Accurate Automatic Papillary Muscle Identification for Quantitative Left Ventricular Mass Measurements in Cardiac Magnetic Resonance Imaging[1]

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Rationale and Objectives. We sought to evaluate the automatic detection of the papillary muscle and to determine its influence on quantitative left ventricular (LV) mass assessment.

Materials and Methods. Twenty-eight Yorkshire-Landrace swine and 10 volunteers underwent cardiac magnetic resonance imaging (CMR) of the left ventricle. The variability in measurements of LV papillary muscles traced automatically and manually were compared to intra- and interobserver variabilities. CMR-derived LV mass with the papillary muscle included or excluded from LV mass measurements was compared to true mass at autopsy of the Yorkshire-Landrace swine.

Results. Automatic LV papillary muscle mass from all subjects correlated well with manually derived LV papillary muscle mass measurements ($r = 0.84$) with no significant bias between both measurements (mean difference ± SD, 0.0 ± 1.5 g; $P = .98$). The variability in results related to the contour detection method used was not statistically significant different compared to intra- and interobserver variabilities ($P = .08$ and $P = .97$, respectively). LV mass measurements including the papillary muscle showed significantly less underestimation (−10.6 ± 7.1 g) with the lowest percentage variability (6%) compared to measurements excluding the papillary muscles (mean underestimation, −15.1 ± 7.4 g percentage variability, 7%).

Conclusion. The automatic algorithm for detecting the papillary muscle was accurate with variabilities comparable to intra- and interobserver variabilities. LV mass is determined most accurately when the papillary muscles are included in the LV mass measurements. Taken together, these observations warrant the inclusion of automatic contour detection of papillary muscle mass in studies that involve the determination of LV mass.

Key Words. Magnetic resonance imaging; papillary muscle; left ventricular mass

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The measurements of left ventricular (LV) function by cardiac magnetic resonance imaging (CMR) are accurate and reproducible compared to those obtained through other imaging modalities (1–4). Measurement of LV mass by CMR is also highly reproducible, but both significant underestimation and overestimation in comparison with LV mass at autopsy have been reported (5,6). In previous CMR studies of LV mass, the papillary muscles were typically excluded because the manual tracing required to measure these complex structures is time consuming. Recent improvements in CMR sequences have increased

both the resolution and contrast ratios, making it easier to distinguish between blood pool and muscle (7). As a result, the papillary muscles are presently easier to identify. These improvements in CMR combined with modern analysis software allow automatic identification of papillary muscle, within a short time frame. This study compares the in vivo measurement of LV papillary muscle mass using automatically drawn contours on CMR scans with those obtained manually as well as with ex vivo LV mass measurements at autopsy.

MATERIALS AND METHODS

Animals

Twenty-eight Yorkshire-Landrace swine (35–50 kg) were sedated with 20 mg/kg ketamine and 1 mg/kg midazolam intramuscularly, anesthetized with 12 mg/kg thiopental intravenously, intubated, and mechanically ventilated with a 1:2 mixture of oxygen and nitrogen. Anesthesia was maintained with fentanyl (12.5 μg/kg/hour). All 28 swine underwent magnetic resonance imaging (MRI) and were sacrificed the next day. Subsequently, the heart was removed and the left ventricle was isolated by dissecting out the mitral and aortic valves, atria, and right ventricle. Experiments complied with *The Guide for Care and Use of Laboratory Animals* of the National Institutes of Health (NIH Publication No. 86-23, revised 1996) and were approved by the Erasmus Medical Center Animal Care Committee.

Volunteers

A total of 10 healthy volunteers with no history of cardiac disease were studied. Their mean age was 30 $\pm$ 4 years. Sixty percent ($n = 6$) of our patient population were male. Exclusion criteria were all the standard contraindications for magnetic resonance studies. The study was approved by the institutional review board, and each subject gave informed consent for participation in this study.

MRI Protocol

A similar imaging protocol was used for the swine and for the volunteers. MR images were acquired using a 1.5-T scanner (Signa CV/*i*; GE Medical Systems, Milwaukee, WI). A dedicated four-element phased-array receiver coil was used for imaging the swine, and an eight-element phased-array receiver coil was used for imaging the volunteers. To minimize the influence of cardiac and respiratory motion on data collection, we used repeated breath-holds, which were achieved in the swine by turning off the ventilator temporarily and gating to the electrocardiogram. Cine MRI was performed using a steady-state free-precession technique (FIESTA). Imaging parameters were 24 temporal phases per slice, 12 views per segment; voxel size of 1.8 $\times$ 1.5 $\times$ 8 mm for the volunteers and 2.0 $\times$ 1.9 $\times$ 8 mm for the swine; repetition time of 3.0–3.6 ms; time to echo 1.4 ms; flip angle 45°; number of averages 0.75. To cover the entire left ventricle, 6–12 consecutive slices of 8 mm were planned in short-axis view perpendicular to the long axis of a four-chamber view and a two-chamber view.

Data Analysis

All the images were transferred to a remote workstation for analysis using the CAAS-MRV program (version 3.1; Pie Medical Imaging, Maastricht, The Netherlands). The algorithm has been previously described (8). In brief, the algorithm for the endoluminal contour draws heavily on the concept of fuzzy objects, in which image elements (pixels, voxels) exhibit a similarity or "hanging togetherness" both in geometry and in gray-scale values. The algorithm will properly differentiate the papillary muscles located inside the left ventricle from the blood volume. In the last step, a smooth convex hull is created to mark the general endocardial border.

For the purpose of this study, the delineation of the papillary muscles should be fully independent of the endocardial border detection, which should not be altered during repetitive analysis. Therefore, the software was extended with an extra procedure for extracting the papillary muscles automatically after the definition of the endocardial and epicardial contours by using a threshold technique and a filter operation to reduce the inhomogeneous gray-scale distribution caused by the surface coil. The threshold is derived from a statistical analysis of the intensity information inside the epicardial contour in each frame after preprocessing. Two observers blinded to the post-mortem results delineated the contours of the papillary muscles manually both in animals and in volunteers. By instruction, structures less than 4 mm^2 and not in contact with the papillary muscle in an adjacent slice should be considered as trabeculations and not be included in the papillary volume. The first observer delineated the papillary contours for a second time to define the intraobserver variability. The automatic contour detection of the papillary muscles was