Low Choline Concentrations in Normal-Appearing White Matter of Patients with Multiple Sclerosis and Normal MR Imaging Brain Scans

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BACKGROUND AND PURPOSE: Spectroscopic studies (1H-MR spectroscopy) of normal-appearing white matter (NAWM) in patients with multiple sclerosis (MS) with MR imaging brain lesions have already been performed, but our intention was to investigate NAWM in MS patients who lack brain lesions to elucidate whether the same pathologic changes could be identified.

MATERIALS AND METHODS: We checked 350 medical files of patients with MS who are registered in our institution. Fourteen patients (11 women and 3 men; mean age, 48.6 years; handicap score, Expanded Disability Status Scale [EDSS] 2.9; range, 1–6.5) with clinically definite MS and a normal MR imaging of the brain were included. 1H-MR spectroscopy was performed in 4 voxels (size approximately 17 × 17 × 17 mm3) using absolute quantification of metabolite concentrations. Fourteen healthy control subjects (11 women and 3 men; mean age, 43.3 years) were analyzed in the same way.

RESULTS: Significant differences in absolute metabolite concentrations were observed, with the patients with MS showing a lower total concentration of N-acetyl compounds (tNA), including N-acetylaspartate and N-acetyl aspartylglutamate (13.5 mmol/L versus 14.6 mmol/L; P = .002) compared with the healthy control subjects. Unexpectedly, patients with MS presented significantly lower choline-containing compounds (Cho) compared with healthy control subjects (2.2 mmol/L versus 2.4 mmol/L; P < .001). The EDSS showed a positive correlation to myo-inositol concentrations (0.14 mmol/L per EDSS; \( r^2 = 0.06 \)) and a negative correlation to tNA concentrations (−0.41 mmol/L per EDSS; \( r^2 = 0.22 \)).

CONCLUSION: The unexpected finding of lower Cho concentrations has not been reported previously. We suggest that patients with MS who lack lesions in the brain constitute a separate entity and may have increased protective or healing abilities.

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lesions in other regions of cerebral white matter. In contrast, our intention was to investigate patients with MS who lack lesions on MR imaging of the brain to elucidate whether \(^1\)H-MR spectroscopy elicits abnormal absolute cerebral metabolite concentrations. Our hypothesis was that these patients show the same pathologic changes as observed in NAWM in patients with MR imaging lesions, that is, a decrease in NAA and an increase in Cho and mIns.

**Materials and Methods**

**Subjects**

Between 1998 and 2001, the medical files of 350 patients with MS registered at the neuropsychiatric clinic of our institution were checked, and 18 patients with normal MR imaging brain scan reported in the files were identified. The MR imaging scans were evaluated by a neuroradiologist for the presence of MS lesions, because the intention of the study was to include only patients with a normal MR imaging scan of the brain.\(^{16}\) Four of these patients had developed brain lesions in the follow-up and were therefore excluded.

Fourteen (4%) of 350 patients who were initially checked were recruited for \(^1\)H-MR spectroscopy. All of these patients fulfilled the Poser criteria for clinically definite MS (CDMS), which implicates at least 2 relapses, separated in space and time.\(^{17}\) There were 11 women and 3 men (mean age, 48.6 years; range, 21–62 years). Nine patients had RR MS, and 5 had the secondary-progressive (SP) form.

Mean disease duration was 10.3 years (range, 4–26 years) and was longer in SP (mean, 14.4 years) than in RR (mean, 8.0 years). Neither immunomodulatory nor immunosuppressive treatment was used in 10 patients before the study; 3 patients were continuing interferon therapy during the study; 1 female patient was treated with intravenous immunoglobulins. None of the patients used steroids or had a relapse 1 month before the study. Disability ascertainment was based on the Expanded Disability Status Scale (EDSS)\(^{18}\) (Table 1). Mean EDSS was 2.9 (range, 1–6.5).

The medical files were checked regarding differential diagnostics excluding other conditions that may mimic MS, such as neuroborreliosis, vitamin B\(_{12}\) deficiency, arteriovenous malformations, mass effects, systemic lupus erythematosus, Behçet disease, sarcoidosis, and neurosyphilis. All of the patients had been confirmed positive for oligoclonal bands in the CSF before inclusion in the study.

