



Iterative reconstruction of radially-sampled ^{31}P bSSFP data using prior information from ^1H MRI

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ABSTRACT

The purpose of this study is to improve direct phosphorus (^{31}P) MR imaging. Therefore, 3D density-adapted radially-sampled balanced steady-state free precession (bSSFP) sequences were developed and an iterative approach exploiting additional anatomical information from hydrogen (^1H) data was evaluated. Three healthy volunteers were examined at $B_0 = 7\text{ T}$ in order to obtain the spatial distribution of the phosphocreatine (PCr) intensities in the human calf muscle with a nominal isotropic resolution of 10 mm in an acquisition time of 10 min. Three different bSSFP gradient schemes were investigated. The highest signal-to-noise ratio (SNR) was obtained for a scheme with two point-reflected density-adapted gradients. Furthermore, the conventional reconstruction based on a gridding algorithm was compared to an iterative method using an ^1H MRI constraint in terms of a segmented binary mask, which comprises prior knowledge. The parameters of the iterative approach were optimized and evaluated by simulations featuring ^{31}P MRI parameters. Thereby, partial volume effects as well as Gibbs ringing artifacts could be reduced. In conclusion, the iterative reconstruction of ^{31}P bSSFP data using an ^1H MRI constraint is appropriate for investigating regions where sharp tissue boundaries occur and leads to images that represent the real PCr distributions better than conventionally reconstructed images.

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1. Introduction

Non-proton MRI has become a matter of intense research in recent years, as a noninvasive approach to obtain functional tissue information in living cells. The high-energy metabolism of the human body is heavily affected by phosphorus (^{31}P)-containing compounds. Hence, the objective of ^{31}P MRI studies is to contribute data for a better understanding of common physiological diseases such as diabetes mellitus, myopathies and cancer [1–3]. Due to a comparatively small gyromagnetic ratio ($\gamma_{^{31}\text{P}} = 17.24 \frac{\text{MHz}}{\text{T}}$, $\gamma_{^1\text{H}} = 42.58 \frac{\text{MHz}}{\text{T}}$), longitudinal relaxation times in the order of seconds, and low *in vivo* concentrations in the human body, ^{31}P MRI suffers from a low signal-to-noise ratio (SNR) and therefore requires long measurement times. Compared to conventional hydrogen (^1H) MRI, the *in vivo* ^{31}P MR signal is about four orders of magnitude smaller [4–6].

Nevertheless, the broad chemical-shift range facilitates *in vivo* ^{31}P magnetic resonance spectroscopy (MRS), which has been investigated for more than thirty years [7–10]. Ultra-high field MRS could improve those investigations conspicuously [11–14]. Also the feasibility of direct ^{31}P mapping has been demonstrated although the spatial resolution

was limited. To overcome the low *in vivo* SNR per unit time, several approaches were proposed including turbo spin echo (TSE) [15–18], fast low angle shot (FLASH) [19,20], or balanced steady-state free precession (bSSFP) [21,22] sequences.

Due to the poor SNR of ^{31}P MRI, only a coarse spatial resolution can be obtained in acceptable acquisition times. Thus, partial volume effects are a major limitation of ^{31}P MRI resulting in differences between represented and expected tissue intensities, which can be described by two phenomena [23]. The finite resolution effect is caused by spillover between regions resulting in blurring and therefore larger but dimmer sources. This is due to the convolution of the actual source with the point spread function of the imaging system. The tissue fraction effect is induced by the image sampling on a voxel grid. Since tissue boundaries typically do not coincide with voxel positions, a single voxel can include various types of tissues. Methods for the quantitative evaluation of partial volume effects as well as partial volume corrections have already been discussed in other scientific publications [24–26].

In order to enhance the SNR and to reduce Gibbs ringing artifacts of radially acquired non-proton images, gridding reconstructions in combination with smoothing filters are applied conventionally [27,28]. However, promising results have been obtained by means of subsampling methods such as compressed sensing [29,30] applied in recent non-proton MRI studies [31,32]. In MRI, compressed sensing is employed for reconstructing undersampled images while reducing

