MR renography based on contrast enhanced T1-mapping

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Introduction: There is a growing clinical demand for assessment of various physiological parameters based on MRI. However, contrary to gamma-emitting modalities, MRI unfortunately does not measure changes in signal intensity in a straightforward way. This means that measurements of injected contrast agent concentration is difficult, which secondarily hinders the possibility to calculate important parameters in absolute units such as ml/min or ml/min/g. In this study, we suggest to employ the Look-Locker sequence for dynamic renography, allowing acquisition of the entire T1-relaxation curve within a few seconds. Further, the proposed method has the enormous advantage that measured T1 is reciprocally proportional with the concentration of contrast agent. The renography observed from the Look-Locker sequence is compared with a conventional T1-weighted renography.

Method: Anaesthetized adolescent pigs were used. Steady-state hydration is reached by infusion with saline and glucose 1-2 hours prior to start of the imaging protocol. Two sets of renography procedures were carried out with an interval of 4 hours to allow washout of the contrast agent. 1) T1map-method: sequence: Look-Locker TFEEPI sequence, artificial gating (30 min^{-1}), TR=57 ms, TE=2.3 ms, flip angle=10 º, 16 phases (e.g. 16 points on the inversion recovery), EPI-factor=7. 2) T1weighting: sequence: RF-spoiled fast 3D-transient-field-echo (3D-T1TFE) sequence with a 120º slice-insensitive prepulse, preparation-delay = 130 ms, TR=shortest (4 ms), TE=shortest (2 ms), flipangle=18º. Both 1) and 2) include: coronal/oblique plane, FOV = 400x400 cm, matrix = 128x50 cm, slice thickness=10 mm, linear k-space encoding, acquisition bandwidth was the minimum available. Gd-DTPA (0.02 mmol/kg) was in both sequences injected iv using a power-injector and flushed with 15 ml of saline. Data analyses were performed offline using Mistar (Apollo Medical Imaging Technology, Melbourne, Australia), allowing pixel-wise analysis. The analysis procedure for the dynamic T1map data was performed by fitting a three-parameter equation to the T1 inversion recovery curve for each dynamic time point:

$$S(t) = \left| A - B \cdot e^{-t(1/T_1 - \chi \cdot \ln(\cos\alpha)/\tau)} \right|$$

where t is the time after the inversion, t is the time between the alpha pulses and α is the flip-angle. A and B are constants depending on the gain of the receiver circuit, the longitudinal magnetization at thermal equilibrium and the transversal relaxation rate. τ is a compensation constant between 0 and 1 to correct for the fact that spins flowing into the slice during the mapping are not exposed to all of the alpha pulses.

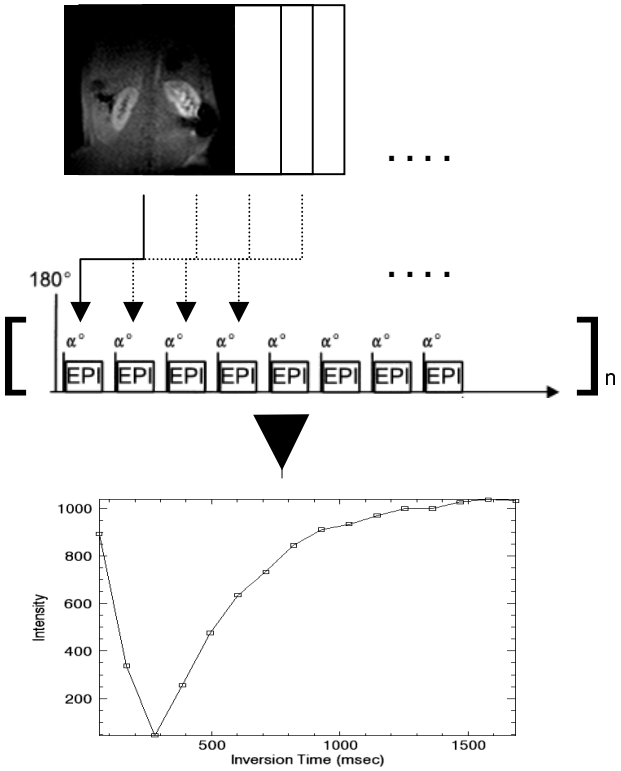

Fig 1: Procedure for dynamic quantitative T1map

Results: MR-renography based on the dynamic Look-Locker sequence and the standard T1-weighted sequence is demonstrated below. The two renographies were comparable, although the curve shape found from the Tmap method exhibited a relatively lower filtration response (the uptake period follo

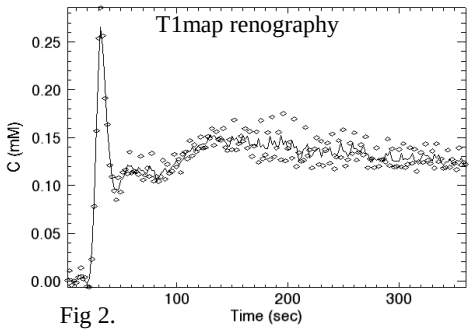

Fig 2.

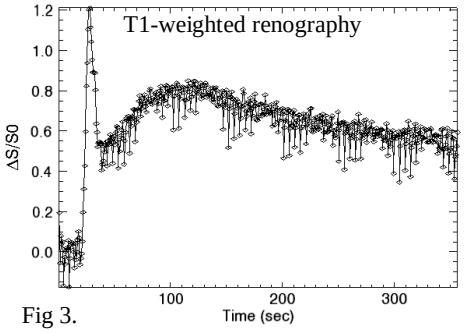

Fig 3.

Discussions and conclusions: This study demonstrated that dynamic Look-Locker sequence combined with a simultaneous bolus of Gd-DTPA is feasible for MR renography. The difference in curve shape should presumably be attributed to changes in relaxivity between different intrarenal compartment, such as blood and cortical tissue. In conclusion, this study presents a novel method for direct quantitative renography with units directly related to the concentration of the contrast agent injected.