

M. K. Ivancevic (Geneva/SWITZERLAND), P. Thévenaz (Lausanne/SWITZERLAND), A. G. Somsen (Geneva/SWITZERLAND), A. Righetti (Geneva/SWITZERLAND), D. Didier (Geneva/SWITZERLAND), J. Vallée (Geneva/SWITZERLAND)

The Abstract

Purpose/Introduction: First-pass cardiac MR perfusion imaging was initially performed only with 1 or 2 slices. With increasing performances of MR scanners due to stronger gradients, and new temporal sampling strategies, 2D multi-slice whole coverage of the heart has been enabled. This, however, increases the data flow to be analyzed. The standard manual ROI-based perfusion analysis getting more time-consuming on an increasing quantity of data raises the interest of an automated data analysis method. In this study we present a pixel-wise, semi-automated and user-independent cardiac perfusion analysis method.

Methods: Eight patients with a history of myocardial infarction and no acute symptoms were included in this study. Infarction was detected in 5 patients by TI-SPECT used as reference. MR Imaging was carried out on an Philips Eclipse 1.5T MR system with an RF-FAST sequence and following parameters: TI/TR/TE 28/3.74/1.5 ms, 50 kHz bandwidth, 40° FA, 90°-180° preparation pulses, 112×128 matrix, mean FOV 37 cm (±2 cm). A cardiac surface coil and ECG trigger were used. Eight slices were acquired during three to six cardiac cycles, depending on patient's heart rate. A bolus of 0.08 mmol/kg Gd-DTPA was injected in a brachial vein at 0.5 ml/s injection rate followed by 10 ml of isotonic saline with a Medrad Spectris MR injector. Central short axis slices were chosen for the analysis. A motion correction algorithm was first applied, using IDL 5.5. LV cavity was segmented manually for the arterial input function, and k1, k2 flow-related blood-tissue transfer coefficients were calculated automatically in each pixel solving the one compartment model equation: $dC_{myo}(t)/dt = k_1 C_{art}(t) - k_2 C_{myo}(t)$

In the k1 maps obtained, pixel values were averaged in myocardial regions of interest (ROI), two per following sectors: anterior, lateral, inferior and septal, corresponding to the segmentation used in the TI-SPECT images.

Results: In 40 analyzed sectors, 12 were infarcted and 38 normal. A 20% (±11) variability was found in normal sectors (s.d./mean per patient, $p > 0.38$), and a 45% (±24) reduction of k1 was found on average in infarcted regions ($p < 0.03$). The variability found in normal regions does not exceed variability reported in literature with manual ROI definition.

Discussion/Conclusion: This study shows the feasibility of a semi-automatic, parametric, cardiac perfusion analysis. Despite initial limits such as spill-over contamination from the cavity, and difficult distinction of the endocardial wall due to partial volume, a hypo-perfusion was detected in the infarcted areas. The algorithm presented here accelerates the myocardial perfusion analysis procedure.