Bloch Equation Simulation with Slice Profile Correction (BLESSPC) T1 Estimation- Enabling accurate and precise myocardial T1 mapping at 3.0T using the FLASH-readout based MOLLI sequence

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Target audience: Scientists and clinicians who are interested in myocardial T1 mapping.

Purpose: Myocardial T1 mapping sequence MOLLI [1] typically use bSSFP readout, which is sensitive to off-resonance and its utility may be limited at higher field strengths [2]. We sought to develop a FLASH-based MOLLI technique for accurate and precise myocardial T1 mapping 3.0T and validate it against bSSFP-MOLLI by phantom studies and on a cohort of healthy volunteers.

Methods: We developed the FLASH-MOLLI sequence by modifying the standard MOLLI sequence to use FLASH readout and incorporated the proposed Bloch equation simulation with slice profile correction (BLESSPC) algorithm for T1 estimation. BLESSPC calculates the 1D longitudinal signal evolution of the FLASH-MOLLI sequence using Bloch equations. To ensure accuracy of the simulated signal, each pixel was divided into 10 sub-slices, where the flip angle α_i of each sub-slice was assumed to follow the expected slice profile of the RF pulse used (Fig.1). The signal evolution of each sub-slice was separately simulated, and the resultant transverse signals $M_{ij}\sin(\alpha_i)$ for all the sub-slices were added together as the final simulated signal for the given pixel. Given the flip angle α, the initial magnetization M0, inversion factor δ, and the T1 value for each pixel, the signal evaluation of each pixel during the T1 mapping sequence could be simulated. Subsequently, the BLESSPC algorithm solves for the 3 parameters (α, M0 and the T1, assuming δ is known) or 4-parameters for each pixel that best match the simulated signal with the actual acquired signal.

The FLASH-MOLLI with centric k-space ordering (flip angle=10°) was evaluated against the bSSFP-MOLLI with the standard linear k-space ordering (flip angle =35°) based on studies over 10 phantoms with different simulated heart rates (HRs) and 10 healthy volunteers in a 3.0T MR scanner (Trio, Siemens Healthcare; Erlangen, Germany) using the same 5-(3)-3 acquisition scheme and pixel resolution (1.8mm x 2.2 mm). For T1 estimation, BLESSPC 3-parameter-fitting was applied to FLASH-MOLLI, and the standard MOLLI fitting with inversion factor correction [3] was applied to bSSFP-MOLLI. Reference T1 values of phantoms were determined by spin-echo experiments. The average inversion factors for phantoms and in vivo were determined by "FLASH-MOLLI+M0" with BLESSPC 4-parameters-fitting, which acquires additional M0 weighted image 6 seconds following the 5-(3)-3 acquisition. Based on results measured by the "FLASH-MOLLI+M0" sequence, the inversion factor was set to be 0.96 for phantom studies and 0.89 for in vivo studies. The precision of T1 estimation at was evaluated using coefficient of variation (CoV = Standard deviation/ Mean T1) at selected ROIs.

Results: Compared to the bSSFP-MOLLI, FLASH-MOLLI yielded lower T1 estimation errors, reducing average T1 estimation error from -58.5±50.6 ms to -1.5±15.3 ms for T1 values from 440ms to 1774ms and HRs from 40bpm to 100bpm (Fig.2). Excluding the results of two phantoms (T1=440ms and 1774ms) with serious off-resonance artefacts by bSSFP-MOLLI, the average CoV was 1.08±0.27% by FLASH-MOLLI and 0.81±0.55% by bSSFP-MOLLI. Based on data from 10 volunteers, the native myocardial T1 values at IVS region by FLASH-MOLLI were significantly higher than that by the standard bSSFP-MOLLI with inversion factor correction by 99.0±31.7ms (1454.9±23.6 ms vs. 1355.8±23.9ms, relative 7.3±2.4%, p<0.001) at an average heart rate of 62.5±9.9 bpm. The average CoV of T1 values at IVS region by FLASH-MOLLI was about 15% higher than that by bSSFP-MOLLI (2.01±0.5% vs. 1.75±0.3%, p=0.13). Compared to the bSSFP-MOLLI sequence, the FLASH-MOLLI sequence is less sensitive to off-resonance artifacts, and provide more homogeneous in vivo T1 estimations at 3.0T (Fig.3).

