Metabolic Assessment of Myositis with 1H Magnetic Resonance Spectroscopy

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Introduction

Myositis is a general term used to define the inflammation of muscles. In the acute forms of myositis, this inflammation is caused by trauma, infection, certain drugs and even exercise. The chronic and sometimes progressive form of myositis is a rare condition that affects 10 in one million people each year. There has been considerable research into the pathological conditions of this disease [1] including the use of 31P magnetic resonance spectroscopy (MRS) for the metabolic evaluation of this disease [2]. To the best of our knowledge, 1H MRS has yet to be applied to myositis. The aim of this pilot study was therefore to investigate the ability of 1H MRS to characterize the metabolism of lesions in patients with myositis.

Methods and Materials

All scans were performed on a Siemens 3T Verio system. Single voxel MRS (PRESS, repetition time 2s; echo time 135 ms, voxel size 2x2x4cc) were collected using a body phased-array receive coil. Spectra were quantified using the phantom replacement method [3]. Both water suppressed and unsuppressed spectra were recorded using the phased array receiver coil, followed by a unsuppressed water signal recorded using the body coil as receiver. The loading of the phased array coil was estimated by the reciprocity theorem, such that the signal intensity from the phantom could be used to estimate the in vivo metabolite concentrations. Correction factors for water and lipid content were applied. A 69 mM NAA phantom was employed as the reference. Peak areas were quantified using the AMARES method in jMRUI [4].

1H MRS spectra were collected in the quadriceps muscle of 10 healthy volunteers (6 males, 4 females, mean age 35, age range 24-49) using the phantom replacement method. Then same spectra were collected from 10 subjects with chronic myositis (5 males, 5 females, mean age 55, age range 27-74). For both the healthy volunteers and subjects with myositis, T1 and fat-suppressed T2 images were acquired. For the healthy volunteers, the voxel was placed in the center of the vastus medialis muscle. For the subjects with myositis (all involved the quadriceps muscles), the voxel was placed in an area of abnormal T2 signal if present, or within the center of the vastus medialis if no abnormal T2 signal was observed. For all subjects, the presence or absence of abnormal T2 signal was recorded. The absolute concentrations of Choline (Cho), creatine and lipid were quantified by the AMARES method in jMRUI [4] and metabolite concentration ratios were determined. Comparisons between the group of healthy volunteers and subjects with myositis were made with the t-test.

Results

A typical 1H spectrum is shown in figure 1. Clear Cho, Creatine and lipids peaks are quantified by the Siemens scanner software. Table 1 shows the Cho concentrations and Cho/lipid ratios for myositis patients with (n=2) and without T2 (n=8) hyperintense lesions. There is a large decrease in Cho concentration (p=0.00066) and Cho/lipid ratio (p=0.017) for patients with lesions. Table 2 shows Cho concentrations and Cho/lipid ratios in the control subjects and myositis patients. While there was a lower Cho/lipid ratio in myositis patients, more data is needed to establish a statistical significance.

Conclusions and Discussions

This is the first report of metabolite differences in myositis determined by 1H MRS. This work indicates that the heightened T2 signal intensity in the muscles of subjects with myositis may be correlated with a decrease in absolute Cho concentration. Abnormal T2 signal is used as a clinical marker of active myositis [5], and these data may help to explain the physiologic basis for this signal abnormality. Second, comparing to healthy subjects, subjects with myositis may have a decreased Cho/lipid ratio, not an unexpected suspicion given that muscle atrophy and fatty replacement is an end stage finding in myositis. 1H MRS may be a potentially useful tool in identifying changes in muscle composition (early fatty replacement), not identified by routine MR anatomic sequences.

References