Initial Comparative Evaluation of a Five-Minute Comprehensive Cardiac MR Examination Using Highly Accelerated Parallel Imaging

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Introduction: The field of cardiovascular MRI (CMR) has evolved rapidly, providing new clinical and research applications across a broad spectrum [1]. CMR examinations may include evaluation of cardiac function (CINE), first-pass myocardial rest perfusion (PERF), coronary artery anatomy (CAI) and myocardial viability via delayed enhancement (DE), each of which is challenging due to the competing requirements of high spatial resolution, immunity to physiological motion, high signal-to-noise ratio, and practical total examination time[2-4].Multiple breath–hold (BH)or navigator-based (NAV) techniques are generally used to examine the entire heart in a standard routine protocols[5-13]. The feasibility of a 5-minute comprehensive whole heart protocol using highly accelerated parallel imaging (PAT) was recently reported [14]. In the current study, we have incorporated this 5-minute comprehensive protocol into routine clinical CMR examinations and have performed initial comparisons between a standard (predominantly 2D) protocol and the new 5-minute 3D comprehensive protocol arranged to occur within a single common scan session.

Methods and Materials: All MRI examinations were performed on a whole-body 1.5T scanner (MAGNETOM Avanto, Siemens, Erlangen, Germany) equipped with a high performance gradient system (max. amplitude: 40 mT/m, max. slew rate: 200 mT/m/ms) and a 32-element cardiac coil array (InVivo, Florida). Following informed consent, 12 subjects (10 healthy volunteers, mean age 33 +/- 13 and 2 patients with suspected CAD) were recruited. In order to allow comparison within a single clinical examination, the 5-minute comprehensive protocol was incorporated into a standard routine protocol before 2D DE. The workflow is shown in Figure 1. Two contrast injections were used – one for the 2D and one for the breath-held 3D perfusion scan – with a single dose each (0.1mmol/kg) of contrast agent (Berlex Magnevist, Schering AG) at 5ml/s followed by a saline flush (20ml at 5ml/s), which yielded a cumulative 0.2mmol/kg does of gadolinium contrast on board to ensure sufficient enhancement for the final DE scans. The time between the first contrast injection and the 3D DE lasted approximately 10-15 minutes. Imaging parameters used in the 2D and 3D protocols are surveyed in Table 1. To make sure that reconstruction time did not impede workflow, most 3D CINE and PERF datasets were retro-reconstructed after the examinations.

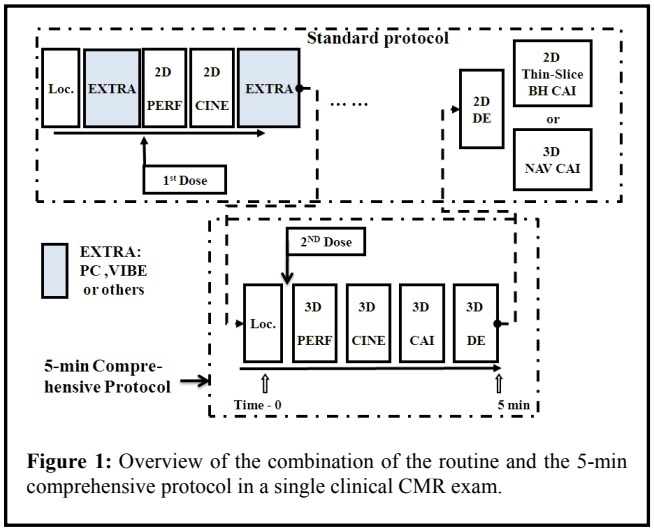

Figure 1: Overview of the combination of the routine and the 5-min comprehensive protocol in a single clinical CMR exam.

Table 1: Typical Imaging parameters used in the standard and the 5-min comprehensive protocol

Type	Perfusion		CINE		DE		CMRA	
	3D	2D	3D	2D	3D	2D	3D (SBH)	3D (NAV)
Pulse Sequence	FLASH	SSFP	SSFP	SSFP	SSFP	SSFP	SSFP	**SSFP**
PAT	TGRAPPA	TGRAPPA	TGRAPPA	TGRAPPA	GRAPPA	GRAPPA	GRAPPA	**GRAPPA**
Orientation	Short axis	Short axis	Short axis	Short axis	Short axis	Short axis	Trans.	**Trans.**
Matrix	76x128x10	122x192x3	109x176x20	139x192x13	144x144x20	101x192x13	192x192x20	**192x192x110**
FOV (mm2)	340x340	287x340	340x340	254x280	340x340	255x340	340x340	**320x320**
Voxel Size (mm)	4.4x2.6x8	2.3x1.8x8	3.1x1.9x5	1.8x1.5x8	2.4x2.4x6	2.5x1.8x8	1.8x1.8x2	**1.7x1.7x2**
Acceleration R	4 x 2	2	4 x 2	2	3 x 2	2	4 x 2	**2**
TI/TR/TE (ms)	130/270/0.9	120/220/1.1	-/45/1.1	-/39/1.2	~250/3.0/1.	~250/3.0/1.	-/2.4/1.2	**-/2.6/1.4**
BW(Hz/pixel)	1392	1370	915	930	500	1350	500	**590**
Flip Angle	10	70	70	70	70	70	70	**90**
Scan Time	**1 BH**	**1BH**	**1BH**	**7~14BHs**	**1BH**	**Multi BHs**	**1BH**	**8~13min**

