Human Gallbladder Bile: Enhancing the Sensitivity of Single-Voxel ^{1}H-MRS using WET Solvent Suppression and Short TE Methodology

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Introduction: The objectives of the present study were (i) to evaluate the potential benefits of using the WET [1] solvent suppression module for extracranial ^{1}H-MRS measurements and (ii) to assess the possible advantages of short TE ^{1}H-MRS methodology for application to human gallbladder bile *in vivo*. This work builds on a recent study that we reported in which a single-voxel ^{1}H-MRS acquisition and data processing strategy was employed for non-invasively characterising human gallbladder bile [2], [3].

Materials and Methods: All measurements were performed on a 1.5 T Siemens (Erlangen, Germany) Vision whole-body MRI scanner. The body coil was used for RF transmission and a commercial circularly polarised RF coil was used for signal reception. Three healthy male volunteers have been examined to date. The gallbladder was localised using three orthogonal MR images acquired using a T_2-weighted TrueFISP sequence (TR/TE; 6.32/3.0 ms, $\alpha = 50^o$, NEX = 4). A PRESS sequence (TR = 1500 ms, TE = 25 / 60 ms, 128 individual FIDs) was used to acquire ^{1}H-MR spectra from a voxel (3.4 ml) positioned within the gallbladder of each volunteer. Two separate ^{1}H-MRS measurements were initially performed in each volunteer using a TE of 60 ms. The first set of 128 FIDs was acquired using the CHESS module for global water suppression whereas the second set was obtained using the WET suppression sequence. The ^{1}H-MR (TE = 60 ms) spectra were reconstructed in the power mode using the post-processing methodology previously described [1]. A third ^{1}H-MRS measurement was performed at each study using the WET module for water suppression and a TE of 25 ms. Post-processing of the short TE (25 ms) ^{1}H-MRS data involved co-addition of the 128 manually phase-corrected spectra (phased using the PtCho resonance at 3.2 ppm). The inverse FT was subsequently applied to the constructed ^{1}H-MR spectrum and a Gauss-Lorentz window function was applied to the time-domain data (LB = -4.0 Hz, GB = 0.15). The FT was applied and the real component of the complex ^{1}H-MR spectrum was presented. In addition, a short TE ^{1}H-MR spectrum was acquired from a phantom containing freshly prepared porcine bile. All signal assignments are based on chemical shift values reported in high-resolution ^{1}H-MRS studies performed on gallbladder bile [4], [5].

Results and Discussion: Figure 1 shows the ^{1}H-MR power spectra (TE = 60 ms) recorded from the gallbladder bile of a male volunteer. The signal assignments are provided in the figure legend. The metabolite resonances observed in the resulting ^{1}H-MR power spectra are strikingly similar in appearance. However, the amplitude of the residual water signal is significantly greater in the data acquired using the CHESS scheme for water suppression, and the baseline of the residual water peak severely affects the neighbouring PtCho resonance at 3.2 ppm. The ^{1}H-MR power spectrum (TE = 25 ms) recorded from the porcine bile phantom is presented in figure 2(a) and the corresponding spectrum recorded from human gallbladder bile *in vivo* is shown in figure 2(b). The assignments are given in the figure legend. The short TE ^{1}H-MR spectra show an increased number of spectral peaks (c.f. TE = 60 ms) in the saturated lipid proton chemical shift region (BA: 0.6 – 2.5 ppm). The majority of these resonances are likely to correspond to the cyclic -CH_2- protons of the conjugated bile acids. In addition to the singlet (-$N^+(CH_3)_3$) of PtCho, the short TE ^{1}H-MR spectra show resonances that may be due to cholesterol (7: 5.38 ppm) and the amide protons of conjugated bile acids (6: 8.0 ppm). The low-intensity signal at 3.1 ppm, which is seen to shoulder the PtCho (-$N^+(CH_3)_3$) resonance in both MR spectra, is tentatively assigned to the taurine -CH_2- protons of taurcholic acid [5]. Finally, the excellent water suppression achieved using the WET suppression module should be noted.

