Refinement of simulated basis set for LCModel analysis

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INTRODUCTION

Quantification of metabolites from in vivo ^{1}H NMR spectra requires a prior knowledge due to strong signal overlap also at very high magnetic fields. Experimental measurement of phantoms with all NMR detectable brain metabolites is very time consuming and it is necessary to repeat it when pulse sequence type, when sequence parameters, such as TE, are changed or when the static magnetic field is drifting. Therefore simulations of the basis sets became very attractive when the detailed set of chemical shifts and coupling constants for the broad range of brain metabolites was available [1]. Highly resolved in vivo spectra indicated that some refinement of the parameter set is necessary, which is the goal of this abstract.

METHODS

Metabolite spectra (pH = 7.1, T = 37^{o}C) measured at 9.4T using STEAM (TE = 2 ms) ware used for the refinement analysis. Spectral simulation and iteration programs on Varian console were used to extract chemical shifts and J-couplings. The series of highly resolved in vivo ^{1}H NMR spectra from the rat brain was summed to generate spectrum with very high SNR for testing purposes.

RESULTS AND DISCUSSION

Twenty brain metabolite spectra were simulated for the same resonance frequency as was used for the measurement of all metabolite phantoms. Then a very detailed comparison of simulated and experimental spectra was performed. When deviation was found chemical shifts and/or J-couplings were updated in the data base. In addition, in vivo NMR spectra with extreme resolution enhanced were used as a control. Then the newly generated database of chemical shifts and J-couplings was used to simulate the new basis set for LCModel analysis. In vivo ^{1}H NMR spectrum with very high spectral resolution and SNR was used as a testing probe for 3 different basis sets: experimentally measured (exp), simulated from the refined parameter set (sim new) and simulated from the original values in the paper [1] (Fig. 1). It is evident from the residuals that the new simulated basis set can fit experimental data better. The whole neurochemical profile is shown in Fig. 2. Concentrations of all strongly represented metabolites were quantified nearly identical. However, significant differences between experimental and simulated basis set in quantification of weakly represented metabolites (Asc, Glc, GSH) were minimized in the new basis set. In addition, the refinement of the simulated basis set resulted in substantial decrease in CRLB (Fig. 3).

REFERENCES: Govindaraju V et al., *NMR Biomed* 2000: 13, 129-153

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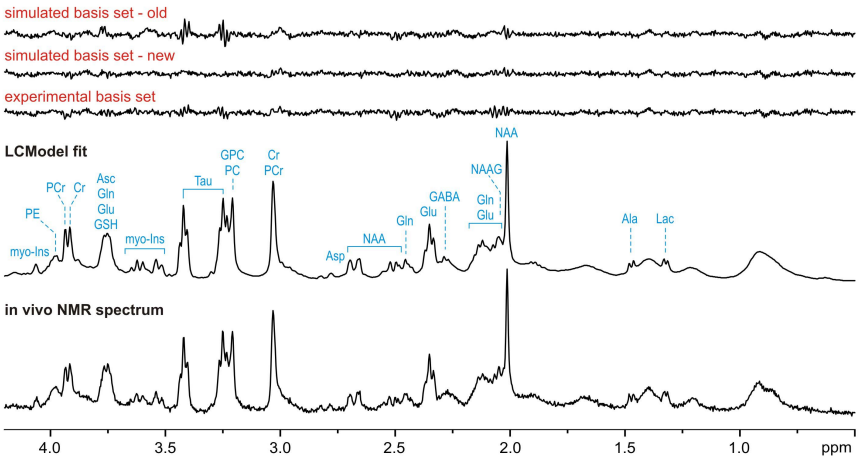

Fig. 1 LCModel analysis of in vivo ^{1}H NMR spectrum measured at 9.4T. STEAM, TE = 2 ms, TR = 5 s, VOI = 12 µL in striatum, NT = 2000 (data summed from 10 rat pups. Upper traces: residuals for different LCModel basis sets.

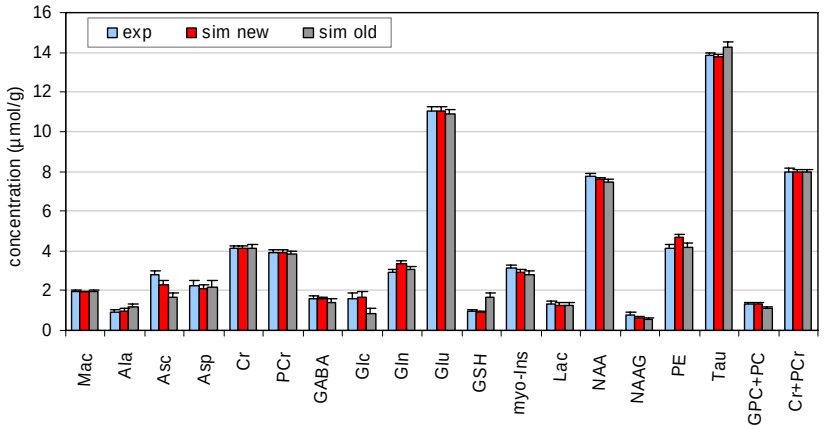

Fig. 2 Neurochemical profile of the rat striatum calculated by LCModel using 3 different basis sets: experimentally measured (exp), simulated using newly refined parameter set (sim new), simulated using parameter set from Govindaraju paper [1]

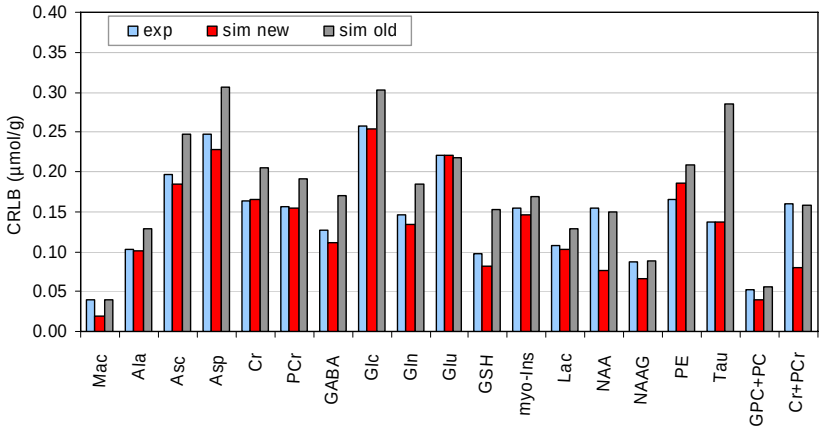

Fig. 3 Cramer-Rao lower bounds (CRLB) for 3 different basis sets described in Fig. 2