Probing Liver Microstructure in-vivo Using Diffusion-Relaxation Correlation Spectroscopic Imaging (DR-CSI)

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Synopsis

Diffusion-relaxation correlation spectroscopic imaging (DR-CSI) is an advanced microstructure imaging approach that can resolve sub-voxel tissue compartments and quantify their fractions. In this work, we investigated the feasibility of DR-CSI with an optimized experiment design for in-vivo liver imaging. Our study showed that DR-CSI can measure multiple sub-voxel compartments in the liver and provide consistent component fraction maps in healthy livers. An initial test on a subject with chronic hepatitis B also demonstrated the potential of DR-CSI to identify and characterize pathological changes in liver parenchyma. Further studies on variable liver diseases are underway.

Introduction

Quantitative multiparametric MR imaging has been of great interest to provide important biomarker to understand various liver pathologies. While multiparametric mapping approaches take advantage of rich information from multiple MR contrast mechanisms, they are limited in probing multiple sub-voxel compartments of the liver because of the single-compartment assumption. Recently, high-dimensional spectrum approaches have been shown to be capable of resolving sub-voxel compartments in various human imaging applications, for example, in the brain, the prostate, the placenta, etc. Diffusion-relaxation correlation spectroscopic imaging (DR-CSI) is one such approach that acquires multidimensional data with the simultaneous encoding of diffusion and relaxation and estimates a 2D diffusion-relaxation correlation spectrum for every voxel in which multiple peaks corresponding to different sub-voxel compartments are observed. This method has not been investigated in the liver, which could be potentially useful for better understanding of liver microstructure. In this work, we demonstrate the feasibility of DR-CSI with an optimized experiment design for in-vivo liver imaging.

Methods

Data acquisition: Seven healthy livers and one liver infected with the hepatitis B virus were scanned with IRB approval. For each subject, abdominal DR-CSI data were acquired using a free-breathing diffusion-weighted spin-echo EPI sequence at 3T (MAGNETOM Vida, Siemens) with TR=7000ms, voxel size=1.6x1.6x5mm³, 35 slices, and 3-scan trace weighted diffusion encoding for each b-value. As shown in Figure 1, a total of 25 combinations of 6 b-values (b = 0, 50, 200, 500, 1000, and 3000 s/mm²) and 5 echo times (TE = 47, 60, 80, 100, and 120ms) were used for contrast encoding as a "fully-sampled" ground truth (total scan time = 28 min). From the 25 contrast encodings, a total of 15 combinations were selected using the Cramer-Rao Bound (CRB)-based experiment design to shorten the scan time to 18min.

Data analysis: DR-CSI assumes a multi-compartment signal model defined by:

\[ M(x, y, b, TE) = \int \int F(z, y, D(T_2)) e^{-A_D TE} D(T_2) dD dT_2, \]

where \( M(x, y, b, TE) \) is the measured diffusion-weighted spin-echo data and \( F(z, y, D(T_2)) \) is the 2D diffusion-T2 correlation spectrum at location (x, y). The DR-CSI spectra from all voxels are estimated by solving a dictionary-based spatially-regularized nonnegative least squares optimization problem. For the analysis, we defined spectral ROIs of a rectangular shape (Fig. 2B) for distinct spectral peaks that represent different sub-voxel compartments. Spatial maps were generated for each spectral ROI that indicate the fractions of individual sub-voxel compartments at each voxel.

Results

Figures 2 and 3 show the results from one healthy subject. The ground truth (25 encodings) and the accelerated acquisition (15 encodings) are compared in Fig. 2(A) and 2(D). We observed consistent five spectral peaks in the spatially-averaged DR-CSI spectra in (A). The spectral ROIs for these peaks are defined in (B) and the fraction maps corresponding to these ROIs are shown in (D). The fraction maps of the accelerated acquisitions were in accordance with the maps from the ground truth. These components seem to correspond to hepatocytes (comp.1), bile ducts (comp.2), connective tissues (comp.3) and a part of blood vessels (comp.4 and comp.5). Fig. 3 shows spatially-varying DR-CSI spectra in a small region from the accelerated scan, clearly showing the transitions of the five components and the partial-volume effects of them. Figure 4 shows the DR-CSI results from another two healthy livers with the accelerated scan (15 contrast encodings), showing good consistency across different subjects. Furthermore, Fig. 4(B) shows one additional spectral peak (component 6) that is not present in other subjects. This component seems to correspond to a cyst, which demonstrates an ability of DR-CSI to detect abnormality. Figure 5 shows the comparisons between a healthy liver and a liver infected by the hepatitis B virus. Five components were observed in both livers. However, the fractions of the components, in particular components 1, 2 and 4, are dramatically different. This suggests that DR-CSI has the potential to identify and characterize pathological changes in liver parenchyma.

Conclusion

We demonstrated that DR-CSI can be feasible for in-vivo liver microstructure imaging with a clinically practical data acquisition time. Our results suggest that DR-CSI has abilities of resolving liver sub-voxel compartments, capturing abnormality, and/or potentially characterizing clinically important pathological changes. Validating the liver sub-voxel compartments and evaluating its utility with various liver diseases are our ongoing work.

Acknowledgements

No acknowledgement found.
References


Figures

Figure 1. Illustration of liver DR-CSI data acquisition. (A) An example of the “fully-sampled” diffusion- and relaxation-encoded images with 25 contrast encodings. Different numbers of averages (N_{avg}) were applied for each b-value, resulting in the total acquisition time of 28 minutes. (B) The Cramer-Rao Bound (CRB)-based sampling scheme with 15 contrast encodings. The same N_{avg} from (A) were used for each b-value, resulting in the total acquisition time of 18 minutes.

Figure 2. DR-CSI results from the 25 contrast encodings and the 15 contrast encodings in the subject shown in Fig. 1. (A) The DR-CSI spectra that are spatially averaged over all voxels of an axial slice. Five major spectral peaks are observed from both the 25 encodings and the 15 encodings. (B) Five ROIs of a rectangular shape are defined to encompass the five spectral peaks. (C) Reference image obtained with TE = 60 ms and b = 50 s/mm^2. (D) The fraction maps of the five components derived from the five spectral ROIs shown in (B).
Figure 3. (A) An example of spatially-varying DR-CSI spectra from a dataset acquired with 15 contrast encodings. The spectra are plotted for the small region (4x4 voxels) corresponding to the red box drawn on the reference image in (B). The five different spectral peaks can be identified in the spectra, and the partial-volume effects and the transitions of the five components are clearly demonstrated. (C) The averaged DR-CSI spectrum from the small region where the five peaks are more distinctive compared to the averaged DR-CSI spectrum from the entire liver shown in Fig. 2(A).

Figure 4. DR-CSI results from livers with and without a cyst. The spectra were estimated from the datasets with 15 contrast encodings for each subject. The five components observed in both (A) and (B) are consistent. Furthermore, one additional peak (comp.6) is observed in (B), which corresponds to a cyst.

Figure 5. Comparison between a healthy liver (A) and a liver infected with the hepatitis B virus (B). Compared to the healthy liver, similar five sub-voxel compartments are resolved from the hepatitis-B liver, but with significantly different fractions. In (C), the percentage of the voxels from the entire liver is calculated as a function of fraction (0.1-1) for each component. Dramatic differences in the voxel percentage are observed in certain fraction ranges for components 1, 2, and 4, respectively, as marked by green-color boxes.