## Signal-to-Noise Ratio Analysis of 31P MRS in Skeletal Muscle: Influence of Localization Schemes, RF Coils and Field Strength

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**Purpose:** Localization in <sup>31</sup>P MRS allows to investigate the metabolism of individual muscles, which increases signal specificity, as averaging over different muscles can be avoided [1]. The signal-to-noise ratio (SNR) may limit its application, mainly because the volume of interest (VOI) contributing to the signal is smaller than for non-localized MRS, and other factors, e.g.  $T_2$  relaxation or partial refocusing (as e.g. with STEAM), may be imposed by the localization scheme. Different pulse sequences and coils were compared at two field strengths, to evaluate the SNR of localized <sup>31</sup>P MRS in human muscle in vivo. **Methods:** <sup>31</sup>P MRS of resting calf muscle in a total of 33 healthy subjects using single channel surface coils ( $\emptyset = 10$  cm) at 3T

and 7T and an in-house custom-built three-channel coil, dedicated for measurements on the calf (7x10 cm per channel) at 7T [2]. All three coils on entry subjects using single channel coil, dedicated for measurements on the calf (7x10 cm per channel) at 7T

[2]. All three coils operated as transceivers. MR sequences applied were a standard pulse-acquire scheme (FID) with a corresponding VOI of ca. 300 ml of calf muscle and two localized sequences STEAM ( $T_E = 7.5 \text{ ms}$ ) and semi-LASER ( $T_E = 23-26 \text{ ms}$ ) [1], selecting 30-40 ml of either medial gastrocnemius or the deeper lying soleus muscle. Non-localized data at 3T were acquired on a Siemens Trio (coil by Rapid Biomedical), localized 3T data on a Bruker Medspec S300 DBX (coil by Bruker), the 7T scanner was manufactured by Siemens (coils by Rapid / in-house built).

SNR was quantified in 3 to 11 partially saturated single-shot spectra (no averaging). Calculation of SNR was done as maximum signal in the real part of the MR spectra (phased to maximum signal) after Lorentzian line broadening with a matched filter, divided by noise, estimated as the standard deviation of an artifact-free region of 1/8 of the total spectral width.

**Results:** The VOI of the STEAM-localized voxels was ca. 1/8 of the VOI muscles from single shots, partial saturation giving signal without localization. Although STEAM inherently refocuses only

50% of the magnetization, the SNR was also 1/8 of the FID's SNR at 3T (see Fig. 1 and Tab. 1). Note however, that the line width with STEAM was half, compared to FID measurements (Fig. 2). Employing 7T approximately doubled the SNR for both methods. Applying semi-LASER instead of STEAM again doubled the SNR of localized measurements. Using our custom three-channel calf coil instead of the single loop coil further increased the SNR by a factor of 2.4, resulting in a value in the order of that of unlocalized FID at 3T. Still half of that could be achieved measuring in the deeper soleus muscle with the latter setup (semi-LASER with custom three-channel coil at 7T). Note that the following values were measured at longer  $T_{\rm R}$ , and were numerically scaled to the expected saturations, via known PCr  $T_1$  (6.4s at 3T [3], 4s at 7T [4]): 3T FID:  $T_{\rm R}$  = 20s to 7s; 7T STEAM:  $T_{\rm R}$  = 8s to 6s.

**Discussion / Conclusion:** The SNR for PCr obtained in localized measurements using the semi-LASER sequence in the gastrocnemius muscle at 7T with the optimized three channel coil was  $97 \pm 13$ . This is not significantly different from the SNR of  $107 \pm 27$  obtained with the well established non-localized acquisition scheme at 3T using a standard single loop surface coil. Even for the deeper lying soleus muscle an SNR of  $59 \pm 8$  could be achieved.



Localized <sup>31</sup>P MRS at 7T, employing dedicated coils, can therefore be used to acquire localized data with similar quality and temporal resolution, but with much higher specificity and thus improved diagnostic value than standard pulse-acquire MRS used for dynamic studies of metabolism at 3T.

**References:** [1] Meyerspeer, M. et al. MRM, 2011. 65(5):1207. [2] Laistler, E. et al., submitted to ISMRM 2013, #5092, [3] Meyerspeer, M. et al. MRM, 2003. 49:620. [4] Bogner, W. et al., MRM, 2009. 62:574.







Fig 2: Line width of PCr