Activated Interstitial Myofibroblasts Express Catabolic Enzymes and Mediate Matrix Remodeling in Myxomatous Heart Valves

Elena Rabkin, MD, PhD; Masanori Aikawa, MD, PhD; James R. Stone, MD, PhD; Yoshihiro Fukumoto, MD, PhD; Peter Libby, MD; Frederick J. Schoen, MD, PhD

Background—The mechanisms of extracellular matrix changes accompanying myxomatous valvular degeneration are uncertain.

Methods and Results—To test the hypothesis that valvular interstitial cells mediate extracellular matrix degradation in myxomatous degeneration by excessive secretion of catabolic enzymes, we examined the functional characteristics of valvular interstitial cells in 14 mitral valves removed for myxomatous degeneration from patients with mitral regurgitation and in 11 normal mitral valves obtained at autopsy. Immunohistochemical staining assessed (1) cell phenotype using antibodies to α-actin (microfilaments), vimentin and desmin (intermediate filaments), smooth muscle myosin (SM1), and SMemb (a nonmuscle myosin produced by activated mesenchymal cells) and (2) the expression of proteolytic activity using antibodies to collagenases (matrix metalloproteinase [MMP]-1, MMP-13), gelatinases (MMP-2, MMP-9), cysteine endoproteases (cathepsin S and K), and interleukin-1β, a cytokine that can induce secretion of proteolytic enzymes. Although interstitial cells in normal valves stained positively for vimentin, but not α-actin or desmin, cells in myxomatous valves contained both vimentin and α-actin or desmin (characteristics of myofibroblasts). Moreover, cells in myxomatous valves strongly expressed SMemb, MMPs, cathepsins, and interleukin-1β, which were weakly stained in controls. Nevertheless, interstitial cells in both groups strongly expressed procollagen-I mRNA (in situ hybridization), suggesting preserved ability to synthesize collagen in myxomatous valves.

Conclusions—Interstitial cells in myxomatous valves have features of activated myofibroblasts and express excessive levels of catabolic enzymes, without altered levels of interstitial collagen mRNA. We conclude that valvular interstitial cells regulate matrix degradation and remodeling in myxomatous mitral valve degeneration.

Key Words: mitral valve remodeling metalloproteinases collagen

Myxomatous degeneration is the pathological substrate of mitral valve prolapse, a common cardiac valvular disorder characterized by redundant, floppy leaflets and associated with progressive mitral regurgitation, thromboembolism, infective endocarditis, and sudden death.1,2 Floppy valves likely result from mechanically inadequate extracellular matrix (ECM), particularly collagen, thereby allowing stretching of the leaflets.2,3 Nevertheless, the mechanisms responsible for the ECM defect and/or reparative processes that bolster the defective ECM are uncertain.

As in other tissues, turnover of the valvular ECM depends on a dynamic balance between synthesis and degradation. In most tissues, degradation of the ECM occurs through the action of matrix metalloproteinases (MMPs) and cysteine endoproteases (cathepsins). In cardiac valves, tight regulation of matrix homeostasis stringently maintains the functional architecture of the normal valve.4 Therefore, we propose that dysregulation of matrix metabolism modulates major features of the abnormalities of collagen and other ECM in heart valves with myxomatous degeneration.

The present study evaluated the role of valvular interstitial cells and catabolic enzymes such as MMPs and cathepsins in the pathogenesis of myxomatous degeneration using valves from patients who required surgery for severe mitral regurgitation, had myxomatous degeneration on pathological examination, and had no other documented condition known to predispose to mitral regurgitation.
TABLE 1. Normal Valves

