Connecting the Dots for Future MR Engineering

SY15-1

Variable Density Magnetization Transfer (vdMT) imaging for 7T MRI: toward quantitative measurement

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Magnetization transfer (MT) imaging technique provides information about changes in the magnitude of restricted protons that are caused by tissue damage. For clinical applications, the MT ratio (MTR) map is typically used. A few studies have reported that the accuracy of quantification of MTR is limited. Quantitative MT (qMT) imaging techniques have been proposed to overcome these limitations. However, because of much higher SAR and longer scan times, qMT methods have not been adopted for routine patient scan protocols. In this study, we introduce a new qMT data acquisition approach using a 7T MR system, Segmented EPI readout variable flip-angle MT [EP-vfMT] technique, which can be reasonably included in a routine patient scan protocol with a much shorter scan time and reduced discomfort to the patient.

Data were collected from an ALS in-situ postmortem brain and three MS patients in a 7T MRI (Siemens; IRB approved). The EPvfMT sequence was developed as shown in Figure 1(A). To cover a 3D volume rapidly and reduce EPI associated artifacts a 3D segmented EPI readout was utilized. In order to reduce SAR while maintaining similar MT saturation to conventional MT, the flip angle of the MT pulse is varied as a function of the slice-encoding index (Fig. 1(B)). In the central k-space region 100% MT RF flip angles are applied every TR. In the remaining outer peripheral k-space area MT RF flip angles are gradually decreased as a function of the slice-encoding index. Imaging parameters are as follows: TR = 50 msec, MT RF flip angle in the central k-space= 500/800°; MT RF offset frequencies = 1000, 2000, 4000, 8000, 10000 Hz, 2.0 mm isotropic voxel-resolution, total acquisition time 8.3 minutes. The fraction of lines of kz space receiving 100% MT RF flip-angle (='H') was 30%. ViSTa aMWF map and qMT results using vdMT sequence were additionally acquired for reference.

For the validation of EP-vdMT, as shown in Fig. 2, MTR maps from 3 different MT methods are compared. All the MTR maps show similar signal distributions and tissue contrast. When compared, the acquisition time for the EP-vfMT is significantly reduced. Figure 3 represents a 3D myelin density map from qMT imaging using EP-vfMT sequence compared to qMT imaging using vdMT sequence and ViSTa imaging. Once the maps are compared, they reveal overall similar spatial distributions although the display range is different. Figure 4 shows the images from a patient with MS. MS lesions demonstrated hyper-signal on the FLAIR, FLAIR* and T2*-weighted images. The corresponding areas in the qMT myelin map demonstrated much reduced signal levels, clearly delineating lesions (Fig. 4D).

In this work, we demonstrated a new approach for acquiring whole brain covered 7T qMT data in a clinically reasonable scan time. The proposed method acquires qMT results in a clinically reasonable scan time while shows similar myelin density map compared to the maps from vdMT and ViSTa imaging. Moreover, it maintains sensitivity to MS lesions. These features make the proposed method appealing for clinical neuroimaging applications in UHF.