Nine patients had negative MR images of the spinal cord (1 of these patients only had the cervical part of the spinal cord examined; another had 1 unspecific thoracic lesion, interpreted as probably not demyelinating; and a third patient had normal MR imaging of the spinal cord a couple of years before MS diagnosis), 2 patients had 1 demyelinating lesion, and 3 patients were not investigated (Table 1). The relapse rate of the patients during the 2 years before the study entry was rather low: only 5 patients had had bouts (Table 1).

Fourteen healthy subjects, 11 women and 3 men, were used as control subjects. The healthy volunteers were recruited from the medical staff or were medical students in our institution (mean age, 43.3 years; range, 34–52 years).

The study was approved by the local ethics committee. All of the patients and control subjects gave their informed consent before inclusion.

**MR Measurements**

MR imaging and the \(^1\)H-MR spectroscopy examinations were performed on a Signa Horizon EchoSpeed Plus 1.5T MR scanner (GE Healthcare, Milwaukee, Wis) using a standard quadrature head coil. Axial scans for evaluating the presence of lesions (~40 sections, depending on head size), were obtained using a double-echo fast spin-echo, with 5-mm section thickness. This gave both proton density (TR, 2300 ms; TE, 14 ms), and T2-weighted images (TR, 2300 ms; TE, 98 ms). The matrix and FOV were 256 × 192 and 24 × 18 cm\(^2\), respectively.

Coronal T1-weighted scans for placement of spectral voxels were acquired using a 3D fast-spoiled gradient recalled acquisition in steady-state sequence (TR, 14.1 ms; TE, 5.4 ms; FOV, 35 cm with 4-mm section thickness) using a flip angle of 20°.

Point-resolved single voxel spectroscopy (PRESS) was used to obtain \(^1\)H-MR spectroscopy spectra at 63.87 MHz using TR at 6 seconds, TE at 35 ms, and voxel dimension at approximately 17 × 17 × 17 mm\(^3\) (= 4.91 mL), with a shape adjusted to the specific white matter

<table>
<thead>
<tr>
<th>Gender</th>
<th>Age at Investigation, Years</th>
<th>Onset</th>
<th>Disease Duration, Years</th>
<th>Course</th>
<th>EDSS, Points during 2 Years</th>
<th>Spectroscopy</th>
<th>Spinal MR Imaging</th>
</tr>
</thead>
<tbody>
<tr>
<td>F</td>
<td>45</td>
<td>Sensory bout</td>
<td>5</td>
<td>RR</td>
<td>1.0</td>
<td>0</td>
<td>One thoracic lesion</td>
</tr>
<tr>
<td>F</td>
<td>52</td>
<td>Optic neuritis</td>
<td>9</td>
<td>RR</td>
<td>1.0</td>
<td>0</td>
<td>Negative (only cervical MR imaging performed)</td>
</tr>
<tr>
<td>F</td>
<td>21</td>
<td>Sensory bout</td>
<td>4</td>
<td>RR</td>
<td>1.5</td>
<td>0</td>
<td>Not done</td>
</tr>
<tr>
<td>F</td>
<td>58</td>
<td>Sensory bout</td>
<td>5</td>
<td>RR</td>
<td>2.0</td>
<td>0</td>
<td>Negative</td>
</tr>
<tr>
<td>F</td>
<td>46</td>
<td>Sensory bout</td>
<td>10</td>
<td>RR</td>
<td>2.0</td>
<td>4</td>
<td>Negative</td>
</tr>
<tr>
<td>F</td>
<td>38</td>
<td>Sensory bout</td>
<td>6</td>
<td>RR</td>
<td>2.0</td>
<td>1</td>
<td>One cervical lesion</td>
</tr>
<tr>
<td>F</td>
<td>50</td>
<td>Optic neuritis</td>
<td>11</td>
<td>RR</td>
<td>2.0</td>
<td>4</td>
<td>Negative</td>
</tr>
<tr>
<td>F</td>
<td>59</td>
<td>Optic neuritis</td>
<td>16</td>
<td>RR</td>
<td>2.5</td>
<td>0</td>
<td>Not done</td>
</tr>
<tr>
<td>F</td>
<td>49</td>
<td>Optic neuritis</td>
<td>6</td>
<td>RR</td>
<td>3.0</td>
<td>1</td>
<td>Negative</td>
</tr>
<tr>
<td>M</td>
<td>51</td>
<td>Sensory bout</td>
<td>12</td>
<td>SP</td>
<td>3.0</td>
<td>0</td>
<td>Negative</td>
</tr>
<tr>
<td>M</td>
<td>36</td>
<td>Sensory bout</td>
<td>15</td>
<td>SP</td>
<td>3.0</td>
<td>3</td>
<td>Not done</td>
</tr>
<tr>
<td>M</td>
<td>57</td>
<td>Optic neuritis</td>
<td>10</td>
<td>SP</td>
<td>5.0</td>
<td>0</td>
<td>One unspecific thoracic lesion</td>
</tr>
<tr>
<td>F</td>
<td>62</td>
<td>Motor bout</td>
<td>21</td>
<td>SP</td>
<td>5.5</td>
<td>0</td>
<td>Negative</td>
</tr>
<tr>
<td>M</td>
<td>57</td>
<td>Motor bout</td>
<td>14</td>
<td>SP</td>
<td>6.5</td>
<td>0</td>
<td>Negative</td>
</tr>
</tbody>
</table>

