Assessment and correction of B1 induced errors in magnetization transfer histograms

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Introduction:

The magnetization transfer ratio (MTR) is widely used as a sensitive tool to study structural changes in lesions and normal appearing tissue of multiple sclerosis (MS) patients. Generally, the MTR is directly related to the strength of the radio frequency field (B_1) that is used for saturating the macromolecular proton pool. While B_1 variations within a single slice are usually small, B_1 variations over the whole head may be more pronounced and therefore can seriously influence whole brain MTR histograms. In a multicenter study we have assessed the typical range of MTR variations which are attributable to B_1 errors. For that purpose MTR maps and the corresponding B_1 distribution maps were measured in healthy volunteers on scanners from different manufacturers at different sites. In addition, a new and simple correction scheme for reducing B_1 induced MTR variations was evaluated.

Material and Methods:

MT data and B_1 measurements were acquired in 23 healthy volunteers on a Philips Intera, two Siemens Magnetom Vision and a GE Signa 1.5 T whole body scanners. The standardized MT scan was a proton density weighted gradient echo sequence (TR = 900 ms, TE = 12 ms, FA = 20°) performed with and without a MT saturation pulse (Gaussian shape, dur = 7.68 ms, eff. FA 500°, offset = 1.5 kHz, bandwidth = 250 Hz) according to the EUROMT-sequence (1). On one scanner the MT pulse was implemented with a Sinc-Gaussian shape.

For B_1 mapping a readily available double angle (fast) spin echo method was used (2). This method is based on two proton density weighted images with single and double values of flip angle for the excitation pulse (e.g. 60°/120° or 45°/90°). Both, the MT and B_1 sequences, were performed with identical geometry parameters (FOV = 250 mm, THK = 5 mm, 24 slices) and covered identical portions of the brain.

The B_1 correction scheme was based on results from numerical simulations, which were done by means of numerical integration of the coupled Bloch equations for the EUROMT-sequence. These simulations showed, that for a B_1 change of up to ±20% there is a linear change of the corresponding MTR values. The slope of this linear relationship was largely independent of the underlying tissue type. Accordingly, the correction scheme was based on a simple linear regression between B_1 and the corresponding MTR values. With the slope found by the regression analysis the MTR was corrected pixel by pixel according to:

$$MTR_{corrected} = MTR_{measured} - slope * B_{1error}, \quad \text{with } B_{1error} = (B_{1measured} - B_{1nominal}) / B_{1nominal}$$

The linear regression was done with data from segmented brain white matter. White matter masks were created with the following steps: (i) removal of non brain tissue with a brain extraction tool; (ii) image segmentation based on a global threshold as defined by an intensity histogram analysis; and finally (iii), erosion of the binary mask by 1 pixel to remove remaining contributions from adjacent grey matter or cerebrospinal fluid.

Results

As predicted by the numerical simulations we found a strong linear relationship between B_1 and the corresponding MTR (Fig.1). In the individual volunteers we observed mean B_1 errors of about 5-13 % which resulted in typical MTR histogram shifts of 2-6 %. Generally, the B_1 characteristic was strongly scanner related which indicates that coil design plays a dominant role. The above correction scheme resulted in a 22 % reduction of the inter-scanner variation and 50 % reduction of the inter-subject variation. A significant reduction of the histogram dispersion was not possible which is most likely due to the fact that sequence related noise usually exceeds the B_1-induced MTR changes.

Conclusion:

Calibration errors and the inhomogeneity of the B_1 field seem to be major sources of inter-subject and inter-scanner MTR variations. We have demonstrated the feasibility of a simple method for the correction of these effects.

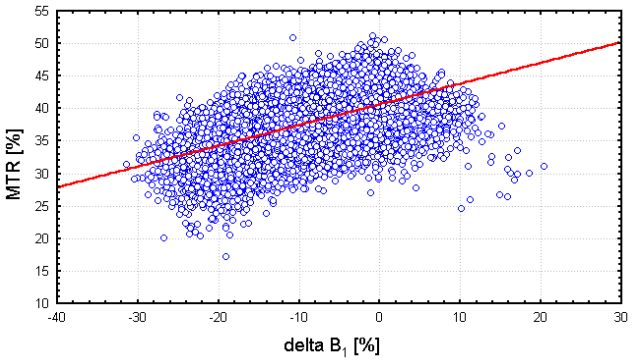

Fig.1. MTR values from segmented white matter of a single volunteer are plotted against their corresponding B_1 values

References:

(1) Barker GJ et al. ISMRM 5th meeting 1997;3:1556.
(2) Stollberger R et al. Magn Reson Med 1996;35:246-25.