Quantitative First-Pass Perfusion with Whole-Ventricle Coverage Using 3D Through-Time Spiral GRAPPA

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TARGET AUDIENCE: Researchers and clinicians working in the field of quantitative myocardial perfusion imaging and cardiac MRI.

PURPOSE: Typical myocardial first-pass perfusion techniques suffer from insufficient myocardial coverage due to the limited time period available for data collection during each cardiac cycle. Because the uptake of contrast agent (CA) changes the image contrast in each RR interval, data collection spanning multiple heartbeats would lead to a misrepresentation of the contrast. Thus, data collection is limited to a single heartbeat, which in turn limits the spatial coverage possible for these types of scans. In order to enable the collection of the full 3D volume of the left ventricle each heartbeat, a highly accelerated 3D FLASH sequence with a stack-of-spirals trajectory has been applied in conjunction with a parallel imaging reconstruction [1]. In this work, these highly accelerated 4D images were used for absolute perfusion quantification over the entire left ventricle.

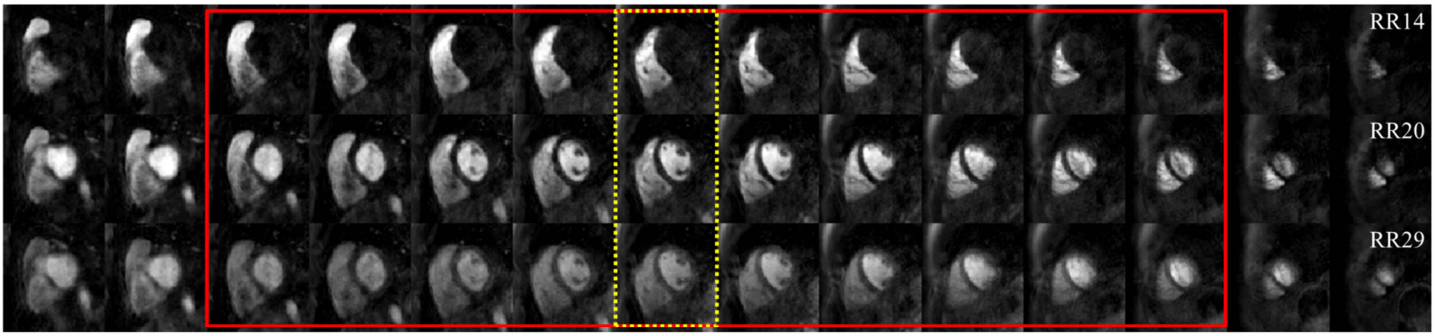

Fig. 1. Reconstructed partitions of the bolus injection for one of the volunteers at exemplary time points (top: peak RV at RR 14, center: peak LV at RR 20, bottom: peak myocardium enhancement at RR 29). The 10 partitions used for the quantification are indicated in red.

METHODS: Acquisition: In this IRB approved study, a myocardial first-pass perfusion experiment was carried out on two healthy volunteers. After the injection of the CA (Optimark™, Mallinckrodt Inc., St. Louis, MO), an ECG-gated, SR prepared 3D FLASH sequence (T_R: 4.7ms, T_E: 0.5ms, α: 10°, reconstructed matrix size: 192×192×16, resolution 1.8×1.8×8.0mm^3, breath-held) with an undersampled stack-of-spirals trajectory (R=6 in-plane: 8 of 48 arms per partition, R=2 and 6/8 partial-Fourier acceleration in partition direction: 6 of 16 partitions per slab) was applied over 40 consecutive heartbeats on a 3T whole-body scanner (Siemens MAGNETOM Skyra, Erlangen, Germany). A trigger delay was used to move the acquisition window of 226ms to diastole. To obtain an unsaturated arterial input function (AIF) for the quantification, a dual-bolus acquisition was applied (prebolus: 1ml, bolus: 4ml, saline flush: 15ml , flow rate: 3ml/s) [2]. Reconstruction: To reconstruct the missing data, two different calibration data sets (total scan time: 42.1s) were acquired post contrast. Each consisted of 10 repetitions of a fully-sampled, ungated and free-breathing version of the sequence described above without any preparation pulse. As described in [3], Cartesian GRAPPA was first performed to reconstruct the missing partitions (R=2) for each of the 8 spiral arms. Next, through-time spiral GRAPPA was used in-plane for the reconstruction of the missing spiral arms (R=6) of each partition. Last, an iterative POCS technique [4] was used to reconstruct the partitions missing due to the 6/8 partial-Fourier undersampling. Finally, the reconstructed datasets were gridded using the IRT toolbox [5]. Quantification: The quantification was performed separately for each partition using a customized software tool based on [6]. First, an AIF was estimated from the prebolus image series [2]. Next, tissue enhancement curves (TECs) were determined from the bolus image series (including rigid motion correction, segmentation of 6 sectors, partial volume and baseline correction [7]). These TECs were deconvolved by the AIF with the constraint of a Fermi function as residuum [8] to obtain absolute perfusion values (in ml/g/min) in 6 sectors of all slices containing relevant parts of the myocardium.

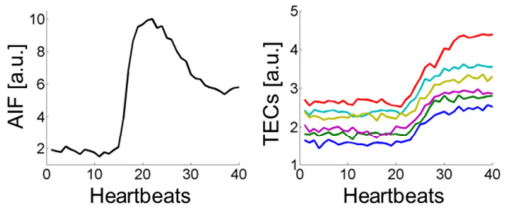

Fig. 2. AIF and TECs (before baseline correction) used for the quantification of the partition indicated in Fig. 1.

RESULTS: Fig. 1 shows 14 reconstructed slices of the bolus acquisition for volunteer 1 at different stages of the first-pass of CA. Aliasing artifacts caused by the high acceleration were removed by the reconstruction. AIF and TECs of a mid-ventricular slice (indicated in yellow in Fig. 1) are depicted in Fig. 2. Absolute perfusion values of all sectors are given in Fig. 3. Although an increase of the values in sector 3 (closest to the receiver coil array) indicates a bias caused by coil sensitivity variations, the mean perfusion value of 0.71 ± 0.22 ml/g/min of all evaluated slices (V1: 10 slices, V2: 7 slices) is in good agreement with standard literature [9].

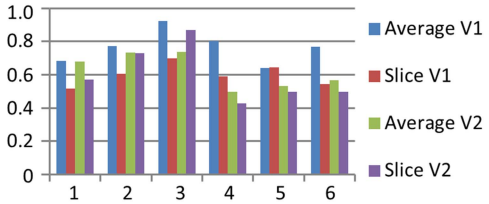

Fig. 3. Absolute perfusion values (ml/g/min) in all 6 sectors. Shown are averages over all partitions of each volunteer (V1: blue, V2: green) and a mid-ventricular partition of each volunteer (V1: red, V2: purple).

DISCUSSION: The stack-of-spirals acquisition with 3D through-time spiral GRAPPA reconstruction enables whole-ventricle coverage (16 partitions) within each cardiac cycle in a diastolic acquisition window of 226ms without any temporal averaging. The spatial resolution of 1.8×1.8×8.0mm^3 more than satisfies the requirements (<3mm in-plane, ≥ 3 slices) formulated e.g. in [10]. It should also be mentioned that in contrast to other comparable 3D techniques that achieve the high acceleration by applying spatial or temporal constraints [11,12,13], only parallel imaging and partial-Fourier techniques were used in this approach for a 16-fold acceleration. Most importantly, the perfusion values demonstrate that the reconstructed images are of a suitable quality for absolute quantification purposes and the obtained perfusion values are comparable to standard literature [9].

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