Overall, T1 values at 40 min post-MnDPDP were 35.9% higher in regions of infarction compared to remote and healthy myocardium (1134±88 versus 843±28 ms, P<0.0001). All infarcts had T1 >1050 ms, whereas remote and healthy myocardium had T1 <950 ms.

Conclusion MEMRI of the myocardium with T1 mapping not only identifies myocardial infarction but also demarcates viability and delineates regions of viability within the infarct zone. This novel contrast imaging technique has exciting potential in ischaemic cardiomyopathy.

Conflict of Interest None

20 REAPPRAISING REMODELLING PATTERN OF LEFT VENTRICLE IN AORTIC STENOSIS: AXIS ORIENTATION AS A UNIQUE SIGNATURE OF POSITIVE REMODELLING

[1]Kenneth Chan*, [1]Masliza Mahmod, [1]Ernesto Zacur, [1]Marzia Rigolli, [1]Michelle D'Souza, [1]Jane Francis, [1]Rina Ariga, [1]Betty Raman, [1]Sairia Dass, [1]Theodoros Karamitsos, [1]Stefan Neubauer, [1]Saul Myerson, [2]Pablo Lamata. *[1]Oxford University; [2]Kings College London*

10.1136/heartjnl-2019-BCS.19

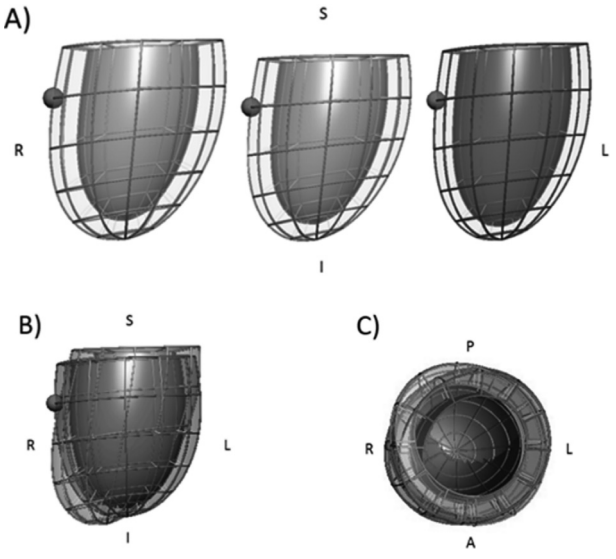
Introduction In aortic stenosis (AS), characterisation of ventricular (LV) remodelling beyond left ventricular mass measurements is lacking. We sought to study the 3-dimensional (3D) geometric LV remodelling pattern in severe AS pre- and post-surgical aortic valve replacement (AVR), and compared it with hypertensive and healthy controls.

Methods Ninety-one subjects (36 severe AS, 19 hypertension and 36 healthy controls) underwent cardiac magnetic resonance (CMR). 18 AS patients had a repeat CMR eight-month post-AVR. 3D meshes were reconstructed from the myocardial contours of the CMR cine images. Principle component analysis and linear discrimination analysis were used to derive shape coefficients.

Results AS patients had a significant shift in LV axis and apex orientation towards the septum, and more spherical LV shape which were not seen in the hypertensive and healthy control groups. As expected severe AS was associated with thicker and larger LV compared to the other two groups. Post AVR, despite significant reduction in LV thickness and sphericity, interestingly the shift in the LV axis/orientation was unchanged/irreversible (Figure 1).

Conclusion Severe AS is characterised by unique remodelling pattern which is not reversible post AVR. The novel shape metrics that comprehensively quantify the LV morphology may be a potential marker for risk stratification in the management of AS.

Conflict of Interest none



Abstract 20 Figure 1 A) Comparison between average LV shape in AS (blue), AS post-AVR (green), and controls (red). B) Overlying shape between AS (orange) and control (purple) showing shift of LV axis to septum. C) Overlying shape of AS post-AVR (orange) and healthy control (purple) showing focal dilatation in the postero-septal region post AVR

Cardiac Rhythm Management

21 THE CARDIOVASCULAR PREDICTIVE VALUE AND GENETIC BASIS OF T-WAVE MORPHOLOGY

[1]Julia Ramirez*, [2]Stefan van Duijvenboden, [1]Andrew Tinker, [3]Pier Lambiase, [3]Michele Orini, [1]Patricia B Munroe. *[1]Queen Mary University of London; [2]University College London; [3]UCL*

10.1136/heartjnl-2019-BCS.20

Background Early prediction of cardiovascular (CV) events in the general population remains an important issue. The T-wave morphology restitution (TMR), an ECG marker quantifying ventricular repolarization dynamics, is strongly associated with CV mortality in heart failure patients. Our objective was to evaluate the CV prognostic value of TMR in the general population and identify any genetic contribution.

Methods ECG recordings from 56,780 healthy individuals undergoing exercise stress testing in the UK Biobank study (EST-UKB) were analyzed. TMR was computed for exercise (TMRex) and recovery from exercise (TMRrec). The primary endpoint was CV death or hospitalizations for CV reasons. The secondary and tertiary endpoints were (1) all-cause mortality or hospitalizations for CV reasons and (2) arrhythmic mortality or hospitalizations for arrhythmic reasons. The median follow-up time was 70.7 months. Genome-wide association studies for TMRex and TMRrec were also performed and genetic risk scores (GRSs) were derived and tested for association with endpoints in the full cohort (FULL-UKB; N=402,746, median follow-up time of 85.3 months).

Results 1,727 (3.0%) individuals met the primary endpoint in EST-UKB, and 2,326 (4.1%) and 120 (0.2%) met the secondary and tertiary endpoints, respectively. TMRrec was significantly associated with the primary endpoint (hazard ratio (HR) 1.15, P=2 × 10–10, table 1), and both secondary and tertiary endpoints (HR 1.13, P=2 × 10–11 and HR 1.28, P=1 × 10–4, respectively) independent of resting