Optimized Detection of Glutamate and Glutamine at 1.5 T, 3 T and 4.7 T

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Introduction

In magnetic resonance spectroscopy, increasing the static magnetic field strength can afford increased spectral resolution and therefore accuracy of metabolite quantification in general. Also, for a particular field strength, optimization of PRESS echo timings can yield better spectral resolution for the resonance of interest. Spectral resolution is of specific importance in the 2.0 – 2.7 ppm range, which suffers from many overlapping resonances, including strongly coupled spin systems that produce complex spectra hindering straightforward quantification. In particular, the similar structures of glutamate (Glu) and glutamine (Gln) (both strongly coupled AMNPQ systems) produce comparable resonance frequencies and therefore their discrimination can be difficult using standard spectroscopic methods. In this study, the optimization of PRESS timings is investigated at three different static field strengths: 1.5 T, 3 T and 4.7 T, to determine the best resolution of Glu and Gln in vivo using the PQ resonances (2.3-2.5 ppm). Previous studies have explored specific optimizations at certain field strengths (1, 2) but have not included an overall description for PRESS quantification of Glu and Gln.

Methods

At each field strength, numerical simulations were performed to determine the response of Glu and Gln to a standard PRESS sequence, using an in-house spin simulation program (3) that incorporates chemical shifts and strong and weak coupling effects for each metabolite. The program was run for various values of TE1 (first echo time) and TE2 (second echo time), ranging from 5 – 200 ms. For each time point, spectra for Glu and Gln were produced using a 3:1 Glu:Gln physiological concentration ratio (4). At short TE, each PQ resonance is comprised of a multiplet with decreasing peak amplitude from its center. Therefore, in order to minimize the overlap, time points were investigated to reduce the amplitude of adjacent Glu and Gln outer wings by essentially collapsing the multiplet into a singlet. At these time points, the contributions of Glu and Gln to the total signal (Glx) were calculated in the 2.0 – 2.6 ppm range, as well as the total amount of overlap. Single voxel experiments were performed on healthy volunteers using the optimized PRESS timings at 1.5 T and 4.7 T. An 8 cm^3 voxel was placed in parietal grey matter to maximize the Glu concentration, and other parameters included a TR of 1500 ms, and 256 averages, yielding a total acquisition time of 6 min 24 s.

Results

The simulated Glu and Gln spectra at the optimal timings determined are shown in Figure 1a-c for 1.5 T, 3 T and 4.7 T, respectively. Each plot contains the Glu (blue) and Gln (red) spectrum, and the resultant Glx (black). The shaded regions correspond to the PQ regions calculated from the simulation to be predominately Gln (left box) and Glu (right). The signal composition was then calculated in these regions to determine the extent of Glu/Gln discrimination. At 1.5 T (1a), the optimal timings for the PRESS experiment were calculated to be TE1 = TE2 = 55 ms. The optimization of the timing parameters offers a drastic improvement in resolution compared to the standard short TE spectrum. Gln suffers the most contamination from Glu at this field strength, with 31 % of the total signal composed of Glu in the Gln region (left box). At 3 T (1b), the timings as determined from the simulation were TE1 = 30 ms, and TE2 = 85 ms, in good agreement with those presented in (2). Fig. 1b shows an improvement in signal composition in the two regions, although the intersection of the Glu and Gln lines in not as sharp as at 1.5 T. The overlap has virtually been eliminated at 4.7 T (Fig. 1c), with Glu and Gln percent compositions of 98.8 and 95.9 in their respective regions. The timings for the 4.7 T simulations were determined to be TE1 = 20 ms and TE2 = 90 ms. The results indicate that the best reduction in signal overlap should occur at 4.7 T, with minimal contamination.