Conclusion: Compared with the bSSFP-MOLLI sequence, the FLASH-MOLLI sequence with proposed BLESSPC algorithm yields accurate T1 estimation and removes off-resonance artifacts at 3.0T.

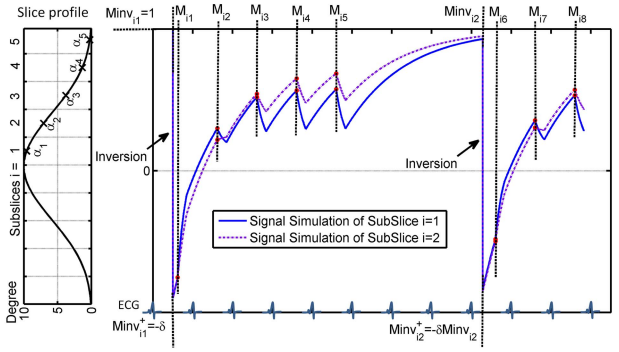

Fig.1: *Illustration of BLESSPC model.This example simulates the longitudinal magnetization signal evolution of the FLASH-MOLLI sequence using 5-(3)-3 acquisition using bloch equations for two of the subslices. δ is the inversion factor,and M_{ij} is the simulated longitudinal signal of subslice i prior to the jth readout. red dots indicate the beginning of a FLASH readout.*

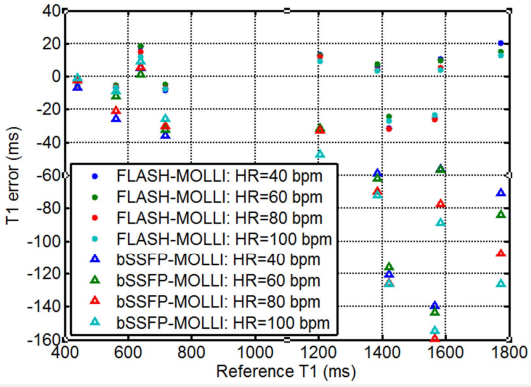

Fig.2: *The T1 estimation error at different heart-rates by the FLASH-MOLLI (dots) and the bSSFP-MOLLI (triangles) in phantom studies. Compared to the* bSSFP-MOLLI*, FLASH-MOLLI with proposed BLESSPC algorithm yielded lower T1 estimation errors.*

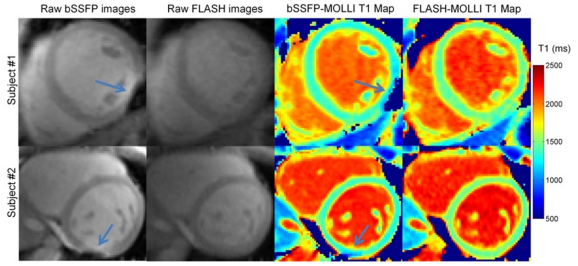

Fig.3: *Example of raw bSSFP-MOLLI and FLASH-MOLLI images and T1 maps of the mid left ventricular short axis at 3.0T in 2 healthy volunteers. T1 values of pixels where data doesn't fit well (R^2 <0.98) were set to zero. Compared to bSSFP-MOLLI, FLASH-MOLLI was less sensitive to off-resonance artifacts (Arrow indicated region).*

References: 1. Messroghli DR et al., *J. Magn. Reson. Imaging*, 2007; 26(4):1081–1086. 2. Kellman P et al., *J. Cardiovasc. Magn. Reson.*, 2013;15(1):63. 3. Kellman P et al., *Magn. Reson. Med.*, 2014;71(4):1428-34.