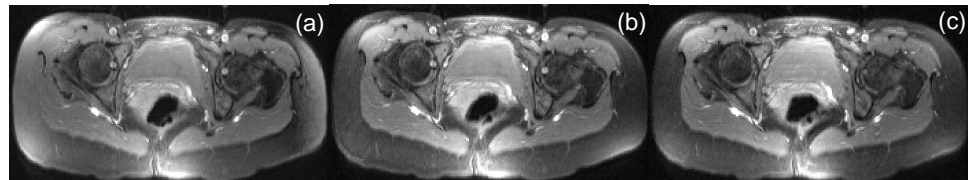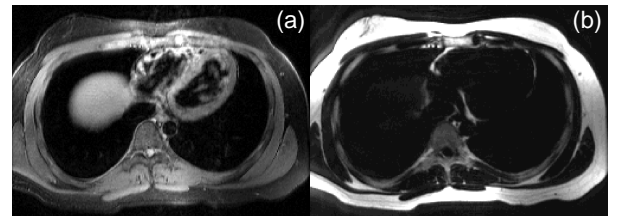**References:** [1] Reeder SB, MRM 51:35, 2004. [2] Reeder SB, MRM 54:636, 2005. [3] Li Z, ISMRM 14:625, 2006.