

Carnosine at 7T: quantification and relaxation times in m. gastrocnemius

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Introduction: Carnosine (β -alanyl-L-histidine) is a cytoplasmic dipeptide present in skeletal muscle, which acts as a buffer to maintain intramyocellular pH in physiological boundaries¹. Its role is interesting especially in relation to exercising muscle, where its concentrations can be noninvasively studied by proton spectroscopy (¹H MRS). One of the most commonly engaged muscle in dynamic studies is the gastrocnemius muscle². For the quantification of the metabolites from the spectra, correction for relaxation times is necessary. Our aim was to measure relaxation constants of carnosine and to quantify its absolute concentration in the gastrocnemius muscle at 7T. The focus was on two carnosine peaks visible in ¹H MRS, raising from two imidazole protons at 8ppm (C2) and 7ppm (C4)³.

Methods: For the study, 7 volunteers (4f/3m, age 28.6±4 years) underwent MR examination in 7T Magnetom scanner (Siemens Healthcare, Erlangen, Germany) using 28 channel ¹H bird cage knee coil (QED, Mayfield Village, OH). Volunteers were measured in supine position, with the right calf placed in the middle of the coil. For localization, T₁ weighted images were acquired. The voxel of interest was carefully placed in the gastrocnemius medialis muscle, with the size varying according to individual gastrocnemius size from 4 cm³ to 7.5 cm³. The excitation frequency was set to 7.5ppm (just between the C2 and C4 peaks of the carnosine). T₁ relaxation constant was measured by an inversion recovery method using STEAM localization sequence with these parameters: TR 10s, TM 20ms, TE 30ms and TI 50, 100, 300, 1000, 1500, 3000, 5000 and 8000ms, 32 avg and 80Hz WS. For the T₂ relaxation constant assessment, STEAM sequence with TR6s, TM 20ms and TEs 20, 30, 50, 70, 90, 120, 150 and 300ms, 20avg, 2 dummy scans and the same WS was used. Residual water and lipid peaks were removed by HSVLD⁴ from the spectra and peaks of carnosine were fitted in Amares⁵, jMRUI. Relaxation curves were fitted in MATLAB exponentially according to the formula $S_1 = M_0 \cdot e^{-TE/T_2} + c$ for T₂ and $S_1 = M_0 \cdot (1 - 2e^{-TI/T_1}) + c$ for T₁. Absolute concentration of carnosine was calculated from the C2 peak of carnosine in the spectra of 4 subjects measured by STEAM, TR10s, TE30ms, 32avg with and 4avg without WS, according to formula $C_{cn} = (S_{cn}/S_w) \cdot (CF_w/CF_{cn}) \cdot c_w \cdot n_w$, where S are signals of metabolites (w-water, cn-carnosine), CF are correction factors for relaxation, $c_w = 0.055$ mM molar concentration of the water and $n_w = 2$ is number of protons in water molecule.

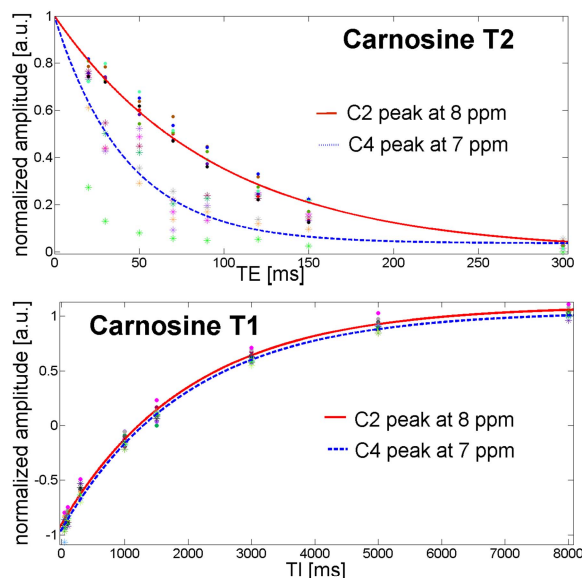


Fig.1. Fitting of T₁ and T₂ relaxation times for C2 and C4 peaks of carnosine (amplitudes are normalized)

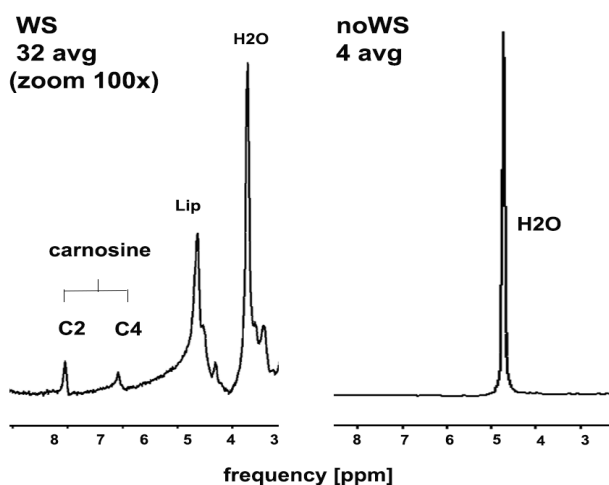


Fig.2. Proton spectra (STEAM, TR/TE=10s/30ms) with WS and with unsuppressed water used for quantification of carnosine

Results/Discussion: Data from all 7 volunteers provided sufficient SNR to fit peaks in the whole echo and inversion times range used. Fitting of T₁'s and T₂'s can be seen in the Fig.1. T₁ relaxation constant for C2 peak is 2002±94ms and for C4 peak 2038±112ms. T₂ times are 96±9ms for C2 and 36±10ms for C4 peak. Measured T₁ and T₂ values are slightly different but in similar range as the values published for m. soleus at 7T⁶. Spectra used for absolute quantification are shown in Fig.2. Measured concentration of carnosine in gastrocnemius muscle is 8.29±4.31mM, what is in agreement with previously published data for the same muscle from the lower field⁷.

Conclusion: In this study we showed the first known relaxation times of carnosine measured *in vivo* in gastrocnemius muscle at 7T. Results were successfully used for absolute quantification of concentration of carnosine in the muscle and will be used for further metabolic studies.

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