Figures

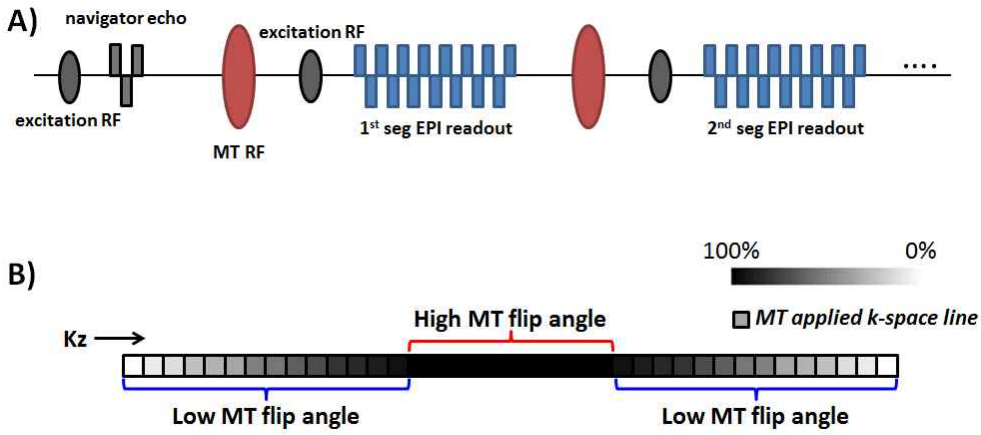
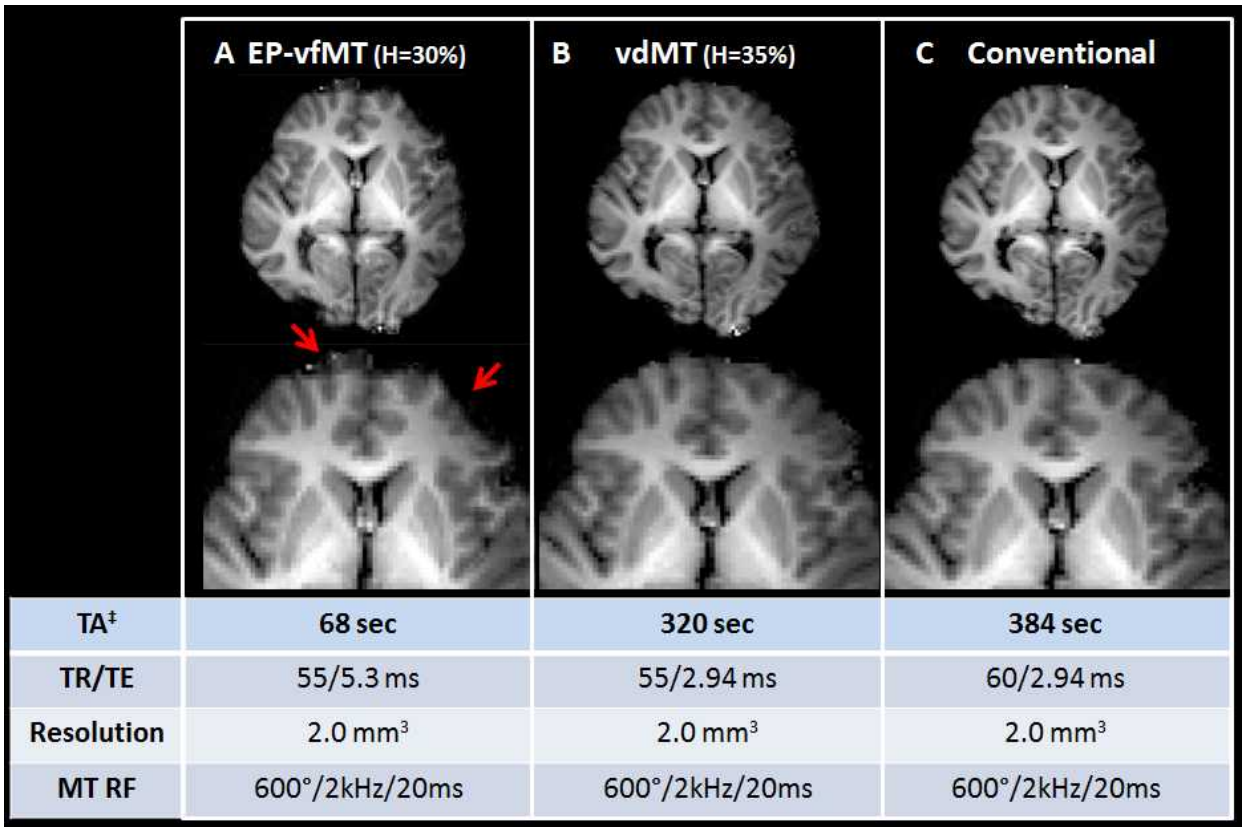


Fig 1.



	A EP-vfMT (H=30%)	B vdMT (H=35%)	C Conventional
TA‡	68 sec	320 sec	384 sec
TR/TE	55/5.3 ms	55/2.94 ms	60/2.94 ms
Resolution	2.0 mm^3	2.0 mm^3	2.0 mm^3
MT RF	600°/2kHz/20ms	600°/2kHz/20ms	600°/2kHz/20ms

Fig 2.