Conclusion: These preliminary data indicate that the WET solvent suppression scheme is capable of achieving high water suppression factors in anatomical regions other than the human brain. The initial short TE ^{1}H-MRS data acquired from human gallbladder bile suggests that this methodology may be useful for identifying additional proton resonances attributable to taurocholic acid and biliary cholesterol. The short TE ^{1}H-MRS sequence might provide a sensitive methodology that is suitable for non-invasively monitoring the biliary excretion of drugs and their metabolites.

References: [1] Ogg *et al*., J Magn Reson B 1994;104(1):1-10. [2] Prescot *et al*., Radiology 2003;229(2):587-592. [3] Dzik-Jurasz *et al*., BJR 2003;76: 483-486. [4] Melendez *et al*., Transplantation 2001;72(5):855-860. [5] Ishikawa *et al*., J Lipid Res 1999;40(10):1920-1924.

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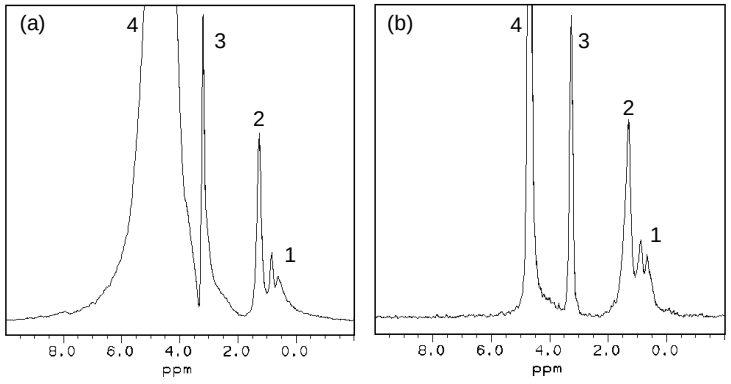

Figure 1: The PRESS ^{1}H-MR power spectra (TR = 1500 ms, TE = 60 ms) recorded from a voxel positioned within the gallbladder of a 38 year-old healthy male volunteer. The spectra were obtained using the (a) CHESS and (b) WET solvent suppression sequences. Signal assignments: 1, conjugated bile acid -CH_3 protons; 2, PtCho (-CH_2-) protons; 3, PtCho (-$N^+(CH_3)_3$) protons; 4, residual water. The ^{1}H-MR spectra in (a) and (b) are presented with identical 1D scaling. The CHESS water-suppressed data was constructed using 115 of the 128 individual power spectra whereas the WET water-suppressed data was constructed using 78 of the 128 power spectra. The different number of power spectra used to construct these data reflects inter-measurement variation as reported in [1].

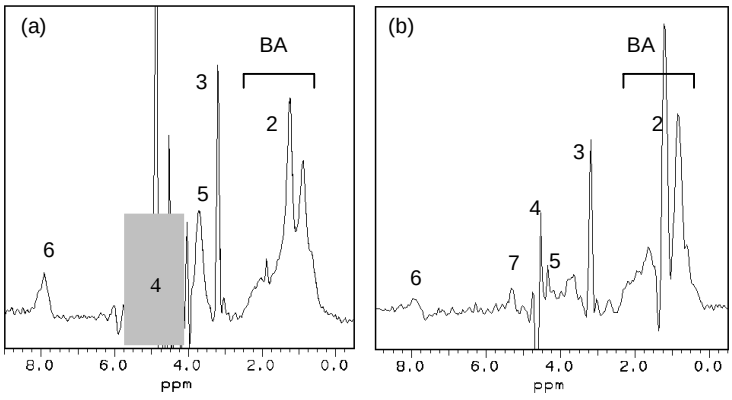

Figure 2: The PRESS ^{1}H-MR real spectra (TR = 1500 ms, TE = 25 ms) recorded from (a) a porcine bile phantom and (b) a voxel positioned within the gallbladder of a 38 year-old healthy male volunteer. Water suppression was achieved using the WET module in both cases. Signal assignments: BA, bile acid protons; 2, PtCho -CH_2- (tentative); 3, PtCho (-$N^+(CH_3)_3$) protons; 4, residual water; 5, conjugated bile acid methine (-C**H**(OH)-) and glycocholic acid -CH_2- (glycine moiety) protons; 6, conjugated bile acid amide protons; 7, cholesterol -C=C**H** (tentative).