Mean 48.6 (21–62) | Mean 10.2 (4–21) | Mean 2.9 (1–6.5) |

**Note:** Mean values are shown as a geometric mean. F indicates female; M, male; EDSS, Expanded Disability Status Scale; RR, relapsing-remitting; SP, secondary-progressive.

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The spectrum of voxel 1 (parietal right). Assignments: 1, Cr-CH₃; 2, Glu-α/Gln-α; 2, Gin (multiple from C₂-C₆); 4, mlns; 5, Gin (multiple from C₂-C₆); 6, scyllo-inositol; 7, Cho (CH₃); 8, Cr (CH₃); 9, NAA; 10, NAA; 11, Glu-γβ; 12, Gin-γβ; 13, NAAG-methyl; 14, NAA-methyl; 15, Lac-CH₃; 16, protein background (“baseline”).

**Outline of the Procedures.** The following main steps were used in the procedures for subject measurements: 1) acquisition of water-suppressed spectra using a short TE and a long TR; 2) acquisition of unsuppressed water spectra as a function of RF pulse amplitude (or “transmit gain,” using the manufacturer’s terminology); 3) acquisition of unsuppressed water spectra as a function of TE; 4) LCModel analysis of the spectra using eddy-current artifact correction and a manufacturer-provided metabolite library, as well as resonances corresponding to lipid signals; 5) correction of the flip angle deviations from the desired in the PRESS sequence; 6) correction of the CSF partial volumes in the spectroscopy voxels (using the water amplitude versus TE measurements); 7) correction of the concentrations for tissue water content; 8) correction for unequal Boltzmann equilibrium magnetization because of differences in temperature between the calibration phantom and the subjects; and 9) correction for differential relaxation between in vitro references and in vivo measurements.

**Additional Procedures.** Data correcting for partial volumes and the reciprocity effects were collected for a single parietal voxel in each subject. The water spectra were collected using different transmit gains (RF pulse amplitude) and TE. The LCModel output concentration values were calibrated periodically during the study to compensate for time variability in scanner parameters using an approximately 50.000 mmol/L of Cr solution in physiologic buffer (“Cr calibration phantom”). Data were recalculated to reflect the tissue concentrations based on the water content in average white matter (71%).

**Correction for Flip Angle Errors.** The deviation between actual RF pulse amplitude (R_actual) (obtained from the scanner auto prescan), and ideal RF pulse amplitude (R_ideal) was determined using the following PRESS-specific signal intensity expression (assuming 180° inversion pulses): 

\[ f(\alpha, TR, T1) = \sin^2\left(\frac{T1}{2} - \sin\left(\frac{T1}{2}\right) \cos^2\alpha\right) \]

where the actual flip angle (\(\alpha\)) was obtained from R_actual and R_ideal in equation 2.

\[ \alpha = \frac{\pi}{2} \cdot \frac{R_{\text{actual}}}{R_{\text{ideal}}} \]

The RF pulse amplitude curves acquired in the subjects were fitted to equation 1 to obtain R_ideal. The flip angle dependence (sin^2(\alpha) and cos^2(\alpha), however, was slightly modified to account for the actual 167° “inversion pulses” used in the manufacturer-provided pulse sequence (see above).

**Relaxation Values.** T1 and T2 values were obtained from the literature. Specifically, the following values were used: T1 satu (in ms) Cho 1150, Cr 1550, mlns 900, NAA 1450; T2 satu (in ms) Cho 330, Cr 240, mlns 110, NAA 450; and T2 satu (in ms) Cho 810, Cr 765, mlns 284, NAA 945. The T1 value of the main Cr resonance in the Cr calibration phantom was determined (using an inversion recovery experiment) to be 1652 ms at 295 K.