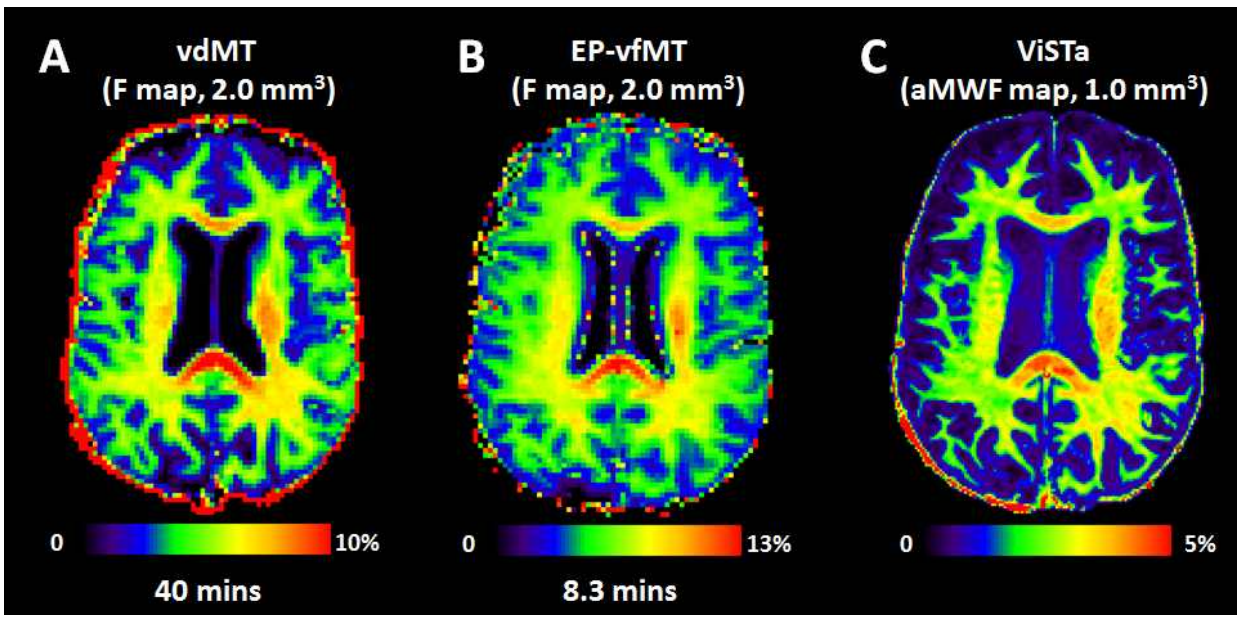


Fig 3.

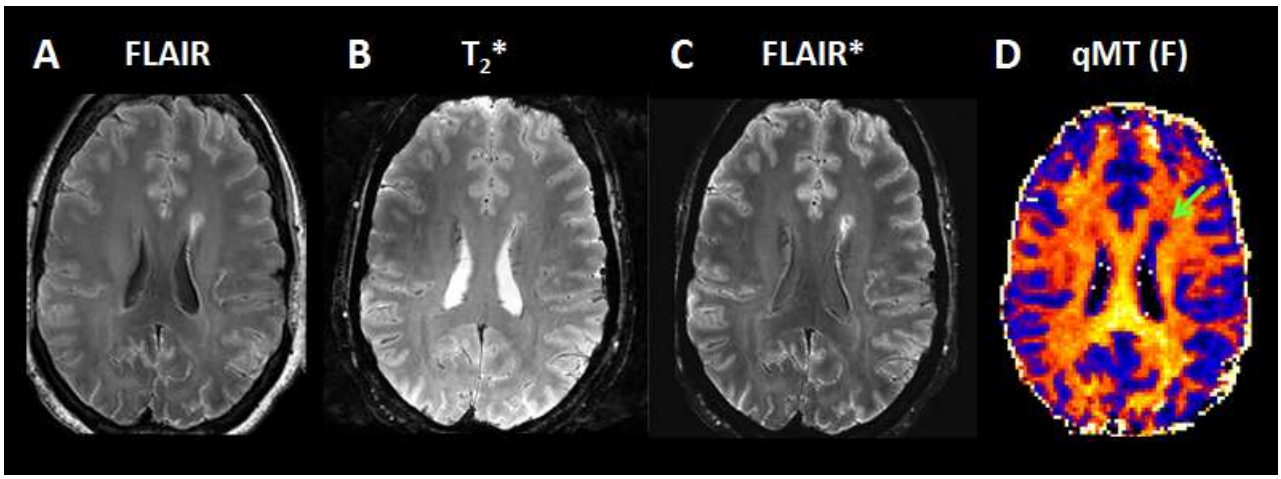


Fig 4.

