Improved delineation of brain tumors: An Automated Method for Segmentation based on Pathologic Changes of 1H-MRSI Metabolites in Gliomas

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Introduction:

In conventional MRI it is often difficult to delineate the heterogeneous structure of gliomas. Even the current methods of choice, T2-weighted MRI and contrast-enhanced MRI are not specific for tumors and can result in ambiguous or misleading results (1). Proton magnetic resonance spectroscopic imaging (^{1}H-MRSI) is a noninvasive tool for investigating the spatial distribution of metabolic changes in brain lesions. Brain tumors show increased levels of choline-containing compounds (Cho) and a reduction in N-acetyl-aspartate (NAA) and creatine (tCr). The range of Cho increase and NAA decrease is compatible with the range of tumor infiltration (2). Exact knowledge of the size of the border zone between tumor and healthy tissue is one of the major problems in therapy planning.

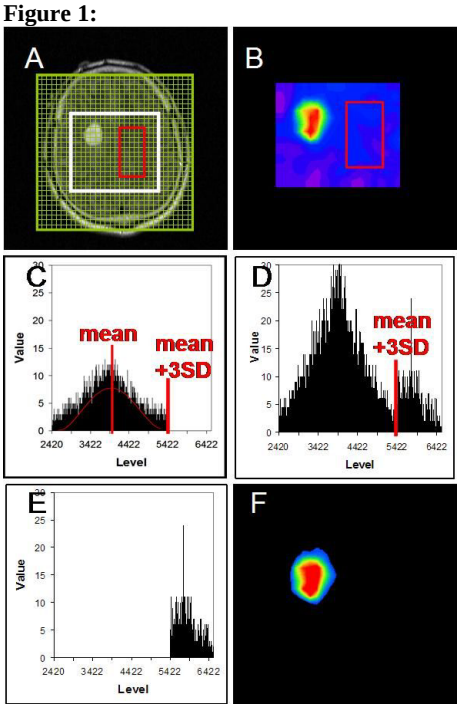
Methods:

10 patients (6 male, 4 female, 40 ± 11 years), all with supratentorial gliomas (WHO grade II and III) were examined. All studies were performed on a 1.5 Tesla clinical scanner (MAGNETOM Sonata, Siemens Erlangen, Germany) equipped with the standard head coil using a standard CSI sequence with PRESS-box and CHESS water suppression, TR/TE = 1600/135 ms, 24 x 24 circular phase-encoding scheme, 16 x 16 cm FOV, slice thickness 10 mm and 2 NEX (total 13 min). The PRESS excitation volume (white rectangle in Fig. 1A) was positioned to exclude lipids of the skull and subcutaneous fat. Metabolic maps for Cho, tCr and NAA as well as the map of the Cho/NAA ratios (Fig.1B) were calculated by integration of peak areas and smooth linear interpolation to a 256 x 256 matrix. A "healthy region" of predominantly white matter (Figs.1A and B, red rectangle) was selected in contralateral brain, at sufficient distance from the lesion to allow segmentation based on the assumption of Gaussian distribution of the Cho/NAA values for normal brain (tested independently). The mean and the standard deviation (SD) were calculated for this region (Fig. 1C) and a cutoff value of mean+3SD was applied to the histogram of the whole metabolic map (Fig. 1D). Segmentation was achieved by zeroing all values less than the cutoff value (Figs. 1E and F). T2w TSE data set of routine tumor MRI of each patient was contoured automatically by the medical imaging software OSIRIS (3). The T2w area was contoured as the area of hyperintensity on the TSE images. The maximum of the calculated T2w hyperintensity areas covered by the PRESS-box delineated on the TSE images (Figs. 2A and B, red line), corresponding to the MRSI slab, was used for comparison with the area of the segmented tumor in the Cho/NAA map (Figs. 2A and B, green line). For integration of the biochemical information into a frameless stereotactic system we developed a method for co-registration of MRI and MRSI data sets (not part of this study) which allowed the obtainment of biopsies from the MRSI/T2w difference areas (Fig. 2B).

Results:

All patients had segmented MRSI tumor areas that were greater than the T2w hyperintense areas covered by PRESS-box. The amount of larger MRSI tumor areas compared to T2w areas was 24% on average (range 6–33%). In nine patients biopsy sampling from a pre-defined area was successful. In one single case a biopsy was impossible because of technical problems. In all nine cases histological findings showed tumor infiltration ranging from about 4–17% (mean 9%) p53 or Map2c positive cells (e.g. Fig. 2C, 5%) in tumor areas detected only by MRSI.

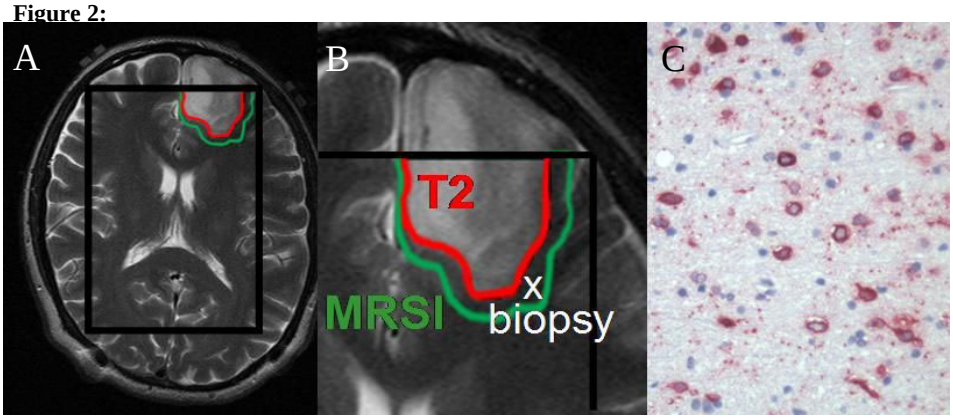
Figure 1:



Discussion:

T2-weighted MRI, and pre- and post-gadolinium contrast enhanced T1-weighted MRI are currently the basis for surgical or radiation therapy treatment planning of brain tumors. We developed an automated method for delineation and segmentation of the lesions related metabolic changes and achieved significantly improved delineation for gliomas compared clinical routine. We demonstrate that increasing spatial resolution in MRSI in combination with our method can improve delineation of tumor borders compared to imaging strategies in clinical routine. Spectroscopic images of the segmented tumor may thus be helpful for therapeutic planning.

Figure 2:



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