# TE averaged PRESS: a better tool for diagnosing early Alzheimer's disease?

I. Hancu[1], E. Zimmerman[2], T. O'Keefe[2], N. Sailasuta[3], R. Hurd[3]

[1]GE GRC, Niskayuna, NY, United States, [2]Albany Med. College, Albany, NY, United States, [3]GE ASL, Menlo Park, CA, United States

## Introduction

$^1$H MRS, and in particular PRESS or STEAM, have been used to diagnose [1] and follow therapy [2] in Alzheimer's disease (AD). Due to repeatability issues and biological variability, a large number of subjects is usually needed to evidence differences between diseased and control groups, or between treated and untreated groups. To possibly overcome this limitation, and decrease the number of subjects who would be enrolled in a clinical trial for an AD drug, eg, we propose here to apply a newly developed technique, TE averaged PRESS (PRESS-J) [3], to the study of AD. In PRESS-J, any signal not belonging to a singlet or triplet is filtered out, leading to less crowded spectra and smaller baselines (some of the macromolecule signals are also suppressed). The singlets and triplets in these spectra are easier to quantify, and we hypothesize that the subsequent improved repeatability associated with the easier quantification might yield a more sensitive separation between the groups of AD patients and normal controls (NC). To test this hypothesis, we compare the results of a PRESS-J acquisition with the results of PRESS, from the same subjects and the same voxel.

## Methods

All the scanning protocols described below were done on a 3T, whole body GE scanner. Ten early AD patients (medium age 71, average MMSE=25, average CDR=0.8) and eight normal controls (medium age 70, average MMSE 29.7, CDR=0) underwent a scanning session, comprising of a whole brain localizer, followed by 2 spectroscopy acquisitions from the same voxel. In the first acquisition, 256 spectra were acquired using PRESS (TE/TR=35/2000), and spectra were quantified using LCModel. In the subsequent PRESS-J acquisition, a total of 256 spectra were also collected, with TE varying from 35ms to 355ms in steps of 2.5ms (2 acquisitions per step). The repetition time for the sequence was 2s. The spectra were then averaged together, and also quantified using LCModel. The posterior cingulate gyrus was chose as the region of interest, following reports [4] about its early involvement in AD.

The concentration of metabolites/ metabolite ratios were then binned in 2 categories (AD and NC), and a one way ANOVA test was performed to estimate whether there is any significant difference between the 2 groups.

## Results and discussion

Figure 1 presents typical spectra (experimental data, as well as fitted spectra and fitted baselines) acquired from the same voxel of an elderly normal volunteer: Figure 1a presents the PRESS spectrum, and 1b the PRESS-J spectrum, displayed between 1 and 4ppm. As mentioned before, the complexity of the PRESS spectrum is greatly reduced in PRESS-J (only Cho, Cr, Glu, mI, NAA and some lipids are visible). Additionally, a flatter baseline is also to be noted (due to the filtering out of some of the macromolecule/lipid signals).

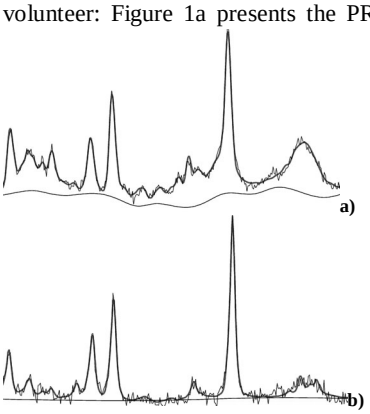
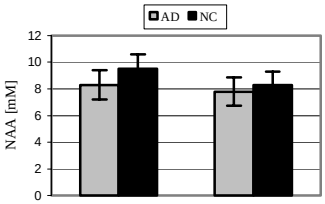



**Figure1: a)** *PRESS and* **b)** *PRESS-J spectra from the same voxel of a normal volunteer.*

The statistical analysis indicates that in this small group studied, a significant decrease in the NAA (p=0.03) and NAA/Cr (p=0.007) levels of the AD patients is observed if data is acquired using PRESS-J. This decrease does not reach statistical significance if data is acquired using PRESS (p>0.1). Figure 2 presents the bar graph illustrating the above statement: The NAA levels for AD vs NC is presented in Figure 2a for both PRESS-J and PRESS, while the ratio NAA/Cr is displayed in Figure 2b. It is hypothesized that this better separation between the diseased and control groups based on the NAA and NAA/Cr levels might be due to the better ability of the fitting program to quantify simpler spectra. This hypothesis is also validated by the Cramer Rao lower bounds (%sd) reported by LCModel. The average %sd for NAA decreased from 4% for PRESS to 2% for PRESS-J. Based on previous literature reports, it is also expected for PRESS to properly separate the AD group from the NC group based on the NAA levels, provided a large enough population is added to the groups studied. Since the separation with PRESS-J is obtained with a smaller number of subjects enrolled in each group, it is expected that this acquisition technique will be more sensitive/specific in separating AD patients from NC based on NAA levels.



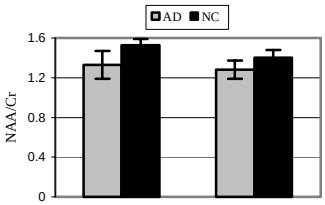




**Figure2:** *a) NAA and b) NAA/Cr for the AD and NC groups, measured using PRESS-J and PRESS.*

## Conclusions

A new method for distinguishing between early AD patients and normal controls has been presented. Spectra from the same voxel were acquired using both PRESS-J and PRESS. Statistical significant decreases in NAA and NAA/Cr in the small population studied were only observable when PRESS-J was used. It is suggested that the simpler spectra of PRESS-J, which can be easier quantified by the fitting program, might be responsible for the better separation of the early AD patients from normal controls. This technique might also become very important in MRS clinical drug trials for AD, possibly being able to reduce the population that needs to be enrolled in a study.

## References

1. Kantarci et al, AJNR **24**, 843 (2003);
2. Krishnan et al, Am J Psychiatry, **160**, 2003 (2003);
3. Sailasuta et al, Proc 11th ISMRM, 267 (2003);
4. Kantarci et al, Proc 11th ISMRM, 437 (2003);