

Whole-body MR imaging with continuously moving table and multiplanar reformations: toward parameter optimization for SSFP imaging in patient examinations

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Introduction: Magnetic resonance (MR) imaging, with its lack of ionizing radiation and its large range of possible image contrasts, has shown increasing clinical utility for the diagnosis of abnormalities. Imaging with continuous moving table and a balanced SSFP sequence has been evaluated and shown to be feasible (1). Such moving table protocols may become increasingly important for extending conventional MR protocols to whole-body coverage, especially for the detection and staging of tumours. An ideal whole-body MRI exam would be able to scan chest, abdomen and pelvis in a single breath hold with a spatial resolution comparable to current clinical protocols. Using multiplanar reformations, ideally all three planes can be evaluated from a single dataset (2). The purpose of this study was to evaluate the performance of a balanced 2D axial SSFP (steady state free precession) sequence with sagittal and coronal reformations, acquired during continuously moving table for whole-body MR imaging, and to optimize sequence parameters.

Materials and Methods: All examinations were performed on a 1.5 T scanner (Avanto, Siemens) using 2D axial SSFP sequences. In a first step a commercially available MR phantom with structures of varying thicknesses (Fig. 1) was used to compare the original axial slices as well as the coronally and sagittally reconstructed images of sequences with different slice thicknesses (3-6mm), table velocities (20-22mm/s) and matrices (128-256) to verify the method's ability to resolve small structures in the direction of table motion (z-direction). The parameters were chosen to allow imaging the chest, abdomen and pelvis in a breath hold of 30 seconds for each sequence (Table 1). Two independent observers evaluated the reconstructed images for sharpness of defined structures (1= extremely sharp, 4= not identifiable) and compared them with the gold standard, a reference scan with stationary table (3D spoiled gradient echo sequence with 1x1x1mm resolution). In a second step, the three best parameter combinations were used for whole-body imaging in volunteers (TR= 2.4/ TE= 1.1/ FOV= 400x300x1800mm, 4/8 partial Fourier). The volunteers were positioned head-first in the MR scanner, and a breath hold was performed during scanning the chest and abdomen. The images were visually inspected by two radiologists. Sharpness of anatomical structures (portal vein, vertebral bodies, ascending aorta, pulmonary arteries) was evaluated for each sequence using the 4-point-scale. Differences were assumed to be statistically significant with a p-value < 0.05 (Wilcoxon rank test).

Results: The best-rated parameter sets in the phantom were those with a slice thickness of 6 mm, both with a mean sharpness value of 2.25 (significantly different compared to 2.5 and 3.1 in examinations with 3 or 4mm slices and lower matrices). Figure 1 shows the reconstructed images with stationary table (a) and the 4 different parameter constellations (b-e). The total scan time for imaging in volunteers was between 81 and 88 s for a z-coverage of 1800 mm. Figure 2 shows axial as well as sagittally and coronally reconstructed images of a healthy volunteer. For all examined parameter combinations, good image quality was obtained not only in the axial slices but also in reformatted planes, with a mean value of 2.3 in the images with 6mm slices compared to 2.6 in the 4mm exam.

Conclusion: Our approach allows scanning the whole body while resolving even small structures while keeping the time constraint for a single breath hold during imaging the thorax and abdomen. Based on these results, we recommend a table velocity of 20-22mm/s with a slice thickness of 6mm to get the best results. A slice overlap does not seem to be necessary in subjects capable of holding their breath. It would be desirable to create also other moving table sequence types in 2D and 3D acquisition modes to compete with current clinical multi-contrast protocols.

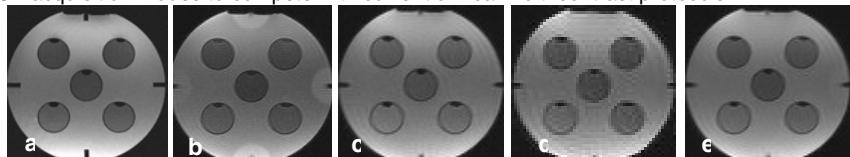
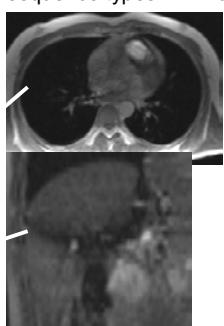
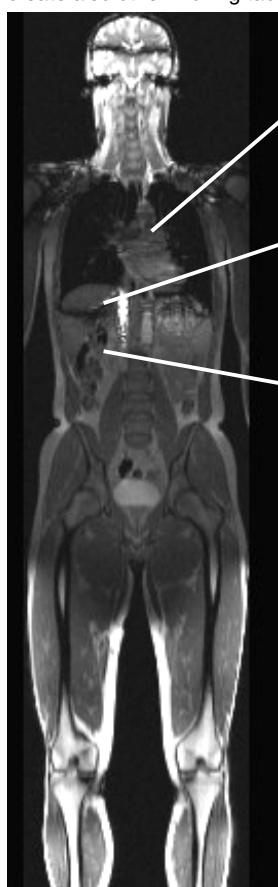


Fig.1: Axial 2D SSFP phantom image using 4 different parameter combinations (Table 1) (b-e). (a) The reference scan.

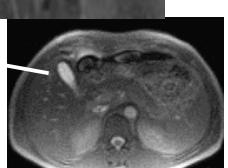


Fig.2: Whole-body MRI with axial 2D SSFP and sagittal and coronal reformatted images. Even smaller structures like the portal veins can be distinguished.

Tab. 1: Parameters of the different SSFP sequences for the phantom acquisitions (Fig.1) and volunteers (Fig.2).

	Slice thickness	Table velocity	Matrix	Total acquisition time	Voxel size (mm)	Slice overlap
Phantom Fig.1b Volunteer	6 mm	22 mm/s	256	0:16 min 1:21 min	1.6x1.6x6	No
Phantom Fig.1c Volunteer	4 mm	20 mm/s	192	0:18 min 1:28 min	2x2x4	No
Phantom Fig.1d Volunteer	3 mm	21 mm/s	128	0:15 min N/A	3x3x3	No
Phantom Fig.1e Volunteer	6 mm	20 mm/s	192	0:18 min 1:28 min	2x2x6	2mm

References

1. Barkhausen J et al. Whole-body MR imaging in 30 seconds with real-time true FISP and a continuously rolling table platform: feasibility study. Radiology.2001;220:252-6.
2. Zenge MO et al. Whole-body magnetic resonance imaging featuring moving table continuous data acquisition with high-precision position feedback. Magn Res Med 2005;54:707-711.