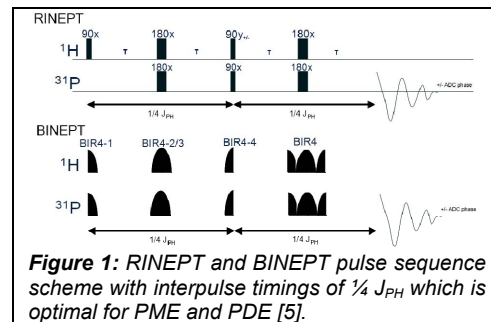
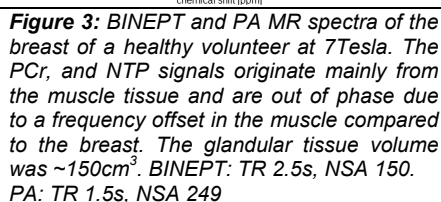
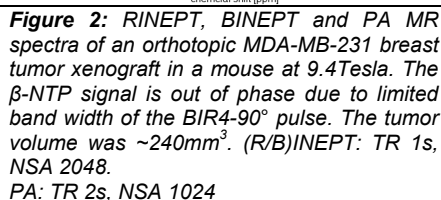


Jannie P Wijnen^{1,2}, Lu Jiang¹, Wybe J.M. van der Kemp², Dennis W.J. Klomp², and Kristine Glunde¹

Introduction:

such as tumor xenografts in preclinical mouse models, and in the human breast, these signals can compromise spectral quality significantly due to susceptibility effects. In this study, we demonstrate that the PT technique results in a flat baseline without any loss of sensitivity, and in uncontaminated detection of PME and PDE only, which are important phospholipid metabolites associated with cancer malignancy [2].



RINEPT and its adiabatic equivalent (BINEPT) sequences were implemented on a Bruker 9.4T Tesla small animal MR scanner (Fig. 1). A home-built solenoid coil tuned to the ^3P and ^1H frequencies, with an inner diameter of 12mm was used. We used short block pulses (100 μs each) for the RINEPT, and segmented BIR4 and BIR4-180 $^\circ$ pulses for the BINEPT. The segments of the BIR4 were 400 μs , driven at 10kHz to achieve a flat excitation profile with a broad bandwidth (24ppm), and the full BIR4-180 $^\circ$ was 800 μs driven at 15kHz.

An MDA-MB-231 breast tumor-bearing mouse was anaesthetized with inhalatable isoflurane, and its tumor was positioned inside the coil in the MR scanner. Non-localized B_0 shimming was done manually by changing first order shim gradients. A RINEPT, BINEPT and direct ^{31}P PA (BIR 4-90°) were acquired in 35 minutes each, using SNR optimized values for TR.

For a direct translation to clinical use, these methods were tuned for ^{31}P MRS in a healthy volunteer at 7T. A two-channel double tuned unilateral RF coil was designed for ^{31}P and ^1H MRI and MRS of the human breast and interfaced to a whole body 7T MR system (Philips, Cleveland, USA) [4]. Shimming with 2nd order shim gradients was based on a manually segmented region of interest in the breast from a B_0 map. A PA (block pulse 39°) and a BINEPT MR spectrum were obtained in 6.25 minutes each.

BINEPT significantly improved the ^{31}P MRS detection of PME and PDE in a breast tumor xenograft model at 9.4T (Fig.2) as well as in a healthy volunteer at 7T (Fig.3) because the polarization transfer removed all signals originating from PCR, Pi, NTP, and macromolecules that overlap with PME and PDE in ^{31}P MRS applications. As a consequence, the BINEPT MR spectrum has a flat baseline, which facilitates PME and PDE analysis using line-fitting algorithms (Fig.2&3). It is even possible to partially resolve the PME signal into phosphoethanolamine (PE) and phosphocholine (PC), and the PDE signal into glycerophosphoethanolamine (GPE) and glycerophosphocholine (GPC). The BINEPT MR spectrum displayed higher PME and PDE signals than the RINEPT MR spectrum (Fig.2) as expected from the non-uniform B1 fields of the coil. When comparing the mouse data with the human data, translational research seems very applicable. The significantly smaller volume of the mouse tumor was able to provide sufficient SNR, caused by the smaller coil, higher field and longer scan time. Nonetheless, the smaller volume did not improve the line shape, which reflects dominant T2^* effects caused by micro-susceptibility effects within (heterogeneous) tumors.

PT techniques at high field strengths (>7Tesla) enable the detection of partially resolved PE, PC, GPE and GPC in experimental breast tumor models and human breast tissue *in vivo* due to the removal of unwanted resonances from PCr, Pi, NTP, and ^{31}P -containing macromolecules. No reduction in SNR was detected when comparing PT techniques to regular PA. Our data suggest that BINEPT can be advantageous for studying phospholipid metabolism in translational research in breast cancer and other cancers *in vivo* at high magnetic field strength.

References: [1] Krishnamachary et al., Cancer Res 2009;69(8):3464-71. [2] Podo. NMR Biomed 1999;12(7):413-439. [3] Glaholm, Leach et al. Lancet 1989: 1326-1327. [4] Klomp, van de Bank. NMR in biomed 2011; Mar 24. doi: 10.1002/nbm.1696. [5] Mancini, Payne, et al. MRM 2003;50:578-8.8
Acknowledgement: This work was funded by the Niels Stensen foundation and NIH R01 CA134695.