**Metabolite Concentrations.** Using these T1 values and the modified equation 1, the metabolite concentration (C_metabolite) could then be evaluated as:
where $S_{metabolite}$ is the signal intensity from a metabolite, $C_{Cr}$ is the concentration of the Cr calibration phantom, $S_{Cr}$ is the signal intensity from the Cr calibration phantom, and $R_{ideal}$ is the RF pulse amplitude, which gives it the peak amplitude of the water resonance. The $f(Cr)$ and $f(in\;vivo)$ refer to equation 1 and the Cr calibration phantom and in vivo voxel, respectively.

**Additional Corrections for Partial CSF Volume, Differential Temperature, and T2.** The CSF fraction of the voxel volume was estimated using bi-exponential decay analysis of the water spectra acquired as a function of TE; in this analysis 40% of water signal intensity was assumed invisible in the conditions used for these experiments. Correction for differences in thermal equilibrium magnetization dependent on the temperature of the body and the Cr calibration phantom was performed using the following expression: $(1/T_{2\beta}^0)/(1/T_{1\beta})$. Finally, differential T2 correction takes into account differences in T2 between in vitro and in vivo measurements as follows:

$$
3) \quad C_{metabolite} = \frac{S_{metabolite}}{S_{Cr}} \frac{R_{ideal,in\;vivo}}{R_{ideal,cr}} f(Cr) f(in\;vivo)
$$

where $S_{metabolite}$ is the signal intensity from a metabolite, $C_{Cr}$ is the concentration of the Cr calibration phantom, $S_{Cr}$ is the signal intensity from the Cr calibration phantom, and $R_{ideal}$ is the RF pulse amplitude, which gives it the peak amplitude of the water resonance. The $f(Cr)$ and $f(in\;vivo)$ refer to equation 1 and the Cr calibration phantom and in vivo voxel, respectively.

**Quantification Aspects**

On System Aspects. The correlation plot between the estimated maximum in vivo water signal intensity ($S_{1/T_2O, in\;vivo}$) and $R_{ideal, in\;vivo}$ for Signa LX (5.8) data showed a strong linear correlation between signal intensity and estimated ideal RF pulse amplitude ($R_{ideal, in\;vivo}$; $r = 0.97$ (data not shown)). This showed that the receiver parameters of the MR scanner are stable as long as the hardware is not modified.

**Error Analysis.** It is important to evaluate the influence of various types of errors in a study based on absolute quantification. The absolute quantification was performed in several separate steps, and the contribution of each of these to the accuracy and precision was subject to an evaluation, which is briefly described here. Here the data for control subjects were used for such an evaluation (Table 2).

**Correction Influence.** The correction for the reciprocity effect was the most significant correction (50% variation between different subjects). It is interesting to note that the other corrections (Table 2) did not alter the (population-wide) precision as expressed by the coefficient of variation (shown for 1 row of data only), which was approximately 10%. The other corrections did not alter the accuracy of the data by more than 5%–10%. The most important (other than reciprocity) correction was the differential T2 correction (approximately +8%), followed by the flip angle correction (approximately –7%). The latter arose from systematic scanner behavior.

**Differential Correction Weights.** It is of interest to note that some of the corrections affect all of the measurements the same way, and their main effect is to achieve more accurate values in terms of biochemical function. Other corrections, notably the reciprocity correction, are very important for intersubject comparisons (such as patients versus control subjects).

**Statistical Evaluation**

Two statistical approaches were used. First, the subjects were analyzed for intrasubject variability for each metabolite between the 4 individual VOIs in the patient and in the control group separately by using analysis of variance (1-way ANOVA). Post hoc, Fisher pairwise comparisons test was performed continuously to show which voxels differed. The Student t test was then adopted to compare metabolite concentrations in respective voxels between the patient group and the control group. In these calculations, we compared sets of data that included 14 measurements, consistent with the number of subjects in the patient group and the control group. In these calculations, we compared sets of data that included 14 measurements, consistent with the number of subjects in the patient group and the control group.