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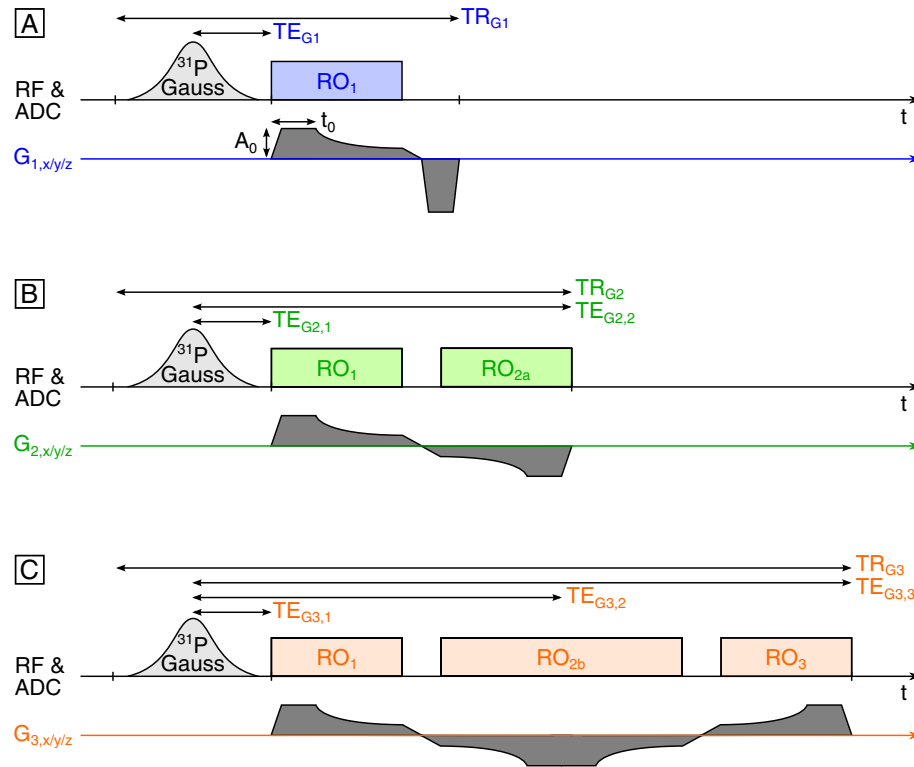


Fig. 1. Schemes of 3D density-adapted radially-sampled bSSFP sequences (not to scale). Frequency selectivity is achieved by Gaussian-shaped ^{31}P excitation pulses. (A) Gradient scheme G_1 features a straightforward layout with a single readout and a rewinder gradient [39]. (B) Gradient scheme G_2 is composed of two point-reflected gradients to sample k -space from the center to the periphery and back acquiring two different contrasts [50]. (C) Gradient scheme G_3 extends scheme G_2 in order to obtain additional contrasts at the expense of a longer repetition time.

incoherent undersampling artifacts. This concept minimizes the acquisition time, but requires three premises in order to reconstruct the compressed images [33]: First, the desired image should have a sparse representation in a known transformation domain. Second, the image should be reconstructed by a non-linear method. Third, the artifacts in the sparsifying domain should be incoherent. This type of incoherence is enhanced in radial rather than Cartesian k -space sampling, since undersampling artifacts already show a noise-like behavior in the image domain [34]. Furthermore, the quality of the reconstruction will be improved if a good balance between undersampling and averaging

is found [35]. Compressed sensing also enables the inclusion of prior knowledge by regularizations [36]. Thus, MR images of different nuclei can be correlated as shown for iterative reconstructions of sodium (^{23}Na) data with an ^1H MRI constraint in terms of a support region that matches the object shape [37,38]. The quality of the ^{23}Na image is thereby improved by employing high-resolution ^1H information.

The aim of this work is to present a method for direct *in vivo* ^{31}P MRI, obtaining a high SNR along with an appropriate resolution within an acceptable acquisition time. Therefore, the conventional gridding reconstruction algorithm for radially sampled sequences is opposed to an iterative reconstruction with an ^1H MRI constraint, assuming that phosphocreatine (PCr) is present with high levels in human muscle tissue. Quality Assessment in terms of artifact reduction and applicability is supported by simulations based on an analytical phantom. Furthermore, three radial bSSFP sampling schemes were compared in order to find a sequence, which is suitable for the iterative approach and additionally provides a high SNR per unit time.

2. Material and methods

2.1. Experimental setup

A 7 T whole-body MR system (Magnetom 7 T, Siemens Healthcare, Erlangen, Germany) was employed to investigate the PCr distribution in the human calf muscle. Three healthy volunteers (all female, 25–28 y/o) were examined using a double-resonant ($^{31}\text{P}/^1\text{H}$) quadrature birdcage coil (Rapid Biomed GmbH, Würzburg-Rimpar, Germany) with an inner diameter of 26 cm. The coil was optimized for examinations of the human head but also enables investigations of extremities. The study was approved by Heidelberg University's ethical review board.

Table 1

Measurement parameters for direct ^{31}P MRI applying the 3D density-adapted radially-sampled bSSFP sequences at $B_0 = 7$ T. The excitation frequency was set on the PCR resonance.

Gradient schemes	G_1	G_2	G_3
Acquisition time TA [min]		10	
Isotropic resolution [mm ³]		$10 \times 10 \times 10$	
Matrix size [px ³]		$32 \times 32 \times 32$	
Flip angle α [°]		30	
FWHM of excitation pulse [ppm]		3.5	
FWHM of excitation pulse [Hz]		420	
Total duration of excitation pulse [ms]		4.58	
Radial read out time T_{RO} per sample [ms]		1	
Number of projections [–]		1000	
Number of radial samples [–]		32	
Maximum gradient amplitude A_0 [mT]		3.7	
Gradient peak time t_0 [ms]		0.5	
Echo times $TE_{x,1}$ [ms]	2.34	2.34	2.34
Echo times $TE_{x,2}$ [ms]	–	4.87	4.87
Echo times $TE_{x,3}$ [ms]	–	–	7.20
Repetition times TR_x [ms]	6.36	7.21	9.54
Number of possible averages in TA [–]	95	84	63

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