**High resolution spectroscopic imaging of the mouse brain using a cryogenic 2x2 phased array coil at 9.4T**

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**Introduction** Spectroscopic imaging (SI) is a useful non-invasive tool to investigate the concentrations of metabolites in different tissues (e.g., brain), which might be linked to pathologies, disease status or therapeutic treatment effects [1]. SI on mouse brain is attractive in view of the many transgenic lines available for mechanistic studies. Due to the intrinsically low signal-to-noise ratio (SNR) resulting in very long acquisition times, the spatial resolution is limited. The use of cryogenic transceiver coils for in vivo imaging of the mouse brain revealed a SNR enhancement by a factor of about 2.5 at high field [2]. However, the inhomogeneous transmit B1-Field across the field of view (FOV) hampered the use for SI applications. In the present study, we show preliminary results of SI data of the mouse brain acquired with a novel cryogenic receive-only phased array coil in combination with a volume resonator for homogeneous excitation. The SNR enhancement according to the cryogenic receiver coil was reinvented into improved spatial resolution, enabling for the first time the acquisition of spectroscopic data with voxel sizes of 0.47 μl in the establishment phase and finally down to 0.32 μl in a pilot study using a glioblastoma mouse model.

**Methods** All experiments were carried out using a BioSpec 94/30 (Bruker Biospin MRI GmbH, Ettlingen, Germany) small animal MR system operating at 400 MHz. A four-element receive-only cryogenic phased array coil (2x2 geometry, overall coil size 20x27mm2) was used in combination with a linearly polarized room temperature volume resonator for transmission. The cryogenic array coil was provided by Bruker BioSpin AG, Fällanden, Switzerland. All in vivo experiments were carried out in strict adherence with the Swiss law for animal protection. All mice were anesthetized using 1.5% isoflurane in a mixture of oxygen/air (20%/80%) and intubated and artificially ventilated. SI experiments used a PRESS excitation scheme with TR/TE: 2000/26 ms. Scans were performed using VAPOR water suppression interleaved with eight saturation slices for fat suppression. Field maps were used for shimming. The acquisition scheme was weighted in k-space following a Hanning filter function. In the establishment phase, we acquired SI datasets on 6 C57Bl/6 mice with following parameters: FOV: 1.7x1.7cm2; slice thickness: 1.5 mm; acquisition matrix: 4096x29x31; reconstruction size: 4096x32x32; scan time: 1.5h; resulting in a nominal voxel size of 0.47 μl while we increased the resolution in the pilot study (acquisition matrix: 4096x37x37, 0.32 μl voxels). The pilot study consisted of 5 nude mice which were imaged 17 days after injection of GL261 brain tumor cells. For data analyses spectra from different coil elements were weighted for each voxel using a water reference scan and individually phase corrected to ensure optimal SNR during reconstruction. The phase correction needed for each coil element in each location was calculated by multiplying the FID signal by the normalized complex conjugate of the highest point in the reference FID. All the corrections and the summation of the spectra were performed in the time domain [3]. Post-processing of spectra: 5Hz Lorentzian filter, jMRUI [4].

**Results** The metabolite distributions resulting from SI data acquired with a resolution of 0.47 μl reflect the anatomy of the brain: Cortical structures and basal ganglia (striatum, thalamus) display high metabolite levels (creatine: Cre, choline: Cho, N-acetylaspartate: NAA, glutamate: Glu, taurine: Tau), while the respective levels were strongly reduced in the tumoral regions. Cre level are strongly reduced, while Cho and Ins level are increased.

**Conclusion** The use of a receive-only cryogenic phased array coil yielded excellent spectral quality in SI experiments with a resolution of down 0.32 μl per voxel. All experiments could be performed in less than 2h. The metabolite distributions over the FOV strongly correlate with brain structures allowing the localization of a tumor and a detailed resolution of the metabolite composition in tumor tissue. Using the established protocol we aim to resolve and characterize compartments of tumor tissue in terms of metabolite content.

**References**