The Helical Ventricular Myocardial Band of Torrent-Guasp

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Contemporary science has to adopt a new way of thinking, which has emerged from rapid accumulation of knowledge at different levels, necessitating integration and linking across multiple scales of biological organization - from proteins to cells, tissues, organs and organ systems - in order to understand a complexity of interactions between form and function, generating a specific behavior (normal or abnormal) in biological system[1].

Within the ventricular mass, structure of every single constituent - defined by composition, size, shape, connections and orientation in a three-dimensional space - determine its global functional behavior. Ventricular architecture allows us to consider the ventricular myocardial mass as the source of complex, interdependent vectorial forces (i.e. electrical and mechanical), being generated at different length and time scales. The ultimate net result of these vectorial forces is to translate uniaxial sarcomere shortening into appropriate and efficient three-dimensional deformation of the ventricular cavities.

The complex architecture of the ventricular mass creates multiple inhomogeneities of electrical and mechanical loads at **cellular and microscopic tissue level**, causing the cardiac function to be stochastic in nature[2]. This fact imposes almost irresolvable problems in ongoing efforts to create a comprehensive mathematical model of the heart, which could fully explain cardiac function and its efficiency from the point of view of vectors of forces, generated during dynamic interaction between the elastic and contractile elements[3,4].

However, at **macroscopic (i.e. organ) level**, these stochastic events become averaged and appear consistent with a continuous medium. Dialectic coexistence of discreetness and continuity, suggests the existence of certain rule-based assignment, which could be applied equally well to all the ventricular myocardial fibers, enabling the ventricular myocardial mass to assemble abundant, dynamic, stochastic vectorial forces and produce apparently smooth, averaged, continuous, global response[2].

The **helical ventricular myocardial band (HVMB)** concept, described in 1972 by the late Spanish scientists, **Francisco Torrent-Guasp** (1931-2005) brings a new light on perennial problem of global, macroscopic, three-dimensional functional architecture of the ventricular myocardium[5-7].

Ventricular mass is heterogeneous structure consisting of cardiac myocytes, connective tissue elements, blood vessels, nerves and interstitial fluid. Ventricular myocardium, being composed of

individual, morphologically discrete, but functionally very-well-coupled cells, should be considered as "functional syncytium"[8]. Individual ventricular "working" myocyte is elongated, branched, cylindrical cell with lengths that range from 50 to 150μm and diameters ranging from 10 to 20μm. Branching outer cell contours resembles the "step-like facades of skyscrapers; the plateau of each step being occupied by an intercalated disc". Each ventricular myocardial cell is coupled by average of 11 neighbors, with 47% of the connections being of side-to-side (i.e. transverse) type and 53% of end-to-end (i.e. longitudinal) type. The branching angle is usually acute so that tightly coupled adjacent cells run almost parallel with one another.[9] Complex hierarchy of connective tissue (i.e. endomysium, perimysium and epimysium) provides a "sponge-like" scaffold for complex hierarchy of myocardial cells, blood vessels and nerves. Thus, the groups of three or more myocytes, surrounded by the perimysium could be distinguished as "myocardial fibers" and predominant local direction of their longitudinal axes defines the "principal fiber direction"[10,11]. These fibers as well as their directions are clearly visible during the macroscopic analyses of the intact ventricles (after removal of fat tissue and epicardium). The Auckland group has demonstrated a higher, laminar level of the ventricular myocardial organization, providing additional evidence that the ventricular myocardium "should not be viewed as a uniformly continuous structure" As they have clearly shown, muscular fibers are arranged into distinct myocardial laminas, four to six myocytes thick, separated from adjacent laminas by the extra cellular collagen network. The cardiac myocytes (fibers) are tightly coupled within the same, but sparsely coupled between the adjacent laminas. The planes of the laminas could be defined locally by the longitudinal axis of comprising myocardial fibers and by their spiral, branching transmural direction on the ventricular mass level[12].

As observed by predecessors[13] and quantitatively demonstrated by Streeter in his histological sections through the ventricular free wall[14], myocardial fibers change their directions gradually from endocardium to epicardium. Subepicardial fibers are becoming subendocardial ones, after helical overlapping around the natural orifices.

The anatomical dissection, revealing HVMB of Torrent-Guasp, accommodates factual difficulties arising from highly complex and anisotropic myocardial architectural design by following **principal fiber direction** at any given point, defining their unique functional (i.e. vectorial) and not any eclectic (i.e. discrete) anatomical personality within ventricular mass. Adopting this reproducible statistical criterion, it was not difficult to understand and prove that myocardial fiber fields have a very consistent and comparable organization between normal hearts of the same species.
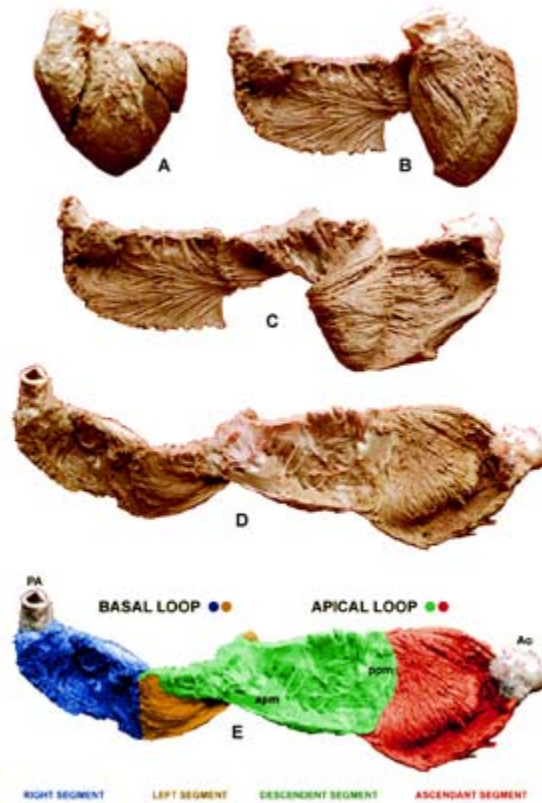
Figure 1 – Bovine ventricles prepared by simple boiling and removal of atria, epicardial fat and coronary arteries. A) Intact ventricles; B and C) Intermediate phases of the HVMB dissection; D) Unraveled HVMB; E) Segmental anatomy of the HVMB (PA – Pulmonary artery; Ao – Aorta; apm – anterior papillary muscle; ppm – posterior papillary muscle).