Second, the single voxel measurements were used as a basis for analysis, according to the assumption that pathologic changes of all of the VOIs in each subject are correlated, irrespective of brain region. Thus, 56 measurements (14 patients × 4 voxels) were compared for each metabolite. Two-way ANOVA was adopted to calculate inter-subject differences in metabolite concentrations between the patients and the control subjects. We also performed the Student t test to compare intersubject general concentrations of respective metabolites in 4 VOIs altogether.
Results

Metabolite Concentrations

Patients versus Control Subjects. The absolute aqueous concentrations of metabolites in NAWM are shown in Table 3. Note that these concentrations reflect the conditions in the aqueous phase, after all of the above-mentioned corrections. The most interesting and unexpected finding was that the absolute concentration of Cho was significantly ($P < .001$) lower in NAWM of patients with MS than in control subjects. In addition, patients showed lower NAA ($P = .003$) and NAA+NAAG (tNA) concentrations ($P = .002$), as well as slightly lower Cr ($P = .03$). In contrast, no significant differences in mIns or glutamine/glutamate concentrations between patients and control subjects were detected.

RRMS versus SPMS. The concentrations of NAA/NAAG were highest in control subjects, lowest in RRMS, and lowest in SPMS, a statistically significant difference, obviously progressing as the disease deteriorates. The corresponding concentrations of mIns showed a slight increase. This is expressed in Table 4 in mM/L (SD), aqueous solution.

Concentrations versus EDSS. The correlation between disability (EDSS) and respective metabolite concentrations in the patient group was also analyzed. There was a weak positive correlation between EDSS and mIns concentration (0.14 mM/L per EDSS; $r^2 = 0.06$), whereas a negative correlation was found for tNA ($-0.41$ mM/L per EDSS; $r^2 = 0.22$).

Concentrations versus Age. Metabolite concentrations versus age were also investigated. In the patient group, we found a weak negative correlation between tNA and age ($-0.04$ mM/L per year; $r^2 = 0.08$), as well as a weak positive correlation for mIns concentration (0.02 mM/L per year; $r^2 = 0.04$). In the healthy control group, a slight positive correlation between Cho and age was observed (0.03 mM/L per year; $r^2 = 0.23$).

Spatial Concentration Differences. No significant difference in Cho, Cr, mIns, and NAA concentrations was found between the 4 voxels in healthy subjects. The tNA concentration was higher in parietal regions compared with frontal voxels on both sides, which may be because of anatomic differences. NAAG and tNA have been shown to be higher in regions with high neuron density, such as the occipital area, compared with lower neuronal density areas, such as the frontal regions. In the MS group, there were no statistically significant differences between patients and control subjects for all metabolite concentrations (RRMS versus SPMS).

Discussion

Our results supported the hypothesis that altered metabolism in NAWM can be detected in patients with MS without brain lesions. NAWM is a term used to express the inability to reveal pathologic changes on the MR imaging brain scan. It has been suggested that it may not be normal, but just a reflection of the restrictions imposed by the measurement device. At higher field strength (>1.5T), it is possible that minute lesions might have been observed. Nevertheless it is quite rare for patients

Table 2: Influence of absolute concentration corrections other than for reciprocity deviations on the relative absolute concentrations of 4 major metabolites averaged in healthy control subjects ($n = 14$)

<table>
<thead>
<tr>
<th>Variable</th>
<th>Cho, %</th>
<th>Cr, %</th>
<th>NAA, %</th>
<th>NAA+NAAG, %</th>
</tr>
</thead>
<tbody>
<tr>
<td>With reciprocity</td>
<td>100.0</td>
<td>100.0</td>
<td>100.0</td>
<td>100.0</td>
</tr>
<tr>
<td>Coefficient of variance</td>
<td>13.5</td>
<td>9.3</td>
<td>11.6</td>
<td>12.3</td>
</tr>
<tr>
<td>Flip angle correction</td>
<td>93.2</td>
<td>94.7</td>
<td>94.2</td>
<td>93.7</td>
</tr>
<tr>
<td>+ CSF</td>
<td>97.7</td>
<td>99.2</td>
<td>98.7</td>
<td>98.2</td>
</tr>
<tr>
<td>+ Differential T2</td>
<td>104.0</td>
<td>109.7</td>
<td>102.8</td>
<td>102.3</td>
</tr>
<tr>
<td>+ Boltzmann</td>
<td>108.2</td>
<td>114.1</td>
<td>107.0</td>
<td>106.4</td>
</tr>
</tbody>
</table>

Note: The top row 100% represents the concentrations without any correction other than the reciprocity correction. Subsequent rows show the accumulated effect of additional quantification step on the concentration values. Fully corrected relative values are shown in the last row. Cho indicates choline; Cr, creatine; NAA, N-acetylaspartate; NAAG, N-acetyl aspartylglutamate.

