3D-liver quantitative perfusion mapping using EGEE grid with MR-DCE imaging and MS-325 blood pool contrast agent

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INTRODUCTION

Liver fibrosis is an important cause of mortality and morbidity in patients with chronic liver diseases. Fibrosis can lead to cirrhosis for which the complications involve 15,000 deaths per year in France [1]. An early detection and a clinical follow-up of liver fibrosis are still needed whereas the histological gold standard is not suitable due to inherent risk, interobserver variability and sampling errors. It has been demonstrated that liver perfusion imaging has the potential to detect and assess vascular modifications associated with liver fibrosis [2,3]. In a previous work, we have developed an MRI protocol and a processing tool for quantitative perfusion assessment based on ROI. Then perfusion parameters such as hepatic perfusion index (HPI) and portal blood flow have been found relevant indicators for the clinical follow-up during antiviral treatments in patients with viral chronic hepatitis [4]. Nevertheless, the evaluation was restricted to a ROI and regional variations, often met in diffuse liver diseases, could not be observed. ROI-based perfusion quantification needs already heavy post-processing methods such as image registrations, unnoising and data fitting. Processing time drastically increase and become really prohibitive for clinical application with 2D or 3D mapping. This abstract presents a post-processing method using EGI grid and parallel processing to allow whole-liver 3D parametric mapping after MR-DCE imaging with the MS-325 blood pool agent.

MATERIAL and METHOD

MR-DCE imaging was performed on a 1.5T Magnetom Symphony *(Siemens Medical Solutions, Erlangen, Germany)*. Dynamic 3D-VIBE sequence was acquired with 1 sec-temporal resolution in free-breathing during two minutes. Acquisition started simultaneously with MS-325 contrast agent injection. For each phase, sixteen coronal 4 mm thickness slices were acquired to explore a 64 mm slab thickness. The total number of images per patient was 1920.

First, images were imported on a personal computer running an in-house developed application writing in Matlab r2010a (*The MathWorks, Natick, Massachusetts, USA*). Images from original stack were sorted in sixteen 2D + t volumes. To correct the offset due to respiratory motions, each volume was automatically registered with an algorithm using maximization of mutual information with affine transformation. Then, pixel intensity was converted in MS-325 mass concentration from a relationship established in our prior work based on phantom study [5]. Arterial and portal input functions were measured from 5-by-5 pixels squared ROIs respectively placed on celiac trunk and main portal vein. These latter are interpolated and modeled using spline curves as functions. In a second step processing was parallelized and executed on the EGI (European Grid Initiative) computing platform. The parallelization was handled at the input data level, by splitting each slice into several pieces. Pieces were processed (jobs) in parallel (on multiple grid resources) and eventually merged. The Matlab code was compiled on a grid compliant operating system (CentOS) and deployed on the fly on the grid nodes. By using the porting and execution platform supporting grid applications at the Creatis laboratory, grid execution is rendered transparent from an end-user point of view. For each piece of image, a pixel by pixel non-linear least-square fit is performed, to a dual-input one-compartment pharmacokinetic model [3]. Data fitting was realized with Levenberg-Marquardt algorithm and multi-start technique to improve fit robustness. Arterial and portal delays were added. They represented the temporal offset between central compartment input and input measured at arterial and portal ROI. For each fit procedure, delays were determined as the delay between the beginning of tissular enhancement and the beginning of arterial enhancement in celiac trunk. These starting points are chosen as the maximum of second order derivative of tissue enhancement curve and arterial input function. Finally, mapped pieces are merged together and four 3D parametric maps were obtained. This method was applied on MR-DCE data from a patient with chronic liver disease (diagnosis from liver biopsy and histological analysis using METAVIR classification). From 3D mapped volume, four 10-by-10 pixel squared ROI were drawn at different location of the liver volume to evaluate spatial fit uniformity.
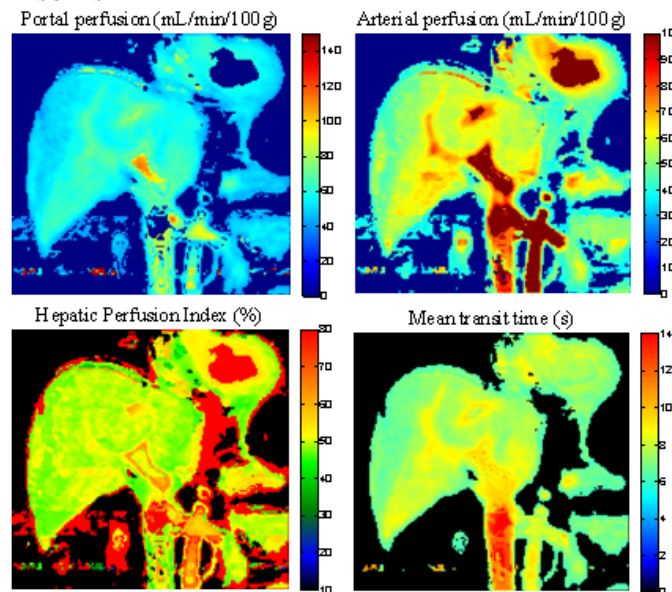
RESULTS

Fig.1: 2D perfusion parametric maps extracted from 3D mapped volumes

Based on histological analysis, fibrosis was scored F2 and steatosis was established with a fat content of 20%. Parametric maps of portal and arterial perfusion, HPI and mean transit time are depicted in Fig. 1. Using the parallel processing procedure described, the processing time was reduced from 240 to 3 hours. Job time was in between 36 min and 1 h 41 min with an average time of 52 min. Total number of failed jobs was about 7% requiring a new run. Results from the 4 ROIs selected were summarized in table 1. Difference in perfusion parameter-values can reach 15% depending on ROI traducing the non uniformity of perfusion maps within the volume. These variations appear linked to signal intensity variations due to coil sensitivity profile. However, no significant uniformity was shown for perfusion parameters on the same slice.

Table.1 Values of quantitative perfusion parameters measured at 4 ROIs

	ROI A	ROI B	ROI C	ROI D
Portal perfusion $(mL.min^{-1}.100g^{-1})$	61.7 ± 1.1	63.4 ± 1.3	58.0 ± 2.2	67.4 ± 1.6
Arterial perfusion $(mL.min^{-1}.100g^{-1})$	59.4 ± 1.6	62.5 ± 1.6	57.9 ± 1.9	64.8 ± 2.2
MTT **(s)**	8.0 ± 0.1	8.2 ± 0.1	7.6 ± 0.2	8.6 ± 0.2
HPI **(%)**	49.1	49.6	50.0	49.0

DISCUSSION

Temporal resolution of DCE-MRI was privileged regarding the number of slice. Hence, acquired 3D volume did not cover the whole liver. However, this method has the potential to realize whole liver volume quantification with MR-DCE imaging acquired on latest MR systems. Processing time was shortened by 80 folds and appears now suitable for clinical research applications. Quantified perfusion parameter-values were similar to perfusion parameters measured based on ROI method for F2 scored patient and quantified in previous works [4]. Portal perfusion decrease was balanced by arterial perfusion increase and leading to an HPI increase compared to physiological values. To conclude, 3D-whole liver perfusion mapping was performed in a reasonable time using EGI computing platform. Further step will be to apply this procedure in a prospective comparative study in patients with chronic liver disease. Its efficiency for fibrosis score discrimination and regional variations will be then investigated.

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