Comparison and optimization of deep learning enhanced 2D APTw-CEST MRI at 1.5 Tesla and 3 Tesla: A clinically relevant phantom study

Lecong WEI[1,3], Andreas VOLK[1], Sophie CAMPANA TREMBLAY[3], Julie Poujol[4], Samy AMMARI[1,2], Gabriel GARCIA[2], Sebastien DIFFETOCQ[2], Tite MOKOYOKO[2], Corinne BALLEYGUIER[1,2], Nathalie LASSAU[1,2], François BIDAULT[1,2]

[1]Multimodal Biomedical Imaging Laboratory (BioMaps), Paris-Saclay University, Inserm (UMR1281), CNRS (UMR9011), CEA, France; [2]Department of Medical Imaging, Gustave Roussy Cancer Campus, Paris-Saclay University, Villejuif, France; [3]Scientific Department, Olea Medical, La Ciotat, France; [4]GE HealthCare, Clinical Research, Buc, France

INTRODUCTION: APTw-CEST can be useful for several clinical applications in oncology, such as differentiation of tumour types and grading, prediction of response to therapy, estimation of overall prognosis, etc[1]. Though preliminary work at lower clinical magnetic field has been recently described[2,3], there is still very limited data available at 1.5T. The recent introduction of deep-learning-enhanced image reconstruction, able to increase spatial resolution and SNR without longer acquisition times, motivates a more detailed investigation especially at 1.5T. The purpose of this preliminary phantom study was to compare the CEST effect at 1.5T and 3T on high resolution 2D images provided by a deep-learning algorithm. In addition, the effect of saturation offset number reduction combined with B0 mapping on CESTasym values was investigated, in order to minimize acquisition time and facilitate integration into clinical workflows.

METHODS: The phantom consisted of 12 tubes inserted into a cylindrical support filled with saline solution. Tubes were filled with BSA (bovine serum albumin) at pH 7 for 3 different physiological concentrations (8%, 10%, 12%)[4]. T1 values of BSA solutions were adjusted to about 1500ms. The phantom temperature was (37±2)°C during all measurements. Acquisitions were performed on 1.5T (GE Artist) and 3T (GE Signa Premier) MR scanners, using 19ch head and neck coil and 48ch head coil, respectively. CEST data were acquired with 2D SSFSE with the AIR™ Recon Deep Learning option (ARDL) activated for image reconstruction. SNR measured inside a saline region was compared with previously acquired data without ARDL (matrix 128^2). CW saturation was used (B1: 2µT, T_{sat}: 2 sec). B0 mapping was performed using a 2D GRE to correct for B0 heterogeneities. The acquisitions were performed with 61 offsets, acquisition matrix: 128^2, reconstruction matrix: 512^2, pixel size: 0.47 mm, slice thickness: 5 mm, T_{acq}: 2 min 28 sec. Acquisition data were post-processed using Olea Sphere 3.0 (Olea Medical, La Ciotat, France) software, which generates the CESTasym maps and Z-spectra. B0 correction was performed by using the chemical shifts of Z-spectra minima ('B0 Map FromZ'), and by using the B0 map ('B0 Map GRE'). The CESTasym values were generated from the 3-4ppm region. Mean values and standard deviations were measured in circular regions of interest (ROIs) in the center of the tubes. For acquisition times optimization, CESTasym was compared for different offset numbers ranging from 6 to 61 (= reference) using 'B0 Map GRE'. Two ΔB0 ranges were distinguished: <0.3ppm and >0.5ppm.

RESULTS: 2D CEST SSFSE using ARDL had 53% and 52% better SNR compared to the sequence without ARDL at 1.5T and 3T, respectively. For 'B0 Map FromZ' correction, CESTasym values increased with protein concentration (from 8% to 12%): from 5.4% to 7.1% at 1.5T, from 4.8% to 7.5% at 3T. Similarly, for 'B0 Map GRE' correction, corresponding CESTasym values increased from 6.7% to 8.1% at 1.5T, from 5.1% to 7.6% at 3T. CESTasym differences between the two B0 correction techniques were less than 20% at 1.5T and less than 3% at 3T (Fig1). The CESTasym varies with the number of offsets. For ΔB0<0.3ppm, CESTasym value differences ranged from 0% to 6%. For ΔB0>0.5ppm, they ranged from 1% to 35%. For each case, 16 and 20 offsets produced similar CESTasym as 61 offsets.

DISCUSSION: This study compared APTw-CEST acquisitions at 1.5T and 3T on the same phantom carried out during the same imaging session. The ARDL option allowed for increased SNR with 16 times smaller voxel volume. Values of CESTasym increased with protein concentration, with similar results at 1.5T and 3T. The comparison obtained with two methods of B0 correction showed that both worked effectively. The use of 'B0 Map GRE' provided the opportunity to reduce the number of offsets to 6 for ΔB0<0.3ppm (T_{acq}: 21 sec), and to 16 for ΔB0>0.5ppm (T_{acq}: 44 sec).

CONCLUSION: This study provided a comparison of 2D CEST SSFSE at 1.5T and 3T on a phantom. The findings open up the prospect of high-resolution time efficient APTw-CEST clinical MRI at 1.5T. However, the results are preliminary, hence repeatability studies and proof of concept in patients should be considered.

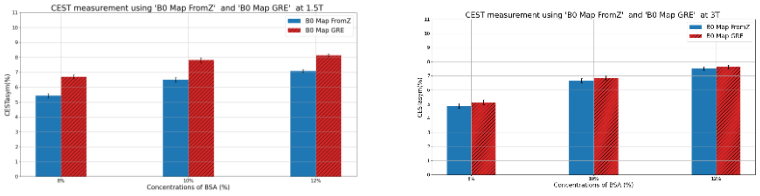

Figure 1: CESTasym values at different protein concentrations using 'B0 Map FromZ' (blue) and 'B0 Map GRE' (red) at 1.5T (left) and 3T (right).

ACKNOWLEDGMENTS: This material is based upon work supported by the ANRT with a CIFRE fellowship granted to L. Wei.

REFERENCES: 1. Vinogradov, *et al*. *NMR Biomed.* **36**, e4906 (2023) 2. Chan, *et al. J. Neurooncol.* **151**, 267–278 (2021) 3. Chan, *et al*. *Magn. Reson. Med.* **82**, 1684–1699 (2019). 4. Ray, *et al. Cancer Res.* **79**, 1343–1352 (2019)