Quantification of the Detailed Cardiac Ventricular Trabecular Morphogenesis in the Mouse Embryo

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1. Introduction

The mammalian heart develops from a simple tubular shape into a complex 4-chamber organ, going through four distinct phases: early primitive tubular heart, emergence of trabeculations, trabecular remodelling and development of the compact myocardium.

To quantify myocardial complexity we developed a framework for regional cardiac ventricular complexity analysis and visualization in 3D, consisting of a standardized, individual-independent representation, fractal analysis and a novel physiologically meaningful complexity measure.

2. Materials

The study was performed on mouse embryos, acquired at different gestational ages (GA): from 14.5, when the ventricular septation is complete and a dense trabecular meshwork is established, to 18.5 embryonic days, when the compact myocardium matures. All specimens were handled and prepared as described in [1]. The prepared samples were then used for high resolution episcopic microscopy (HREM) analysis as described in [2].

3. Methods

The HREM datasets were pre-processed, aligned and The LV myocardium was segmented. Segmentations were then mapped to the standardized representation [3] and were subdivided into 361 regions.

The regional tissue complexity analysis was performed on 50 subjects, 10 subjects per GA. For each GA, mean and standard deviation of the segment complexity values were calculated and visualized on continuous bulls-eye plots. The complexity metrics used were 3D fractal dimension, and regional myocardial volume and surface area.

4. Results and Discussion

The tissue complexity results using the surface area metric are shown in Fig.1. Results confirm the known decrease in trabecular complexity with GA in normal embryos and are in agreement with the results in [1].

The proposed approach allows inter-individual and longitudinal quantification and comparison of normal, as well as abnormal, trabecular development and provides a way for a more objective quantification of alterations induced by genetic mutations.

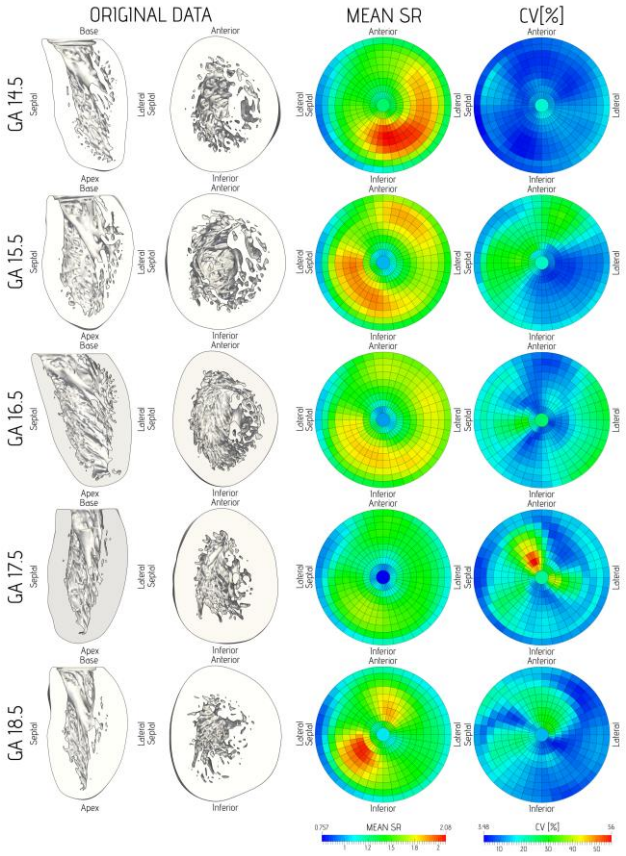

Fig.1: Continuous bull's eye plots representing average regional surface area ratios per GA (2nd column) and coefficient of variation of regional surface area ratios per GA (3rd column).

References

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