Figure 1(A-D) depicts successive steps of dissection technique applied in unraveling the ventricular mass into HVMB. The HVMB is topographically divided in two loops, each of them comprising of two segments (Figure 1E). The central 180-degree fold of the HVMB defines two loops: the basal loop (from the root of the pulmonary artery to the beginning of the central fold - i.e. to the anterior papillary muscle) and the apical loop (from the beginning of the central fold to the root of the aorta). Each of these two loops could be further divided in two segments.

The posterior interventricular sulcus, which coincides topographically with the posterior linear border of the RV cavity, divides the basal loop into two segments: the right segment - coinciding with the RV free wall; and the left segment - coinciding with the LV free wall. It is interesting to notice here, that the right segment also defines the outer (non-septal) border of the tricuspid orifice and the left segment defines the outer (non-septal) border of the mitral orifice. These particular borders are common targets in AV surgical annuloplastic procedures.

The apical loop could be also divided in two segments. After the 180-degree twist (at the central fold of the HVMB), the descendant fibers of the apical loop, make a 90-degree turn around the apex becoming the ascendant fibers. Posterior papillary muscle (belonging to the descendant

segment), demarcates the border between the descendent and the ascendant segments of the HVMB apical loop.

The elegance and astounding simplicity of this dissection is reflected in the capacity to easily reverse these unraveling steps, with ready re-establishment of the well-known three-dimensional ventricular architecture that existed prior to beginning of dissection.
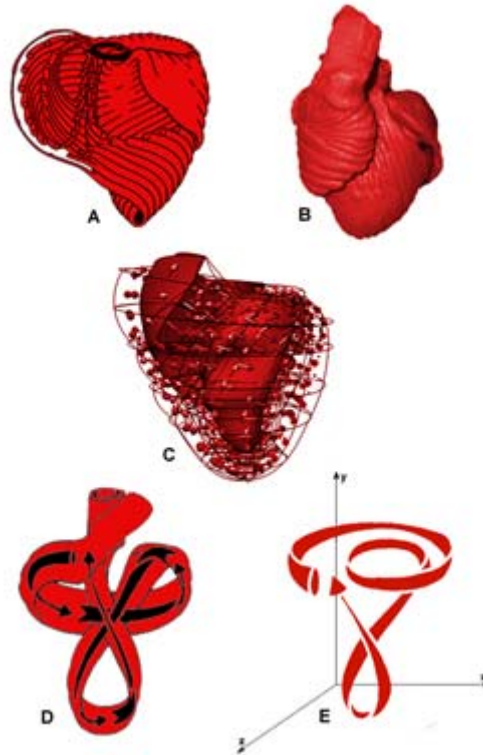

Figure 2 – Functional significance of the HVMB. A) Schematic 3D architecture of the ventricular myocardium; B) Silicone rubber model of the HVMB; C) A myriad of spatially and temporary dependent finite vectorial forces within ventricular mass (reproduced with kind permission from Peter J. Hunter, The University of Auckland, Bioengineering Institute); D and E) HVMB as the spatial and temporal continuum integrating the tissue architecture (i.e. form) and net forces developed (i.e. function) within the ventricular mass.

Although anisotropy within ventricular myocardium is evident at microscopic and macroscopic level – it is well documented that resultant vectors of electrical and mechanical forces coincide with the long axis of myocardial cells and fibers, having the greatest values along the predominant myocardial fiber orientation. Accordingly, the HVMB concept defines principal, cumulative vectors, integrating the tissue architecture (i.e. form) and net forces developed (i.e. function) within the ventricular mass (Figure 2). Arbitrary, there are four principal curvilinear vectors within ventricular myocardial mass, named after corresponding segments of the HVMB. According to their predominant orientation in three-dimensional space, they are grouped in two homologue pairs, named after corresponding loops of the HVMB. As idealized approximation of reality, HVMB concept integrates the ventricular form and function into single helicoid three-dimensional vector (Figure 2E). Appropriate mathematical formulation of this spatial and temporal

continuum may lead to new constitutive equation of the ventricular myocardium, which could overcome some limitations encountered in contemporary efforts to create a mathematical model of the heart.

During the last decade, three successive, international, multidisciplinary symposia were organized in order to set up fundamental research principles, which would allow us to make a significant step forward in understanding heart structure and function. We cannot continue to develop new diagnoses and therapies for heart diseases, without serious scientific consensus on these fundamental questions[15]. That goal shall be helped by further understanding of the **helical ventricular myocardial band of Torrent-Guasp**.

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