Legend : Figure 1. (A) Proposed Segmented EPI readout variable flip-angle MT (EP-vfMT) sequence diagram and (B) one-dimensional EP-vfMT k-space acquisition diagram. Each dot indicates MT applied k-space line. Color scale represents applied MT RF flip-angle. In the central k-space region, which determines most of the information regarding signal intensity and contrast of the image, 100% MT RF flip angles are applied every TR. In the remaining outer peripheral k-space area, which provides most of high spatial frequency information, MT RF flip angles are gradually decreased as a function of the slice-encoding index. Figure 2. MTR maps from the (A) EP-vfMT, (B) vdMT and (C) conventional MT imaging. Imaging parameters and acquisition time for both MT and non-MT data for each imaging scan were listed at the bottom. Figure 3. Comparison of white matter quantification in a recently-deceased ALS subject. Preliminary data demonstrates feasibility of in situ acquisition of maps of myelin density as determined by (A) qMT imaging using vdMT, (B) qMT imaging using EP-vfMT and (C) ViSTa imaging. Reasonable patterns of myelin density are observed within white matter throughout the brain. Figure 4. (A) FLAIR, (B) GRE T2*, (C) FLAIR*, and (D) myelin map (determined by qMT imaging using EP-vfMT sequence) images from an MS patient.

Keywords : Quantitative magnetization transfer imaging, MRI, Myelin map

Connecting the Dots for Future MR Engineering

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Precision Medicine: Hopes and Fears

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One of the most important overarching concepts of "Precision Medicine" is that more specific and precise separation of patients into the subpopulations that differ in susceptibility to particular disease, biology and/or prognosis of those disease they may develop, and response to a specific treatment. The way to achieve this separation is through combining data about clinical phenotype and genotype or gene expression. Since the President Obama's Precision Medicine Initiative, there have been explosive and fervent response especially among the researchers working in the field of basic science such as genomics, proteomics, and medical informatics because of the hope that precision medicine will contribute to better understanding of diseases and physiology. In the clinicians' side, Precision Medicine is expected to provide them with genomics-based precise diagnosis of the disease and more importantly with targeted treatment for individuals belong to a genome-based specific subgroup by developing the specific drugs.

On the other hand, there have been concerns regarding the future of genomics in two point of views. First one is the time and money issue. Especially the expertise of public health raise the question of "From the perspective of the broad pattern of morbidity and mortality, is precision medicine what is needed now?" On their view point, more money should now be invested to the well-being and life expectance of the least-advantaged people instead of putting enormous amount of money to the research with uncertain future. For example, the iconic drug of precision medicine, Ivakaftor, is not only working on in less than 5% of total patients with cystic fibrosis, but also it took decades to develop and costs $300,000 a year per patient. Second point of view comes from the fundamental questions regarding the limitations in genomics. The proportion of total variation explained by genome-wide significant variants is only 10% - 20% for a number of disease. And in terms of disease risk prediction, relative risk of vast majority of gene variants rarely exceed 1.5. Furthermore, cancer, the main target of Precision Medicine, is genomically the most heterogeneous disease, and therefore when intra- and inter-tumor heterogeneity is combined with interpatient heterogeneity, treatment planning reaches a very high grade of complexity.

In healthcare system, research is mandatory for the bright future; patients' wellbeing and better care is today's task. What we need to keep in mind is how to balance the amount of invested time and money between for the future of research and for today's patients care and wellbeing. Together with that, by clearly understanding the limitations of genomics we can reach the goal of Precision Medicine in an efficient way while trying to get rid of hypes and excessive expectations.

Keywords : precision medicine, genomics, radiomics, expectations, limitations