Results: All subjects completed the full protocol. Figure 2 shows that only 3 slices were acquired in 2D PERF; while 10 slices covering the heart from base to apex were acquired in 3D PERF. Figure 3 shows typical results for whole heart 2D CINE (8 out of 13 slices acquired in 7 BHs) and single BH 3D CINE (8 out of 20 slices). Figure 4 shows representative views of the LCX and LAD derived from a 3D BH and NAV CAI. Figure 5 shows representative single BH whole heart 3D DE images with acceleration factor R=6, which enabled acquisition of all data at the same time point of the contrast agent kinetics, ensuring uniform suppression of healthy myocardium.

Conclusions and Discussions: A 5-min comprehensive whole heart protocol offering comparatively high quality results in few BHs was successfully incorporated into and compared with a standard routine protocol. 3D PERF and 3D DE imaging showed relatively low SNR due to noise amplification caused by the use of high acceleration factors. However, complementary acceleration techniques such as compressed sensing have already shown promise for further acceleration of 3D PERF without sacrificing SNR [16]. Building on our preliminary results, studies in a growing patient cohort are underway to evaluate the clinical efficacy of the proposed accelerated 5-min protocol as compared with the conventional protocol.

Reference: [1]Kramer, C.M., et al., JCMR, 2008; [2]Plein, S., et al., Radiology, 2002; [3]Foo, T.K., et al., Radiology, 2005; [4]Gutberlet, M., et al., 2006; [5]Mascarenhas, N.B., et al., AJR 2006; [6]Parish, V., et al., JMRI, 2010; [7]Davarpanah, A.H., et al., Radiology, 2010; [8]Niendorf, T., et al., MRM, 2006; [9]Okada, T., et al., EJR, 2009; [10].Zhu, Y., et al., MRM, 2004; [11]Park, J., et al., MRM, 2005; [12]Shin, T., et al., JCMR, 2008; [13]Foo, T.K., et al., Radiology, 2004; [14]Xu, J., ISMRM, 2009, P725; [15]Xu, J., ISMRM, 2010,P670;[16] R. Otazo, et. al,ISMRM 2010.

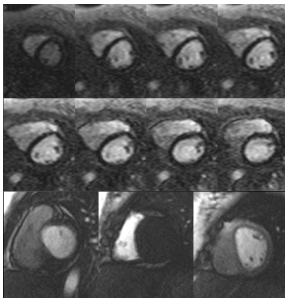

Fig. 2: Top 2 rows show 8 of 10 slices from 3D PERF. **Bottom)** representative 3 of 3 slices from 2D PERF.

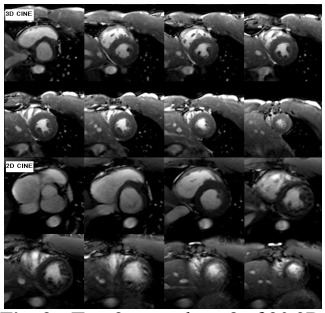

Fig. 3: Top 2 rows show 8 of 20 3D CINE slices, all acquired in a single BH; **Bottom** 2 rows show 8 of 13 2D CINE slices acquired in 7 BHs.

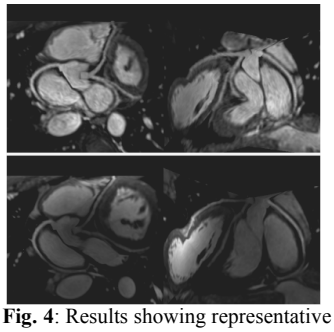

Fig. 4: Results showing representative views of the LCX /LAD obtained from **Top)** single BH CAI and **Bottom)** NAV CAI in 8 min.

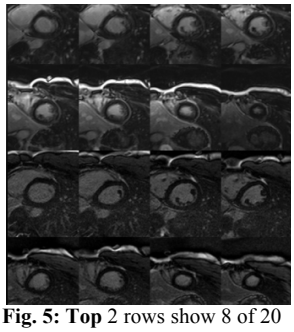

Fig. 5: Top 2 rows show 8 of 20 3D DE slices acquired in a single BH; **Bottom** 2 rows show 8 of 13 2D DE slices in 13 BHs.