MP2RAGE, a self-bias field corrected sequence for improved segmentation at high field.

J. P. Marques[1,2], T. Kober[1,3], W. van der Zwaag[1,2], G. Kruegger[1,3], and R. Gruetter[1,4]

[1]Laboratory for functional and metabolic imaging, Ecole Polytechnique Federale de Lausanne, Lausanne, Vaud, Switzerland, [2]Department of Radiology, University of Lausanne, Lausanne, Vaud, Switzerland, [3]Advanced Clinical Imaging Technology, Siemens Medical Solutions-CIBM, Lausanne, Switzerland, [4]Department of Radiology, University of Lausanne and Geneva, Switzerland

Introduction MPRAGE images provide a very good contrast between different brain tissues (1). The contrast between CSF\GM or GM\WM can be optimized by varying the inversion times and flip angles. At high B_0 fields (>3T), the inhomogeneity of the transmit, B_1^+, and receive B_1^- fields necessitates taking into account a bias field. This bias in GRE based sequences scales images with a factor $B_1^-(\mathbf{r})\sin(\gamma B_1^+(\mathbf{r})t)$, where **r** represents the image space spatial coordinates. Two main approaches have been developed to combat these undesired large-scale signal fluctuations: An estimation of the bias field by post-processing techniques, or acquisition of a second GRE image with similar scan parameters as those used in the MPRAGE (2). This GRE image serves as a reference scan to correct for both the B_1 and B_0 inhomogeneities. This second approach promises better results despite the extra scan time for the GRE image.

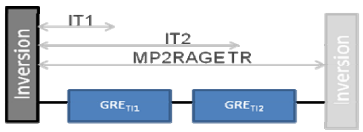

Fig.1 MP2RAGE sequence diagram. The MP2RAGE block is repeated for each phase-encode step. Within each GRE block the phase-encode steps in the third dimension (slab) are acquired.

Methods The predicted MP2RAGE (see fig. 1) signal amplitudes for several tissues were numerically calculated by solving the Bloch Equations for a wide range of inversion times and flip angles assuming values of longitudinal relaxation for WM/GM/CSF=0.8/1.3/2.3 s at 3T and a proton density of 0.8, 0.8 and 1 respectively.

In the simulations, the constraints regarding number of excitations per gradient echo module inside each inversion was set to be 160, which typically allows a final resolution of 1*1*1 mm^3. The maximum MP2RAGE TR, being the time between two inversions, was limited to 4 seconds. The signal contrast was considered to come entirely from the center k-space point, and the flip angles for each gradient echo block were fixed to a constant value.

A combination of GRE_{TI1} and GRE_{TI2} which resulted in a good removal of the bias field (in the low flip angle regime) as well as good CSF-GM and GM-WM contrast was:

$$S = \frac{GRE_{TI1} \cdot GRE_{TI2}}{GRE_{TI1}^2 + GRE_{TI2}^2} \quad (Eq.1)$$

The parameters TR, TI1, TI2, α_1 and α_2 were chosen from simulations in order to optimise the contrast to noise ratio between GM-WM and CSF-GM in S (the noise of the S image was estimated by error propagation of eq.1).

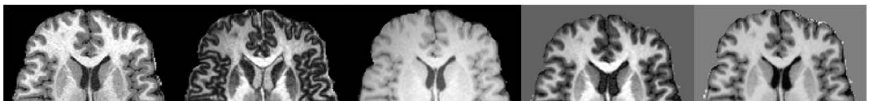

Fig. 2. a) MPRAGE /FLASH image; b) 1st contrast of MP2RAGE; c) 2nd contrast of MP2RAGE; d) 1st contrast of MP2RAGE after phase correction; , note that b, c and d have not been 'bias field' corrected and WM has a significant range of intensities e) Image obtained from Eq. 1. (d) and (e) have a gray background because the brain contains positive and negative values.

