Automated quantification of myocardial perfusion SPECT using simplified normal limits

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Background. **To simplify development of normal limits for myocardial perfusion SPECT (MPS), we implemented a quantification scheme in which normal limits are derived without visual scoring of abnormal scans or optimization of regional thresholds.**

Methods and Results. **Normal limits were derived from same-day TI-201 rest/Tc-99m-sestamibi stress scans of male (n = 40) and female (n = 40) low-likelihood patients. Defect extent, total perfusion deficit (TPD), and regional perfusion extents were derived by comparison to normal limits in polar-map coordinates. MPS scans from 256 consecutive patients without known coronary artery disease, who underwent coronary angiography, were analyzed. The new method of quantification (TPD) was compared with our previously developed quantification system and visual scoring. The receiver operator characteristic area under the curve for detection of 50% or greater stenoses by TPD (0.88 ± 0.02) was higher than by visual scoring (0.83 ± 0.03) ($P = .039$) or standard quantification (0.82 ± 0.03) ($P = .004$). For detection of 70% or greater stenoses, it was higher for TPD (0.89 ± 0.02) than for standard quantification (0.85 ± 0.02) ($P = .014$). Sensitivity and specificity were 93% and 79%, respectively, for TPD; 81% and 85%, respectively, for visual scoring; and 80% and 73%, respectively, for standard quantification. The use of stress mode–specific normal limits did not improve performance.**

Conclusion. **Simplified quantification achieves performance better than or equivalent to visual scoring or quantification based on per-segment visual optimization of abnormality thresholds. (J Nucl Cardiol 2005;12:66-77.)**

Key Words: Myocardial perfusion single photon emission computed tomography • total perfusion deficit • visual scoring

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Methods for the quantification of myocardial perfusion SPECT (MPS) allow automated detection and localization of coronary artery disease (CAD). Various parameters such as defect extent, defect severity, summed stress score (SSS), summed rest score (SRS), and location of the defect[1] can be computed automatically by comparisons of patient data to normal limits in polar-map coordinates. However, one major difficulty in clinical application of quantitative MPS perfusion tools is the dependence on normal limits distributed with quantitative software. These default normal limits may not be suitable for a particular acquisition protocol, radiopharmaceutical, or patient population.

In previous approaches the development of normal limits from studies of patients with a low likelihood of CAD was often coupled with an optimization process for regional abnormality thresholds.[2,3] These modified thresholds may need to be determined for each quantification method and each population studied. For example, in the method proposed previously by our group, optimization of individual segmental thresholds by using a large training data set was required.[4] To accomplish this, segmental scoring of abnormal cases was performed by an experienced observer and thresholds for each segment were subsequently derived by maximizing the agreement between visual scores and computer-generated scores. This process required a large number of abnormal samples in each segment to be reliable. It also required a well-defined set of abnormal cases as well as low-likelihood scans for the generation of normal limits. Because of these facts, to our knowledge, the system

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