Towards translation of advanced MRS methodology to clinical setting

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Target audience: MR spectroscopists interested in translational research

Introduction: PRESS and STEAM are the two most commonly used pulse sequences in the clinical setting for ^{1}H MR spectroscopy (MRS). The vendor-provided standard PRESS sequence has a large chemical shift displacement (CSD) error while STEAM suffers a loss of signal intensity by a factor of 2. The recently introduced sLASER sequence[1,2] provides full intensity signal with minimal CSD in addition to reduced T_2-relaxation and *J*-coupling evolution relative to standard PRESS. Using sLASER with voxel-based B_0 and B_1 calibrations, highly reproducible neurochemical profiles were obtained on clinical 3T scanners at two different sites[3]. Prior to clinical translation, the applicability of the advanced, non-standard MRS protocol in the clinical setting needs to be established. The aims of the present study were therefore: **1)** to investigate if the sLASER protocol, including FASTMAP shimming, can be utilized in a clinical setting where the scanners are operated by trained clinical MR technicians and **2)** to compare quantification precision between the in-house sLASER vs. the standard PRESS protocols at 3T.

Methods: 30 healthy elderly volunteers (age 80±5 years, 17M/13F) were studied at 3T (Siemens Verio) with body coil excitation and 32-channel head coil reception. Two spectra (T_R = 5 s, 64 averages) were acquired from an 8 mL VOI located in the posterior cingulate cortex in the same session in *randomized* order using sLASER (T_E=28ms) after B_0 shimming with FAST(EST)MAP[4] (FM) and using vendor-provided PRESS (T_E=30ms) after vendor-provided advanced 3D shimming (Adv. shim). All scans were carried out by 3 rotating neuroradiology MR technologists. Spectra were quantified with LCModel[5] with water scaling option. The sLASER data were post-processed and fitted as described previously[3], including single-shot phase/frequency correction and a simulated basis set that contains experimentally measured macromolecule spectra while the PRESS data were fitted using standard LCModel parameters and a basis set obtained from Dr. Stephen Provencher. Metabolite concentrations were corrected for T_2 relaxation, and for tissue water and CSF content (determined using the fully relaxed unsuppressed water signals acquired at different T_Es[6]) in the selected VOI.

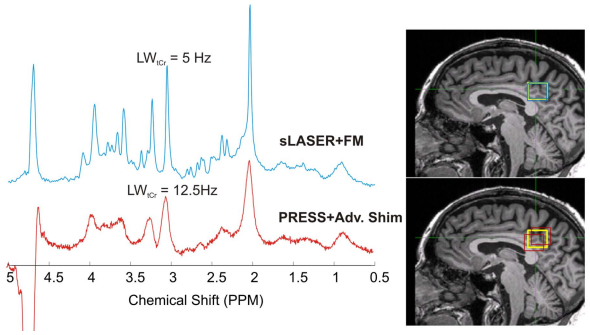

Fig. 1: Proton spectra (LB=0.5Hz) acquired from one subject. CSD for the PCC voxel (yellow) with sLASER (blue) and PRESS (red) between the upfield and downfield edges of the spectrum.

Results: The MR technicians were able to run the non-standard MRS protocol (including all steps required by the randomized protocol, such as resetting the B_0 shims between acquisitions) after 3 training sessions on average. sLASER and PRESS spectra acquired from the same subject (Fig. 1) showed similar spectral pattern although PRESS spectra had consistently broader spectral linewidths, likely due to both shimming performance of FM vs. Adv. shim and the single-shot phase/frequency correction in sLASER. The better shimming performance of FM was demonstrated by the water linewidths obtained with each protocol (Fig. 2). Notably, 18 out of 30 subjects had water linewidth > 10Hz with PRESS+Adv. Shim vs. 1 subject with sLASER+FM, a linewidth criterion previously determined for exclusion of spectra at 3T[3]. In addition, better water suppression was achieved with VAPOR in sLASER compared to CHESS in PRESS (Fig. 1, residual water was always higher than NAA singlet in PRESS). The CSD in sLASER was ~2% per ppm and ~10-12% per ppm with PRESS (Fig. 1). The quantification precision was improved with sLASER+FM compared to PRESS+Adv shim protocol: of the 5 major metabolites, CRLBs of tCr, tNAA, *myo*-inositol and glutamate were significantly different between the protocols (Fig. 3).

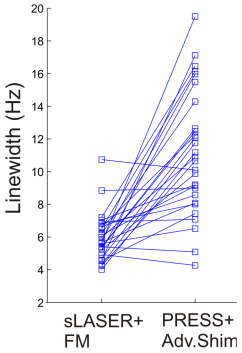

Fig. 2: Measured water linewidth from each subject (P<0.05).

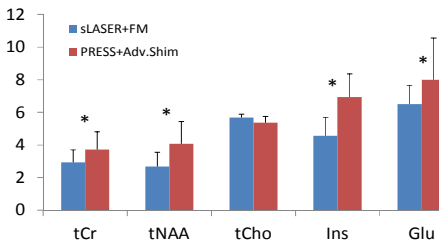

Fig. 3: Mean CRLB (%) from 30 subjects where error bars represent std. P<0.05 is represented by *.

Conclusion: The current study shows the feasibility of obtaining excellent quality MR spectra using a non-standard protocol in the clinical environment by trained clinical MR technicians; however the requirement for ~3 training sessions per technologist also demonstrated a need for further automation of the protocol. Specifically, a need to automate the voxel-based B_1 and B_0 calibrations was emphasized when the MR technologists were surveyed after the study. In addition, better quantification precision was achieved using the sLASER protocol. It remains to be determined which aspects of the non-standard protocol (sequence, shimming protocol, differences in post-processing & fitting) result in the observed differences in CRLB. In conclusion, the sLASER+FM protocol seems to be suitable for use in the clinical settings and further automation of all calibrations would facilitate ease-of-use of the MRS protocol.

References: 1. Scheenen et al MRM 2008; 2. Oz & Tkac MRM 2011; 3. Deelchand et al. MRM 2014; 4. Gruetter & Tkac MRM 2000; 5. Provencher MRM 1993; 6. Ernst et al. JMR 1993.

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