Table 3: Differences in absolute metabolite concentrations (and SE, in mM in aqueous fraction) in NAWM between patients with MS (and normal MRI scan of the brain) and control subjects

<table>
<thead>
<tr>
<th>Absolute Metabolite</th>
<th>Control Subjects</th>
<th>RRMS, mM</th>
<th>SPMS, mM</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cho</td>
<td>Mean</td>
<td>10.96</td>
<td>10.34</td>
</tr>
<tr>
<td></td>
<td>SE</td>
<td>0.19</td>
<td>0.19</td>
</tr>
<tr>
<td>NAA</td>
<td>Mean</td>
<td>3.73</td>
<td>3.59</td>
</tr>
<tr>
<td></td>
<td>SE</td>
<td>0.25</td>
<td>0.25</td>
</tr>
<tr>
<td>NAAG</td>
<td>Mean</td>
<td>14.62</td>
<td>13.88</td>
</tr>
<tr>
<td></td>
<td>SE</td>
<td>0.26</td>
<td>0.26</td>
</tr>
<tr>
<td>tNA</td>
<td>Mean</td>
<td>6.18</td>
<td>6.35</td>
</tr>
<tr>
<td></td>
<td>SE</td>
<td>0.13</td>
<td>0.18</td>
</tr>
</tbody>
</table>

Note: CHO indicates choline; Cr, creatine; m-Ins, myo-inositol; NAA, N-acetylaspartate; tNA, total N-acetyl compounds including NAA and NAAG; n.s., not significant; MS, multiple sclerosis; NAWM, normal-appearing white matter.

Table 4: Absolute metabolite concentrations (and SE, in mM in aqueous fraction) in NAWM between patients with MS (and normal MRI scan of the brain) and control subjects

<table>
<thead>
<tr>
<th>Absolute Metabolite</th>
<th>Control Subjects</th>
<th>RRMS, mM</th>
<th>SPMS, mM</th>
</tr>
</thead>
<tbody>
<tr>
<td>NAA</td>
<td>Mean</td>
<td>10.96</td>
<td>10.34</td>
</tr>
<tr>
<td></td>
<td>SE</td>
<td>0.19</td>
<td>0.19</td>
</tr>
<tr>
<td>NAAG</td>
<td>Mean</td>
<td>3.73</td>
<td>3.59</td>
</tr>
<tr>
<td></td>
<td>SE</td>
<td>0.25</td>
<td>0.25</td>
</tr>
<tr>
<td>tNA</td>
<td>Mean</td>
<td>14.62</td>
<td>13.88</td>
</tr>
<tr>
<td></td>
<td>SE</td>
<td>0.26</td>
<td>0.26</td>
</tr>
<tr>
<td>mIns</td>
<td>Mean</td>
<td>6.18</td>
<td>6.35</td>
</tr>
<tr>
<td></td>
<td>SE</td>
<td>0.13</td>
<td>0.18</td>
</tr>
</tbody>
</table>

Note: mIns indicates myo-inositol; NAA, N-acetylaspartate; NAAG, N-acetylaspartylglutamate; tNA, total N-acetyl compounds including NAA and NAAG; RRMS, relapsing remitting multiple sclerosis; SPMS, secondary-progressive multiple sclerosis; NAWM, normal-appearing white matter. The MS patients were separated into RRMS and SPMS. Significant difference between RRMS and SPMS, $P < .05$ (Mann-Whitney).
with MS to have a negative MR imaging brain scan. Approximately 5% of patients with MS, assigned previously to a group of CDMS according to the Poser criteria, do not exhibit pathologic changes on MR imaging of the brain. In this study we found that 4% of our patients with MS had normal MR imaging scans. In a study of patients with suspected MS and negative brain MR imaging, all ($n = 20$) had lesions in the spinal cord. The authors proposed that a combination of brain and spinal MR imaging can reach almost 100% sensitivity. Of course, this raises the question of whether MS diagnosis is plausible in case subjects with a negative brain and spinal MR imaging. In our patient population, many fewer subjects (14%) had spinal lesions (although not all of the patients were investigated; Table 1). From our point of view, the large fraction of negative spinal MR imaging in our patients (64%) suggests that there is indeed a subtype of MS with minimal demyelination. However, some of the spinal MR imaging examinations of our patients were not recent.

