Wavelet-encoded MR spectroscopic imaging incorporating parallel imaging to further reduce acquisition time: in-vitro results.

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Introduction: It has been shown that wavelet encoding spectroscopic imaging (WE-SI) reduces both acquisition time and voxel bleed in magnetic resonance spectroscopic imaging (MRSI) as compared to chemical shift imaging (CSI) for equal number of encodes, with an associated loss of signal-to-noise ratio (SNR) [1, 2]. It has also been shown, from simulation results, that wavelet encoding (WE) combined with parallel imaging (PI, WE-PI) reduces further the acquisition time by approximately the well known acceleration factor R, and preserves the spatial metabolite distribution with minimal loss of the signal-to-noise ratio (SNR) of the WE-SI technique [3]. Here we report phantom results confirming simulation results and demonstrating that WE-PI decreases the acquisition time of the standard WE-SI technique, while preserving its metabolite spatial distribution, and an associated SNR decrease, which is given by $SNR_{WE-PI} = (1/g)\sqrt{(N^2+2)/(N^2+2R^2)}.SNR_{WE-SI}$. In wavelet encoding, shaped RF pulses with profiles resembling dilated and translated wavelet (Haar) functions are used to acquire amplitude-modulated MR signals from sub-spaces with variable sizes and positions to fill wavelet domain lines [1, 2]. Similar Fourier encoding with PI where a number of k-space lines are not acquired and reconstructed from the acquired MR signals, in wavelet encoding, a set of wavelet domain lines are either simultaneously acquired or skipped and reconstructed from the collected ones. The first line of the wavelet domain corresponding to Haar scale function is always acquired (Fig. 1). The subsequent wavelet domain lines are either acquired or reconstructed depending on coil region versus sub-space. If the excited sub-spaces are larger than the coil regions, wavelet domain lines are reconstructed from the previous acquisitions (dashed yellow line in figure 1). If the excited sub-spaces are equal or smaller in size than the coil regions, the corresponding wavelet domain lines are simultaneously acquired using composite RF pulses (red and blue lines in figure 1). Figure 1 displays the WE-PI data acquisition steps for resolution N = 8 and acceleration R = 2.

Material and Method: The one dimension WE-PI scheme is implemented on a 3 tesla Siemens clinical scanner, using a Siemens multi-receive head coil. The pre-combined CP signal [5] from the posterior part of the head coil is used for an acceleration factor R = 2 in the left-right direction. Excitation RF pulses with single and dual-band profiles (Fig. 1) are applied along the acceleration direction (left- right) with 9 kHz bandwidth and 5.2 ms duration. Phantom studies using both WE-SI and WE-PI are conducted at resolution N = 4 and N = 8 with the following acquisition parameters: TR = 2 sec, TE = 75 ms, FOV = 180 mm by 20 mm, slice thickness = 30 mm, ADC bandwidth = 2 kHz, 1k points, and 2 averages. The phantoms are made from cylindrical tubes filled with aqueous solutions of metabolites with known concentrations, placed in holes of an inner plastic chamber. The latter surrounded by water and in turn immersed in an outer plastic chamber filled with canola oil. Data reconstruction combines both the inverse wavelet transform and SENSE technique. The g factor is calculated from the coil sensitivity maps à la SENSE technique.

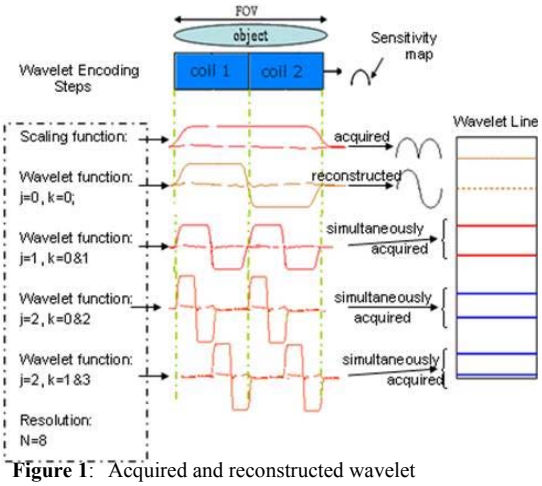

Figure 1: Acquired and reconstructed wavelet domain lines with N = 8 and R = 2. Translation and dilation values k and j are displayed for each wavelet encoding step.

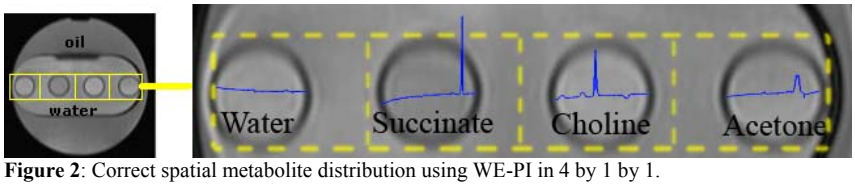

Figure 2: Correct spatial metabolite distribution using WE-PI in 4 by 1 by 1.

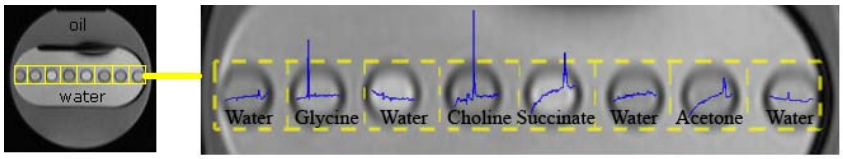

Figure 3: Correct spatial metabolite distribution using WE-PI in 8 by 1 by 1.

Table 1: Acquisition time and SNR of CSI, WE-SI, and WE-PI; CSI results are from calculation, SNRcsi is set to one. The experimental SNR values for WE-SI and WE-PI are calculated as peak intensity/noise standard deviation of the succinate. The g factor is calculated from the coil sensitivity map which at the succinate position is equal to 1.35 and 1.64 for 4x1x1 and 8x1x1 respectively.

Resolution	4x1x1			8x1x1		
Technique	CSI	WE-SI	WE-PI	CSI	WE-SI	WE-PI
Acquisition Time (s)	16	14	8	32	23	14
SNR (experiment, a.u)	---	0.82	0.49	---	0.61	0.33
SNR (calculated, a.u)	1	---	0.71/g=0.52	1	---	0.58/g=0.35

Result/Conclusion: The WE-PI method provides accurate spatial metabolite distribution at both resolutions (Figs. 2, 3). Table 1 reports acquisition time and SNR for WE-PI and WE-SI compared to the calculated CSI values considered as a gold standard. Acquisition time and SNR results are comparable to the theoretical ones for WE-PI technique. Acquisition time in WE-PI is reduced by approximately the factor R as compared to that for WE-SI. The calculated SNR is given as function of the g factor calculated from coil sensitivity maps. The use of more receiver channels will reduce the g factor and consequently increase the SNR. The SNR of CSI with PI will drop by $1/\sqrt{R}.g$ approaching 0.52 (R = 2 and g = 1.35), which is comparable to the WE-PI value at resolution N = 4. In conclusion, phantom results show that WE-PI provides accurate results with further reduced acquisition time and minimal SNR loss. Further tests are being conducted to reduce g factor for improvements in SNR.

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References: [1] Serrai H. et al. J. Mag. Reson., 177:22, 2005. [2] R. Young, H. Serrai, Mag. Res. Med. 61:6, 2009. [3] Y. Fu, et al., ISMRM, Toronto, 1582, 2008. [4] D. Sodickson, et al. Mag. Reson. Med. 591:38, 1997. [5] A.Reykowski, M. Blashe Mag. Res. Med. 1587:11, 2004