Dynamic contrast enhanced MRI in patellofemoral pain syndrome: perfusion quantification of patellofemoral joint tissues

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Target Audience: Our target audience consists of MRI physicists as well as researchers and clinicians applying DCE-MRI.

Purpose: Patellofemoral pain syndrome (PFPS) is a common knee pathology with unknown etiology. A leading hypothesis on the etiology is a disturbed blood flow in the patellofemoral joint. Quantitative dynamic contrast-enhanced MRI (DCE-MRI) of bone provides a means to visualize and quantitatively analyze blood perfusion changes in bone, and shows promise as a novel imaging biomarker that can be applied in research to advance the knowledge on the pathogenesis of bone diseases, such as PFPS.[1] Because quantitative DCE-MRI of bone is novel, there is no consensus regarding optimal analysis methods and pharmacokinetic models and there is no tailored method for the patellofemoral joint yet. In this study, we assess several aspects of DCE-MRI in the patellofemoral joint and develop standardized methodology for DCE-MRI analysis, with the purpose to contribute to the further understanding, development, validation, and implementation of this promising technology.

Methods: We evaluated our method in 5 healthy control subjects from an ongoing DCE-MRI study in patients with PFPS and healthy control subjects without PFPS, aged 18-40 years. All examinations were performed on a 3T MRI scanner (Discovery MR750, GE Healthcare, Milwaukee, USA) using a dedicated 8-channel knee coil. The image protocol for DCE consisted of a sagittal, superior-inferior phase encoded, 3D spoiled gradient-echo (SGPR) sequence with fat suppression, 35 phases (approximately 10 seconds per phase) with intravenous contrast administration (0.2 mmol/kg Magnevist (Bayer, Berlin, Germany)) 2 ml/s starting after the first phase. Other parameters were: field of view of 38x38cm, with an acquisition matrix of 256 x 128, zero filled to 256 x 256, giving an in-plane resolution of 1.5 mm, slice thickness of 5 mm without gap, number of slices in the sagittal plan =14. In addition, a high resolution 3D SPGR sequence before contrast administration was acquired for delineation of the patellar bone for the DCE analyses. In-house developed software[4] was used to correct for patient motion during acquisition of the DCE images. All phases were rigidly registered in 3D using the image of the first phase as fixed image, the first phase image was registered to the high resolution SPGR image, and subsequently all DCE images were transformed accordingly. Our volume of interest (VOI) consisted of the patellar bone. Voxel-wise quantitative perfusion parameters (*k*ep) were calculated with a Tofts model using an arterial input function (AIF) computed from the popliteal artery.[2] Since precision of *k*ep varies spatially, weighted mean and standard deviation were computed over the VOI, with weights given by the reciprocal Cramér-Rao-Lower-Bound (indicating fit uncertainty).

Results: The Tofts model successfully fitted the measurements, see as example figure 1a. Over the entire dataset, the residue is close to the acquisition noise level. Weighted mean *k*ep values of the patellar bone of the 5 control subjects ranged between 0.27-0.42 min^{-1}. The mean weighted standard deviation in the VOI of the 5 control subjects was 0.186 min^{-1}, which was more than four times larger than the statistical uncertainty of this measurement, suggesting heterogeneous blood perfusion within the patella, see as example figure 1b.

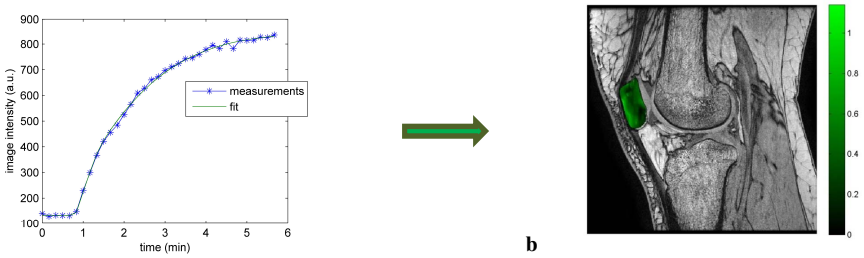

Figure 1: a. the fitted pharmacokinetic Tofts model (green) to the measured data (blue) in a single voxel. b. map of the perfusion parameter k_{ep} (values in 1/min) in the patella.

Discussion: Our patellar bone *k*ep values differ from reported *k*ep values for bone in the literature. For example, *k*ep values for the femur ranged between 3,48-3,85 min^{-1} in a study of Breault et al. using the Tofts model.[3] A possible explanation might be the use of an AIF measured from the data, which could be more accurate than an *a priori* assumed model. Our *k*ep value in muscle (approximately 1 min^{-1}) does corresponds to values reported in the literature. Comparison of values, however, is difficult due to a variety of different (semi)quantitative methods being used in literature. As consensus regarding optimal analysis methods and pharmacokinetic model is needed, we proceed optimizing our current method and have planned a systematic comparison of different methods.

Conclusion: The results suggest that our tailored DCE-MRI protocol and post-processing tool successfully extract the dynamic contrast enhancement from the measurements, and thus can be used to study patellar blood perfusion. Quantitative *k*ep maps even allow study of regional perfusion. This may yield important information on the etiology of PFPS.

References:

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