MR Techniques for Quantifying Myocardial Perfusion

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Synopsis

Myocardial perfusion imaging is an essential tool for characterising ischemic heart disease. Moreover, quantitative myocardial perfusion methods that provide pixel-wise quantitative myocardial perfusion maps are increasingly being applied as an alternative to visual inspection. Newer methods combine quantitative imaging with acceleration techniques and motion compensation to overcome current limitations of the technique, and thus, improve spatial resolution and heart coverage, reduce image degradation due to motion and accurately detect perfusion defects. In addition, fully automated workflows are facilitating the integration of quantitative myocardial perfusion into clinical practice by making it faster and easier to use.

Introduction

First-pass perfusion cardiac MR (pCMR) enables the non-invasive detection of ischemic heart disease.¹⁻³ This technique captures a series of images during the rapid passage of a contrast bolus through the heart. Acquisitions are electrocardiogram (ECG)-synchronised with the cardiac cycle and patients are instructed to hold their breath for as long as they can, to reduce image degradation due to cardiac and respiratory motion. Thus, conventional pCMR only permits the acquisition of 3-4 non-contiguous short-axis slices with moderate spatial resolution (~2.5mm). Moreover, diagnostic accuracy of pCMR may be compromised by respiratory motion artefacts because breath-holding can be challenging for patients, incomplete heart coverage, and dark-rim artefacts (false positives) due to low image resolution. In addition, images are often interpreted based on visual assessment, which only has high diagnostic accuracy when performed by highly trained operators.⁴ Recently, there has been a growing interest in developing automated pCMR methods that provide pixel-wise quantification of myocardial perfusion since they provide operator-independent, objective and reproducible results.³

Technical Aspects

Quantitative imaging: Tracer kinetic modelling

Perfusion quantification refers to the estimation of physiological parameters related to the microvascular environment (e.g., myocardial blood flow in ml/min/g, MBF) from the contrast enhancement obtained during the first pass of the contrast bolus, through the cardiac chambers and myocardium (Fig. 1).³ Quantitative imaging requires knowledge of the contrast agent concentration in the myocardial tissue and arterial input function (AIF; typically measured in the left ventricle blood pool). It is often assumed that there is a linear relationship between the MR signal intensities and the contrast agent concentration.

Quantitative pCMR has been performed using either the Fermi deconvolution method or (more complex) tracer-kinetic modelling.^{3,5,6} The Fermi method determines MBF through deconvolution of the AIF from the myocardial tissue concentration curve and by fitting an empirical-mathematical model. On the other hand, tracer-kinetic models are based upon physiological assumptions about the interaction between the contrast agent and different tissues and thus, can be used to extract several quantitative physiological parameters. However, the fitting problem can be less stable.

Sequences for quantitative pCMR: How to get data for accurate quantification of myocardial perfusion

The most commonly used pulse sequence for pCMR is a 2D saturation recovery pulse sequence. One major challenge with quantitative imaging is the lack of linearity between the MR signal intensity and the contrast agent concentration at high contrast agent concentrations. The concentration of contrast in the blood is much higher than in the myocardium, resulting in the saturation of the AIF.

The dual-bolus and dual-sequence methods have been proposed to handle the AIF saturation.⁷⁻¹¹ The dual-bolus method uses a low dose bolus to measure the AIF followed by a high dose bolus for myocardial imaging. The dual-sequence method acquires a low-resolution slice with a short saturation-recovery time to estimate the AIF, together with high-resolution myocardial slices, without the need for additional contrast injection, but requires specialised CMR software.

Accelerated pCMR: Quantitative imaging with high resolution and/or heart coverage

Parallel imaging, compressed sensing and low-rank reconstruction methods have been proposed to accelerate 2D pCMR scans and achieve the necessary spatial resolution to eliminate dark-rim artefacts and improve diagnostic confidence.¹²⁻¹⁷ These methods explore the redundancies or compressibility of pCMR images to reduce the amount of (k-t)-space data required for image reconstruction. However, these methods still suffer from limited cardiac coverage. 2D simultaneous multi-slice sequences have been combined with undersampling techniques to improve both spatial resolution and coverage.^{18,19} 3D pCMR with whole-heart coverage has been achieved using advanced k-t undersampling strategies without ECG-synchronisation and/or breath-holding.²⁰⁻²³ However, 3D pCMR methods often sacrifice spatial resolution.

Typically, acceleration methods indirectly generate quantitative myocardial perfusion maps by first reconstructing individual dynamic contrastenhanced images, which are then converted to contrast agent concentration and, finally, tracer-kinetic modelling is used to generate quantitative maps (Fig.1). Recently, a model-based reconstruction method has been proposed to directly estimate quantitative perfusion maps and achieve extremely high acceleration rates.^{24,25}

Deep learning-based methods have gained popularity in CMR due to their potential to significantly speed up reconstructions.²⁶ Unfortunately, large amounts of fully sampled reference data are required for training these methods, which are not available in pCMR. Therefore, self-supervised deep learning pCMR methods have been proposed to reconstruct the dynamic pCMR times series from undersampled data without requiring fully sampled data.²⁷⁻²⁹

Automated workflows: Making quantitative pCMR easier to use and more accessible

Quantitative pCMR can be complex and time consuming, requiring manual segmentation and labelling of regions of interest in a large number of images. Automatic in-line vendor specific and vendor neutral commercial quantitative pCMR solutions have been proposed to enable fast, reproducible and operator-independent estimates of myocardial perfusion.^{11,30} These methods include respiratory motion correction, automatic detection of the AIF, segmentation and pixel-wise estimation of perfusion maps.

An in-line dual-saturation multi-echo Dixon QFPP-CMR framework (FOSTERS), with low-rank and sparsity constrained reconstruction, has been proposed to facilitate free-breathing and high-resolution pCMR.³¹ It automatically estimates non-rigid respiratory motion from fat-only images and generates high-resolution pixel-wise perfusion maps from motion-corrected water-only images.

Artificial intelligence-based solutions have also been proposed to automate the time-consuming and subjective pre-processing step of quantitative pCMR, such as segmentation and identification of the AIF.³²⁻³⁴

Conclusions

Quantitative pCMR is an established non-invasive test for the detection of ischemic heart disease. However, accurate quantification requires timeconsuming manual processing steps and expert knowledge. This has prevented the widespread clinical adoption of quantitative pCMR. Recently, fully automated quantitative pCMR methods have been proposed to provide operator-independent, accurate and reproducible results in a faster and simpler way. These methods automate several tasks, such as reconstruction, motion correction, segmentation, AIF estimation and pixel-wise estimation of myocardial perfusion maps. Automated qCMR methods can also be combined with acceleration techniques to increase the spatial resolution and/or heart coverage, to improve the detection of perfusion defects.

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Figures



Figure 1. The general steps of quantitative myocardial perfusion MR. 1) Acquire perfusion CMR perfusion data, 2) reconstruct, 3) convert signal intensity data to contrast agent concentration and 4) estimate the quantitative myocardial perfusion maps.