Our main finding of a low absolute concentration of Cho in the NAWM of patients with MR imaging-negative MS was unexpected but interesting. It could indicate a lack of inflammation, but we believe that it may also be possible because of increased uptake of Cho from the free phase for the building of cell membranes (only mobile choline-containing compounds are observed under the conditions of the present experiments). If this is true, it might reflect the onset of a healing process in these patients with MS. The only report with similar findings was from Richards et al dealing with a model of experimental acute encephalomyelitis in primates. They described a decline in Cho concentration in animals with no lesions in voxels seen on $^1$H-MR spectroscopy examination, though the animals developed lesions in other regions of the central nervous system. The cause for this finding still remains unknown. Sarchielli et al detected no significant difference in apparent Cho concentrations between patients with MS and control subjects when investigating NAWM in patients with lesions. Aging affects Cho concentration slightly; levels increase very slightly with age in a young and middle-aged healthy population (Cho versus age; $r = 0.38$). This is consistent with our finding in the healthy control group ($r = 0.48$). The patient group had a slightly higher mean age compared with the healthy control subjects, but the effect of this on Cho concentration is opposite of the observed difference; the age difference can therefore not explain our results.

One of the most important limitations in the interpretation of Cho changes in $^1$H-MR spectroscopy is that the Cho resonance, under the conditions of in vivo spectroscopy, is complex and represents several metabolites, including phosphocholine and glycerophosphocholine, and changes in any of these may result in similar spectral changes in proton spectra. One should also realize that the major Cho-containing metabolite of the brain, phosphatidylcholine, remains invisible for $^1$H-MR spectroscopy, because it is immobilized in membranes to a large extent. Any Cho alterations should therefore be interpreted very cautiously. Thus, absolute Cho concentration determined by using $^1$H-MR spectroscopy might therefore be a “tip of an iceberg” of all Cho intermediates taking part in brain metabolism.

It is possible that to maintain myelin sheath integrity, mIns can be replaced by Cho in phospholipids in the form of lecithin (phosphatidylcholine), a major component of the myelin membrane. Some subjects may have an enhanced ability to repair their myelin sheaths effectively, and they therefore do not develop typical MS lesions.

It seems that as soon as the myelin sheath is irreversibly damaged, Cho concentration increases and, consequently, lesion foci develop. It has been reported that Cho is an essential nutrient for cell function, and deficiency of Cho leads to apoptosis. In addition, recent genetic research has revealed altered gene expression in NAWM in patients with MS, compared with control subjects. This should be kept in mind when considering our results. Further study, including genetic, is therefore warranted in this field.

NAA and NAAG are regarded as markers of neuron cells. A decrease in absolute concentration of these metabolites reflects loss of neurons in the course of illness, either reversible or persistent. Interestingly, we also found significantly lower tNA concentrations in patients with SPMS compared with those with RRMS, consistent with a progression in the course of the disease. In the work by Pouwels and Frahm, it was shown that there are more pronounced differences in regional intrasubject concentrations of tNA than of NAA alone, comparing frontal, parietal, and occipital white matter. This variability was attributed to NAAG distribution. We, therefore, assume that NAAG is a typical marker for neuron cells, because its distribution is correlated with neuron density.

In our study, we noticed statistically significant differences in tNA between control subjects and patients. It is important to note that tNA was not strongly correlated with age, as has been shown previously. Therefore, tNA concentration differences should not be influenced by a nonoptimal age matching between patients and control subjects. In patients with MS with brain lesions, axonal damage in NAWM is associated with retrograde degeneration of fibers transversely by the remote lesions. No apparent lesions were detected in brain MR imaging, but this does not exclude the presence of small lesions, which are smaller than the resolution of conventional 1.5T MR systems. These may be associated with relatively maintained myelin shear integrity. We suggest that this might explain the observation of parallel tNA and Cho alterations.

Furthermore, we believe that the weak correlations among EDSS, tNA (negative), and mIns (positive), respectively, are likely to reflect actual metabolic changes. Other investigators have described a similar but stronger correlation between mIns and disability (EDSS).

Conclusion

We report a lower absolute concentration of Cho in NAWM of patients with MS with a normal MR imaging brain scan. These patients may represent a subtype of MS characterized by an increased ability to protect against or a decreased ability to form lesions. Thus, $^1$H-MR spectroscopy may help to elucidate the metabolic variability in MS patients with different clinical expressions.

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