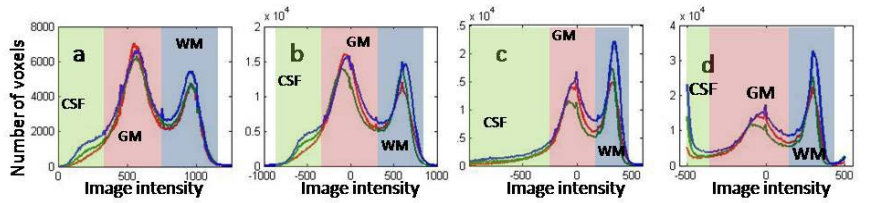

Fig. 3 Histograms of image intensities obtained in three different subjects represented by the red green and blue linesof: a) MPRAGE/FLASH; b) $MP2RAGE_{TI1}$/FLASH ; c) $MP2RAGE_{TI1}$/ $MP2RAGE_{TI2}$; d) Image obtained using Eq.1; Green, red and blue areas represent CSF, GM and WM. All the image intensity values of histograms b)-d) are multiplied by 1000

Experiments The MP2RAGE sequence was implemented on a clinical 3T MR scanner (Magnetom Trio, Siemens Medical Solution). Data from three different subjects was acquired using a 12-channel product head coil using the following sequences: (a) MPRAGE TR=2300ms, TI=900ms; α=9 which resulted in a total acquisition time of 9 mins; (b) MP2RAGE TR=4000ms, TI1=700, TI2=1900 ms; α_1=6, α_2=5 with a factor of two acceleration and 6/8 k-space coverage, resulting in a total acquisition time of 7 mins; (c) GRE with BW=270, TE=3.5ms and TR=7ms, as in the GRE blocks of the MPRAGE and MP2RAGE, and α=3 was acquired in 2 mins with a factor of two acceleration and 6/8 k-space coverage. Before combining the images as in Eq. 1, the magnitude image GRE_{TI1} was corrected by applying $GRE_{TI1} = \mathrm{Re}(abs(GRE_{TI1})\exp(i(\phi_{TI2} - \phi_{TI1}))$ where ϕ_{TI1} and ϕ_{TI2} are the phase of GRE_{TI1} and GRE_{TI2}. This correction was necessary because at the TI1 not all signal had passed the zero-crossing point (3).

Results Figure 2 shows images of one of the subjects acquired at 3T, after skull stripping. A precise description is given in the caption. Note the high GM-WM contrast in D and E. Fig. 3 shows the intensity histograms of skull stripped images obtained for each subject through different combinations of the acquired images. Fig. 3*(c)*, resulting from the ratio of the two MP2RAGEs provides a very good GM\WM contrast, but the CSF intensity distribution is too wide. Visual inspection of Fig. 3*(d)* shows 3 very distinct peaks which are highly correlated with CSF, GM and WM respectively, (the subject represented with a red line in Fig. 3 has a low CSF volume which is only visible in histogram *d)*. It should be noted that the information present in the histograms *(c)* and *(d)* was achieved in 7 minutes compared to the eleven minutes of histogram (a). MP2RAGE, holds obvious advantages; 1) Point spread function broadening, or blurring, introduced by the multiple excitations per inversion is reduced; 2) Motion artifacts are identical in the two images, whereas with separate acquisitions different amounts of blurring may occur. 3) There is no need to perform motion correction (which introduces extra smoothing in at least one of the images) because the two contrasts are inherently coregistered.

Conclusions We conclude that 3D imaging using a new sequence, MP2RAGE, is able to yield T_1 contrast independent from spatial variation in B_1^+ and B_1^- and therefore is likely to be useful at higher field strengths.

References 1 Mugler, J. P.et al,, Magnetic Resonance In Medicine 15(1): 152-157. 2 Van de Moortele et al, Efficient Bias Reduction for High Resolution T_1w Imaging in the Human Brain at 7 Tesla, Workshop on Advances in High Field MR, 2007 (3) Totman et al., Null point Imaging, Proc. ISMRM, 15 (2007)

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