Lipid Fraction Measurement Incorporating T1 and RF inhomogeneity Correction

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INTRODUCTION

The content and distribution of fat in humans has received increased attention in recent years because of its relationship to many diseases including cancer, coronary heart disease, diabetes, and obesity. Quantification of lipid, therefore, is very significant for diagnoses, treatment, and understanding disease processes [1, 2]. At short TR, lipid content measured strongly depends on relaxation times, RF inhomogeneity, and pulse sequences [3, 4]. Here, the lipid fraction in skeletal muscle is accurately estimated by incorporating T_1 and RF inhomogeneity corrections.

METHODS

All experiments for three normal volunteers were carried out with Siemens knee coil at 1.5T Siemens Sonata system.

Flip angle map: The transmit field map was estimated using three images which were acquired by a segmented gradient echo EPI sequence with excitation flip angles of 30°, 60° and 120°, respectively. The other acquisition parameters were: TR/TE 2500/7 ms, FOV 200 x 200 mm^2, matrix 128 x 128, slice thickness of 3 mm, 10 slices, and 3 segments.

Lipid Fraction: All images for three point IDEAL [5] were collected using a spoiled gradient echo sequence (SPGR) (Siemens Medical Solution, Erlangen, Germany). The imaging parameters were: matrix size = 256x256, FA= 13°, TR = 8.1 ms, TE's = 2.68/4.21/5.74 ms (sampling interval $\Delta\theta$ = 120° or Δt = 1.53 ms; asymmetric sampling phase angle θasym = 90°), bandwidth = 1028 Hz/pixel, 8 average, slice thickness = 5 mm, number of slices = 1. In this set up, the maximum number of signal average (NSA) of 3 for a three-point data collection was obtained independent of lipid content in the pixels [5]. Additionally, the experiments for the volunteers were repeated with TR=5000ms and flip angle of 90° for estimating the lipid fraction of the phantom. The other parameters were identical.

Relaxation: T_1 of lipid and water in skeletal muscle at 1.5 can be obtained from the literature [6]. With the T_1 of lipid and water, and an estimated transmit field map, the proton spin density of lipid can be estimated by the signal intensity of an internal reference (water). It is noted that the effect of TE should be corrected if TE is comparable to the T_2^* of water and lipid in skeletal muscle.

RESULTS AND DISCUSSIONS

At the flip angle of α, the signal intensity for the SPGR sequence spoiled gradient echo is given by [4]:

$$SI = M_0 \cdot (1-E_1) \cdot (\sin\alpha) / (1-E_1 \cdot \cos\alpha) \quad (1)$$

where M_0 is the equilibrium magnetization and $E_1 = \exp(-TR/T_1)$. The accuracy Φ for lipid fraction is defined to describe the influence of flip angle for quantification

$$\Phi = SI_{C\text{-}Lipid}/(SI_{C\text{-}Lipid}+SI_{C\text{-}Water}) - M_{0\text{-}Lipid}/(M_{0\text{-}Lipid}+M_{0\text{-}Water}) \quad (2)$$

where $SI_{C\text{-}Lipid}$ and $SI_{C\text{-}Water}$ are the signal intensity of lipid and water calculated from Eq (1), respectively. $M_{0\text{-}Lipid}$ and $M_{0\text{-}Water}$ are the equilibrium magnetization of lipid and water, respectively. $M_{0\text{-}Lipid}/(M_{0\text{-}Lipid}+M_{0\text{-}Water})$ is a true lipid fraction. **Fig. 1** shows simulated results for accuracy Φ for TR = 10 ms. The results indicate that the lipid fraction is overestimated for all flip angles and all lipid fractions because of the approximation of $SI_{C\text{-}Lipid}/(SI_{C\text{-}Lipid}+SI_{C\text{-}Water}) \approx M_{0\text{-}Lipid}/(M_{0\text{-}Lipid}+M_{0\text{-}Water})$. The calculated lipid fraction becomes more accurate with smaller flip angles.

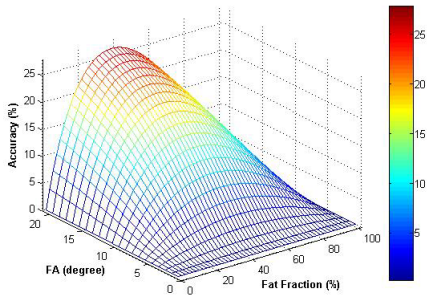

Fig. 1. The influence of flip angles (FAs) on the accuracy of lipid fractions at the different lipid fractions.

Fig. 2 shows that the lipid fractions obtained using an SPGR sequence with the three point IDEAL method and aTR of 8.1 ms (left) and 4000 ms (middle). The lipid fraction is obtained by water-only and fat-only images which are calculated by the IDEAL algorithm [5]. Since TR= 4000ms is much larger than T_1 of water and fat at 1.5 Tesla, the effect of T_1 and flip angle on the estimated can be neglected. Thus, the lipid fraction at the TR of 4000 ms can be regarded as a standard to evaluate the results which are estimated at short TR with / without T_1 and RF inhomogeneity correction. The results indicate that the lipid fraction is overestimated at the TR of 8.1 ms without any correction. For a true lipid fraction of around 10%, the resulting error can be as high as 40%. However, for voxels with pure lipid, there is no error for both short and long TR. All the experimental results are consistent with the simulation in **Fig. 1**.

CONCLUSIONS

(1) Simulated results indicate that both T_1 and RF inhomogeneity strongly affect the accuracy of lipid fraction estimation using SPGR. (2) With the measured flip angle map and known T_1 of lipid and water, accurate lipid fractions can be estimated using SPGR imaging with a short TR. The experimental results in skeletal muscle are consistent with the simulation. In order to maximize the accuracy of the estimated lipid fraction at a short TR, the influence of T1 and RF inhomogeneity should be corrected.

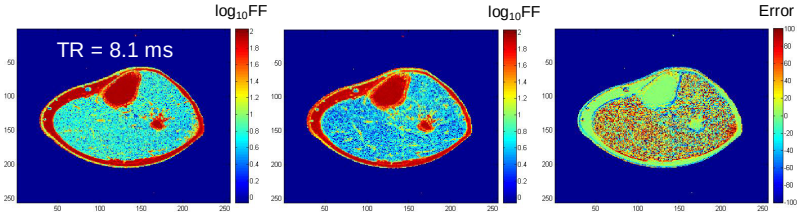

Fig. 2. The lipid fractions acquired by three point Dixon method at the TR of 8.1 ms (left) and 4000 ms (middle), and their difference (right). The lipid fraction is estimated by original IDEAL algorithm.

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