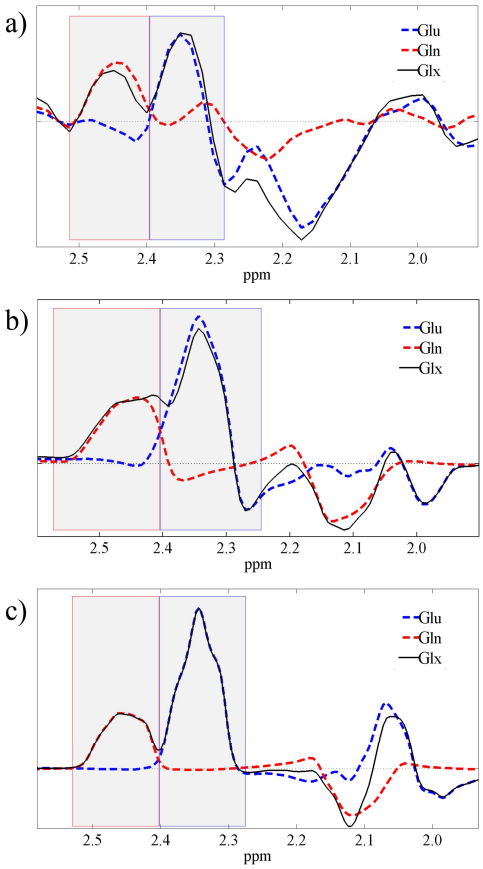

Figure 1: *Simulated spectra at optimized timings for Glu (blue line), Gln (red line) and the resultant Glx (black) for a) 1.5 T, b) 3 T and c) 4.7 T. The shaded regions denote the areas where the overlap is computed.*

The in vivo data is shown in Fig. 2 for a) 1.5 T and b) 4.7 T using the optimized timing parameters. The theoretical line shapes for Gln (red) and Glu (blue) are also shown. The resolution shown for the simulated spectra for 1.5 T (Fig. 1a) is not apparent in the in vivo spectra, due to the large linewidth, and therefore the expected possibility of discrimination is not realized. The increased resolution in the 4.7 T experiment allows the overlap to be minimized similar to the simulations. The theoretical line shapes agree with the in vivo spectrum, and therefore cross-contamination between the two is expected to be minimal as predicted.

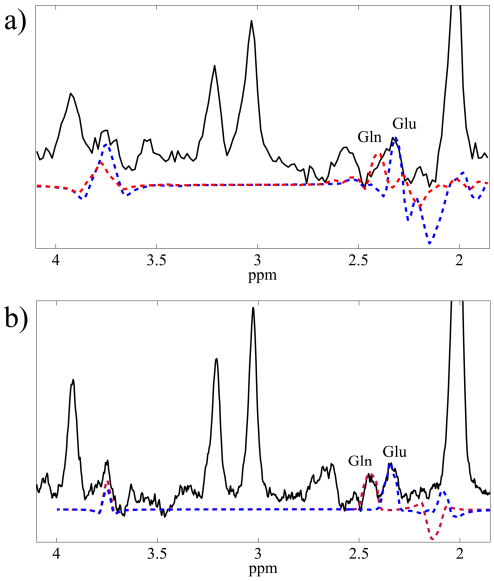

Figure 2: *In vivo spectra acquired at optimized timings determined from the simulation at a field strength of a) 1.5 T (TE1 = TE2 = 55 ms), and b) 4.7 T (TE1 = 20 ms, TE2 = 90 ms). The simulated spectra for Glu and Gln are shown in blue and red, respectively.*

Discussion

The resolution at the optimized parameters for 4.7 T illustrated excellent discrimination of Glu and Gln, with good line shape agreement between in vivo and simulation. Although the amount of spectral overlap in the simulated spectra at 1.5 T was greater that that at 3 T, the 1.5 T line shape may prove useful if the line broadening can be reduced further in vivo. In addition to the reduction in spectral overlap, improved quantification of Glu and Gln may require inclusion of contributions from other overlapping metabolites, particularly GABA with Glu (2.28 ppm) and aspartyl resonances with Gln (2.5-2.65 ppm).

References

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