Quantitative perfusion measurement of liver metastasis using DCE-MRI: Comparing a 3D-Flash vs. a IR-trueFISP protocol within a clinical phase II study

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Introduction

For assessing treatment response to novel cancer therapeutics dynamic contrast enhanced magnetic resonance imaging (DCE-MRI) is a valuable tool. With appropriate data acquisition, quantitative functional parameter estimates can be obtained by fitting a physiological model to the data. Here a DCE-MRI protocol using a 2D Inversion Recovery trueFISP (IR trueFISP) sequence for DCE-MRI examinations of liver metastasis [1] was implemented and compared with a 3D Flash protocol.

Methods

Within a clinical study a subset of twelve patients with liver metastasis received two baseline examinations using two different protocols. Protocol A consist of a conventional 3D Flash sequence while protocol B, which was run 24h later, used a 2D Inversion Recovery trueFISP (IR-trueFISP) sequence[1]. Both protocols used a matrix size of 128x128, FOV of 400mm and a total acquisition time of 6min. The parameters in detail were for 3D-Flash: TR/TE=3.23ms/1.12ms, 72 time point's Δt=5s, 20 slices a 3.5mm, α=13° and 4 pre scans with α=2/8/13/25° and for IR-trueFISP TR/TE=3000ms/1.28ms, 120 time point's Δt=3s, single slice of 10mm, α=40°. To minimize through-plane movement during breathing data is acquired in a mainly coronal oriented view.

Phantom studies using a Eurospin phantom set with the same two protocols and a TSE protocol for reference were performed.

Data analysis: As shown in Figure 1 three slices of the 3D Flash data covering the same volume as the corresponding IR-trueFISP data were analysed with a custom-built software package developed under Matlab. Data processing consists of several steps

1. A ROI spanning the metastasis is defined and then semi automatically tracked using a correlation analysis-based algorithm.
2. T1 quantification is performed by a Levenberg-Marquardt (LM) routine using the analytic expression as published [2]. Concentration values are calculated according to $C(t)= (1/T1-1/T1_0)/kt$, with kt the relaxivity of Gd-DTPA taken from literature (4.3 mmol/ml*s).
3. Data-driven analysis is performed assessing initial area under curve (iAUC) [3] and pharmacokinetic modelling is done using the multi-compartment model from Tofts assessing the transfer constant Ktrans, which equals the permeability surface product under permeability limited conditions [4].

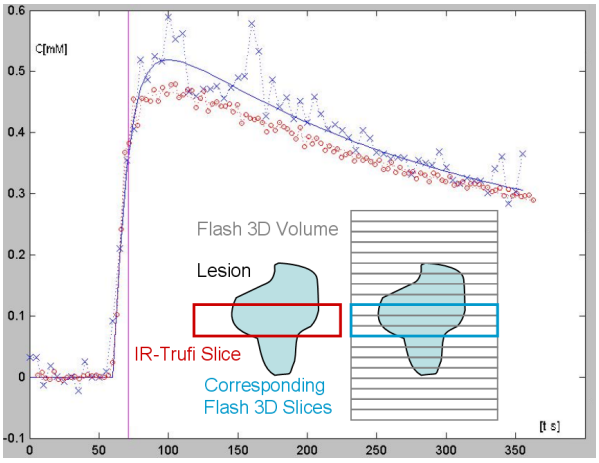

Fig 1: Slice positioning scheme and resulting concentration-time curves.

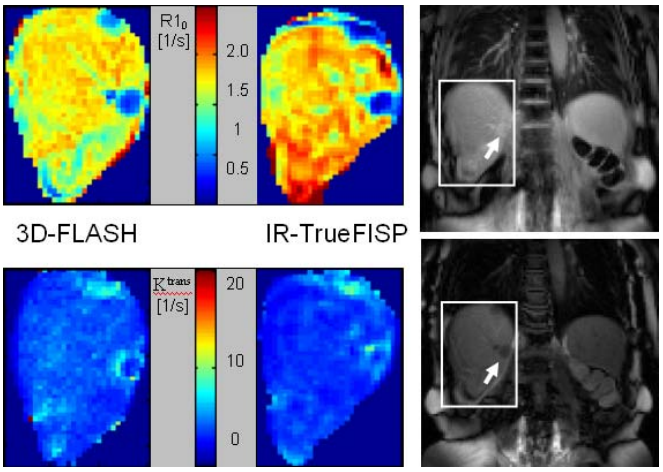

Fig 2: Comparison of calculated parameter maps for data of both methods.

Results

Phantom results of the TSE sequence showed the validity compared to T1 reference values. Phantom data showed on average a 26% higher T1 values measured with the 3D-Flash protocol compared to the IR-TrueFISP protocol. While 3D Flash R1 values showed random differences from -44% to +25%, IR-TrueFisp R1 values showed a linear (R^2 = 0,83) decreasing deviation from +25% to +3% over the T1 range of the phantom. A correction for this systematic deviation was applied.

The correlation coefficients of the IAUC60 and Ktrans values calculated from data acquired with both methods are 0.91 and 0.95 respectively over the whole subject group. This good agreement is also reflected in the direct visual comparison of parameter maps as in Figure 2.

Discussion

In conclusion IR-TrueFISP was successfully applied as DCE-MRI method and results were comparable with a data acquired using 3D-Flash protocol. It was shown that the IR-TrueFISP protocol with its high temporal resolution and good accuracy is a suitable DCE-MRI acquisition method assessing treatment response to novel cancer therapeutics or in other applications of DCE-MRI.

References

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