Short echo time MR spectroscopy of brain tumors: grading of cerebral gliomas

J. Weis, P. Ring, T. Olofsson, F. Ortiz-Nieto, and J. Wikström
1Dept. of Radiology, Uppsala University Hospital, Uppsala, Sweden, 2Dept. of Radiology, Karolinska Institute, Stockholm, Sweden, 3Dept. of Pathology, Uppsala University Hospital, Uppsala, Sweden

Introduction

1H MRS is extensively used for characterization of brain lesions [1]. Recent studies have shown that pattern recognition techniques can improve classification and grading of brain tumors [2-5]. There is however not yet a consensus about optimal technique. In this study, single voxel spectra were acquired from normal-appearing white matter (NAWM) and from histologically diagnosed gliomas grade II, III and IV (g-II, g-III, g-IV). The primary goal of the current study was introducing the correlation analysis of the scatter plots of normalized spectral amplitudes as a pattern recognition tool for the classification and grading of brain tumors. A secondary goal was to propose a new spectrum processing approach that improves the differentiation of proton spectra with dominating macromolecule and lipid peaks.

Materials and Methods

Twenty patients with gliomas were included to this study. Six patients were g-II, three were g-III and eleven were g-IV. An additional two patients were selected for demonstration purposes: one each with recurrent g-IV and meningioma grade 1 (MNG-I). Five healthy volunteers were evaluated as a control group. The subjects were scanned on a 1.5 T scanner (Siemens Avanto). The single voxel spectra were measured using PRESS sequence (TR/TE 5000/30 ms, BW 1000 Hz, 1024 points, 16 phase cycle steps). Four dummy excitations were followed by 16 non-water-suppressed and 128 water-suppressed scans. Spectra of NAWM were acquired in the parietal and occipital lobe. MRS of the patients was performed after the intravenous administration of Gd-based contrast agent followed by T1W imaging. The size and location of the voxels were adjusted to include as much viable tumor as possible avoiding necrosis with minimum contamination from normal tissue. Quantification of absolute concentrations was accomplished by LCMModel [6]. Only LCMModel fits of the spectra were used in further processing. The fits were normalized by summing the squares of the intensities of each spectral point and then dividing the amplitude of each point by the square root of this sum [4, 5]. Three groups of fitted spectra were used: (a) measured spectra (MS), (b) macromolecules and lipids spectra (ML) in the range 1.4 – 0.9 ppm, and (c) difference spectra DS = MS-ML-Lac. Mean MS, ML and DS spectra were computed for NAWM, g-II, III and IV, by averaging the values at each data point. A novel feature of our spectrum processing approach is the correlation analysis of the scatter plot of normalized spectral amplitudes. This spectrum processing approach consists of two steps: (i) construction of the scatter plot for the pair of considered spectra. Coordinates of each point are normalized spectral amplitudes of both spectra for defined chemical shift. (ii) Correlation analysis of the scatter plot. Correlation coefficient r was used as a measure of common features of the spectra, i.e., how the first spectrum resembles the second one.

Discussion

Described spectrum processing approach improves differentiation of the spectra with dominating macromolecule and lipid peaks, e.g. g-IV, metastases, abscess, MNG and lymphoma. These spectra have very similar patterns, characterized by dominant lipids, macromolecules and Lac peaks in the range 1.3 and 0.9 ppm. These spectral intensities mainly represent the volume of necrotic tissue instead of the tumor type. Our method emphasizes that difference spectra (DS) are most suitable for such analyses. The main reason is the strong dependence of the normalization constant from the elevated intensities of macromolecules and lipids at 1.3 and 0.9 ppm. These spectral intensities mainly represent the volume of necrotic tissue instead of the tumor type. Our method enables pairwise comparison of the measured spectrum with the mean database spectra and might be helpful in narrowing the clinical diagnosis.

Conclusion

Correlation analysis of the patient’s normalized spectral amplitudes and mean (database) normalized spectral amplitudes were used for classification of the tumors. It was found advantageous to perform correlation analysis using DS spectra. The shape of the ML spectrum was found to be good marker to discriminate between different glioma grades.

References


Fig. 1

Fig. 2

Fig. 3