A Method of Reducing Fat-Caused Bias in DCE-MRI Perfusion Measurement

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Introduction

Perfusion imaging via dynamic contrast-enhanced (DCE) MRI is an important technique widely applied in clinical practice nowadays to characterize inflammation, tumors, and various lesions. It has been proved that the fat-saturation (FS) technique influenced the perfusion parameter measurements up to two-fold in comparison with those obtained without fat-saturation (NFS) in fat-rich tissues such as the parotid glands [1]. Prior study has shown the main difference to be due to the presence of fat signals in the pre-contrast baseline used for normalization. We therefore hypothesize that the use of a baseline signal measured from a fat-free region could minimize the sequence-induced measurement bias for the perfusion parameters.

Materials and methods

Our study included both phantom and in vivo experiments. The phantom consisted of 18 bottles of 20ml fat-water emulsion solution at three fat contents (0%, 30%, and 50%) and six concentrations of Gd-DTPA (0, 0.5, 1.0, 1.5, 2.0, and 2.5 uM), which underwent both NFS and FS T1-weighted imaging at 1.5T (TR/TE = 400/6.3). Percentage signal enhancements at all concentrations were calculated with the zero-dose intensity of the same fat-content as the baseline. To reduce the difference between FS and NFS scans, in the phantom analysis, we also apply the 0%-fat phantom as the normalization baseline of each fat content phantom. In vivo studies included 9 healthy volunteers (2 men and 7 woman, aged 43.4±11.6 years). The images were obtained on a 1.5T MR system (Signa, GE Healthcare, Milwaukee, Wis) using a contrast-enhanced MRI head and neck multi-slice 2D T1-weighted fast spin-echo sequence. The volunteers received two MR scans separately by one week apart, each with 0.1 mmol/kg dose of Gd-DTPA injection. NFS and CHESS FS used identical scanning parameters: axial view with 6 slices, field of view of 282×282mm, matrix of 256x160, slice thickness of 5 mm and TR/TE of 400/12.6 msec. The total acquisition time of each scan was 264 seconds including 24 phases equally spaced by 11s.

For perfusion parameter analysis, the Brix model was used for curve fitting on the percentage signal increase relative to the baseline signal before contrast injection. The three Brix model parameters (A, k21, and Kel) were also measured to calculate the percentage peak enhancement (PE) defined as the percentage increase at maximum value of the fitted curve. Difference between PE values obtained with FS and NFS, as well as other perfusion parameters such as the wash-in slope, was assessed using two baseline signals: One selected from the parotid gland (about 50% fat content) and the other selected from the spinal cord which contains about 10-20% fat content only. Paired student t-test was used for statistical analysis.

Results

Results from the phantom study shows that the percentage signal enhancement in FS scan is always higher than the corresponding NFS scan. The higher fat content, the larger difference in percentage signal enhancement is found between FS and NFS scans (Fig.1a). Such discrepancy is removed when the signals from 0% fat phantom is used as baseline signal for normalization (Fig.1b). Results from in vivo human experiments further show substantial disagreement in PE between FS and NFS scans when using the fat-rich parotid glands. Baseline normalization using signals from the spinal cord, although also showing statistically significant difference between FS and NFS scans, demonstrates prominent improvements in the agreement (Fig.2). Brix model perfusion parameter A (amplitude) and the wash-in slope exhibit the similar trend to PE (not shown). The fat-content and perfusion parameters show negative association (R^2~0.5) in NFS scans but not in FS scans (R^2~0.07). With spinal cord selected as the baseline, disagreement between FS and NFS scans (R^2~0.25, 0.3) reduces (Fig.3).

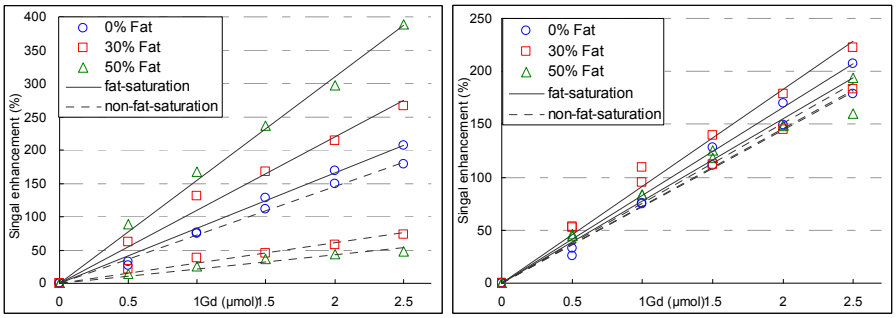

Figure 1 *(a) Higher percentage signal enhancement is found for FS scan than the corresponding NFS scan. Larger discrepancy appears at high fat content. (b) The discrepancy is largely removed when the signals from 0% fat phantom is used as baseline signal for normalization.*

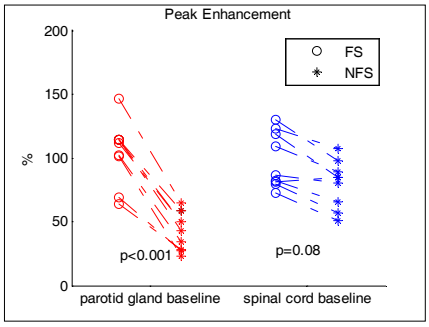

Figure 2 *Discrepancy between FS and NFS scans is found in human parotid glands (left), but is prominently reduced with the spinal cord chosen as the baseline signals (right).*

Discussion and Conclusion

It is widely recognized that DCE perfusion with FS yields results substantially different from those with NFS scans. Since the fat signals are not enhanced with contrast administration, signal enhancement is restricted to the water compartments. As a result, the proportion of fat signals affects the signal enhancement by introducing baseline bias, thus influencing subsequent derivation of perfusion parameters even with identical contrast agent concentraton (Fig.1a). This phenomenon is clinically crucial, as aging, gender, and disease status are all known to cause alterations in fat content for many tissues. Perfusion parameters derived from FS scans are shown to exhibit less dependency on fat contents (Fig.1b), but may be prone to imperfect FS in the head-and-neck region due to susceptibility effects near the oral cavity, especially in the presence of dental implants [2]. To compensate the baseline bias on NFS DCE MRI, we propose to select pre-contrast ROI from the spinal cord to replace parotid gland as baseline. The less fat content in spinal cord used as baseline signals improved the agreement between perfusion parameters derived from FS and NFS scans (Fig.2). We therefore conclude that the selection of a relatively fat-free tissue for pre-contrast baseline is a simple and effective method to reduce bias from fat content in DCE perfusion MRI of the parotid glands. Possible limitations resulting from the use of a different tissue for baseline signal are under continuous investigation.

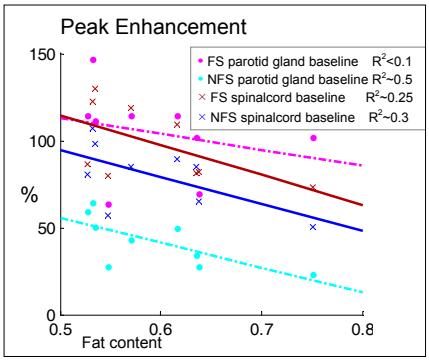

Figure 3 *Fat-content and perfusion parameters show negative association in NFS scans but not in FS scans. With spinal cord selected as the baseline, disagreement between FS and NFS scans reduces.*

References

1. Chiu SC et al. ISMRM 2010;1732. 2. Suenaga S et al. AJR 1998;171:511.