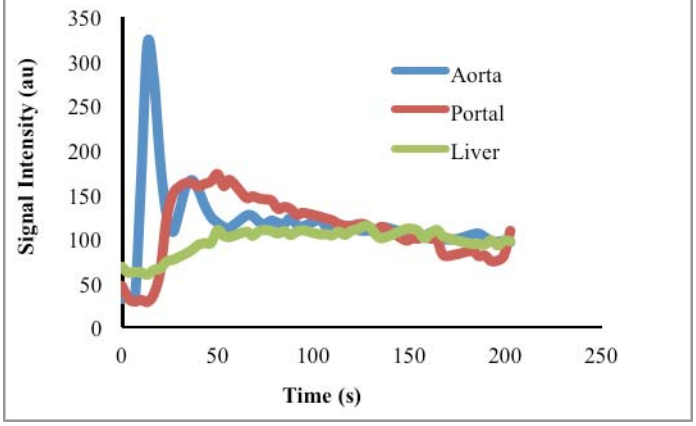
EFFECT OF PRE-CONTRAST T1 ON THE REPRODUCIBILITY OF LIVER PERFUSION PARAMETERS

Shimon Aronhime[1], Claudia Calcagno[1], Hadrien Arezki Dyvorne[1], Philip Robson[1], Henry Rusinek[2], Maria Isabel Fiel[3], Douglas Dieterich[3], and Bachir Taouli[1]
[1]*Radiology, Mount Sinai School of Medicine, New York, New York, United States,* [2]*Radiology, New York University, New York, New York, United States,* [3]*Department of Medicine/Liver Disease, Mount Sinai School of Medicine, New York, New York, United States*

Introduction: Pharmacokinetic modeling of perfusion-weighted (PW) MRI of the liver has made it possible to quantify perfusion changes for liver fibrosis detection and for the assessment of tumor angiogenesis [1-3]. Reproducible calculation of perfusion parameters partially depends on the ability to reliably determine gadolinium concentration ([Gd]) from the acquired MR signal intensity (SI). Numerous techniques are available in this regard. The simplest technique assumes a linear relationship between SI and [Gd] for the range of expected concentrations in the liver and blood [1]. Other techniques utilize the SPGR signal equation [4], which requires a pre-contrast baseline T1 measurement that can be calculated or assumed using published values [5]. The objective of our preliminary study was to evaluate the reproducibility of liver perfusion metrics using various post processing techniques aimed at optimizing the calculation of [Gd].

Materials and Methods: PW-MRI of the liver was performed twice on 5 patients (4 male, mean age 53 y) with chronic viral hepatitis C at 1.5T (Siemens Avanto) using a 3D SPGR sequence (3D FLASH) in the coronal plane, with TR/TE 2.67/0.94, FA 12°, 192x121, interpolated slice thickness 3 mm, GRAPPA 3. 64 coronal volumes were acquired every 3.5-5 sec before and after injection of 0.05 mmol/Kg of gadobenate dimeglumine (Multihance, Bracco Diagnostics). T1 mapping of the liver was acquired using a breath-hold Look-Locker sequence [6]. SI versus time curves **(Fig. 1)** were obtained by placing ROIs in the abdominal aorta, portal vein and liver. SI was converted to [Gd] using 3 different methods: the 1st assumed a linear relationship between SI and [Gd]. The other 2 methods utilized the SPGR signal equation, which was used to estimate post-contrast T1. Pre-contrast T1 was either measured directly with the Look-Locker sequence for the 2nd method **(Fig. 2)** or assumed using published values for the 3rd method. [Gd] vs. time curves were fitted using a dual-input single-compartment model [7]. Estimated perfusion parameters included arterial flow (Fa), portal venous flow (Fp), total liver blood flow (Ft), arterial fraction (ART=Fa/Ft), distribution volume (DV) and mean transit time (MTT). Reproducibility of perfusion parameters was assessed by calculating coefficients of variability (CV).

Fig. 1



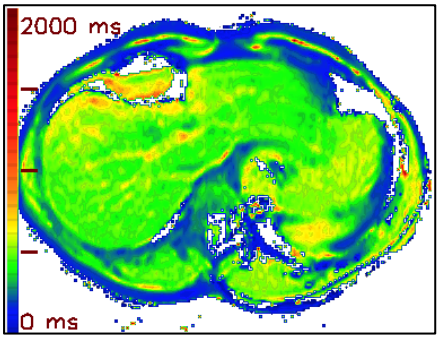


Fig. 2: Liver T1 map obtained from the Look-Locker sequence

Results: Mean calculated pre-contrast liver T1values obtained from the Look-Locker sequence were 555 ± 65 msec (range 425-643). All conversion techniques demonstrated acceptable to poor reproducibility. CVs ranged from 9 to 44%, 11 to 54% and 13 to 50% for linear conversion, SPGR with assumed pre-contrast T1 and SPGR with T1 mapping conversion techniques, respectively **(Table 1)**.

	Linear conversion	SPGR with assumed T1	SPGR with calculated T1
ART	9.0	11.4	13.1
Fa	34.8	53.5	50.8
Fp	37.6	50.5	50.5
Ft	36.5	50.8	50.3
DV	19.8	23.0	18.2
MTT	44.0	38.2	38.8

Table 1: CVs (%) of perfusion parameters using different [Gd] conversion techniques

Discussion: There is limited published data on the reproducibility of liver perfusion metrics [8]. Our preliminary results indicate that liver perfusion reproducibility is not affected by the method of [Gd] calculation. ART and DV which have been shown previously to be predictors of advanced liver fibrosis [2] were the most reproducible parameters for all 3 conversion techniques. The other parameters, including Fa, Fp and MTT were not as reproducible. This may partially be due to the small size of the study. These findings are significant because they may hel simplify the complex post processing image analysis required for PW-MRI by obviating the need for T1 mapping. Knowledge of reproducibility of perfusion parameters is important in assessing new antifibrotic drugs in liver fibrosis and cirrhosis and antiangiogenic drugs in liver tumors. Future studies will be needed to investigate whether the accuracy of PW-MRI is affected by the method of [Gd] calculation.

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This work was supported by NIDDK grant # 1R01DK087877