<table>
<thead>
<tr>
<th>Age, y*</th>
<th>Sex</th>
<th>Cause of Death</th>
<th>Post Mortem Interval, hr</th>
</tr>
</thead>
<tbody>
<tr>
<td>34</td>
<td>F</td>
<td>Adenocarcinoma</td>
<td>6</td>
</tr>
<tr>
<td>52</td>
<td>F</td>
<td>Carcinoma</td>
<td>20</td>
</tr>
<tr>
<td>77</td>
<td>F</td>
<td>Cerebral aneurysm</td>
<td>4</td>
</tr>
<tr>
<td>78</td>
<td>F</td>
<td>Pseudomembranous colitis</td>
<td>3</td>
</tr>
<tr>
<td>36</td>
<td>M</td>
<td>Subarachnoid hemorrhage</td>
<td>8</td>
</tr>
<tr>
<td>55</td>
<td>F</td>
<td>Sclerosis</td>
<td>15</td>
</tr>
<tr>
<td>46</td>
<td>F</td>
<td>Sickle cell disease</td>
<td>20</td>
</tr>
<tr>
<td>80</td>
<td>M</td>
<td>Liposarcoma</td>
<td>5</td>
</tr>
<tr>
<td>61</td>
<td>F</td>
<td>COPD</td>
<td>19</td>
</tr>
<tr>
<td>30</td>
<td>F</td>
<td>Leukemia</td>
<td>12</td>
</tr>
<tr>
<td>53</td>
<td>M</td>
<td>Mesothelioma</td>
<td>9</td>
</tr>
</tbody>
</table>

MR indicates mitral regurgitation; MVP, mitral valve prolapse; HT, hypertension; TR, tricuspid regurgitation; AI, aortic insufficiency; CR, chordal rupture; P, posterior; and A, anterior.

COPD indicates chronic obstructive pulmonary disease.

*Mean age was 54.7±5.3 years.

Methods

Mitral valves with myxomatous degeneration derived from valve repair (n=13) or replacement surgery (n=1) and normal mitral valves from autopsy (n=11) were obtained according to a protocol approved by the Human Research Committee at the Brigham and Women’s Hospital. Detailed review of clinical charts revealed that none of the patients with myxomatous valve degeneration had documented coronary artery disease or other conditions known to predispose to mitral regurgitation (Tables 1 and 2).

TABLE 2. Myxomatous Valves

<table>
<thead>
<tr>
<th>Age, y*</th>
<th>Sex</th>
<th>Clinical Diagnosis/Operative Findings</th>
<th>Tissue Examined (leaflet)</th>
</tr>
</thead>
<tbody>
<tr>
<td>58</td>
<td>F</td>
<td>MR4+, MVP, HT</td>
<td>P</td>
</tr>
<tr>
<td>36</td>
<td>M</td>
<td>MR4+, MVP, CR</td>
<td>P</td>
</tr>
<tr>
<td>68</td>
<td>M</td>
<td>MR4+, MVP, HT, CR</td>
<td>P</td>
</tr>
<tr>
<td>64</td>
<td>M</td>
<td>MR4+, MVP</td>
<td>P</td>
</tr>
<tr>
<td>50</td>
<td>F</td>
<td>MR4+, MVP</td>
<td>P</td>
</tr>
<tr>
<td>51</td>
<td>M</td>
<td>MR4+, MVP</td>
<td>P</td>
</tr>
<tr>
<td>57</td>
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<td>M</td>
<td>MR4+, MVP</td>
<td>P</td>
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<tr>
<td>58</td>
<td>M</td>
<td>MR4+, MVP</td>
<td>P</td>
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<tr>
<td>71</td>
<td>F</td>
<td>MR4+, MVP, AI, TR</td>
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<tr>
<td>57</td>
<td>M</td>
<td>MR4+, MVP, CR</td>
<td>P</td>
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<tr>
<td>65</td>
<td>F</td>
<td>MR3+, MVP, CR</td>
<td>P</td>
</tr>
<tr>
<td>47</td>
<td>F</td>
<td>MR3+, MVP, TR</td>
<td>P</td>
</tr>
<tr>
<td>42</td>
<td>M</td>
<td>MR4+, MVP</td>
<td>P=A</td>
</tr>
</tbody>
</table>

*Mean age was 55.4±2.7 years.

Characterization of Myofibroblasts and Detection of Catabolic Enzymes

Myofibroblasts were distinguished by antibody reaction to cytoskeletal filaments (smooth muscle α-actin [microfilaments] and vimentin and desmin [intermediate filaments; DAKO]); and by negative staining to the myosin antibodies SM1 (differentiated smooth muscle cells) and SM2 (mature smooth muscle cells)9,10 (Table 3). Combined use of these antibodies serves as useful markers to distinguish smooth muscle cells from myofibroblast-like cells. A classification system of myofibroblasts is based on immunohistochemical staining of cytoskeletal filaments.11 Myofibroblasts that express vimentin and α-actin are called VA type, those that express vimentin and desmin are called VD type, and those that express vimentin, α-actin, and desmin are called VAD type. Differentiated smooth muscle cells were determined by immunoreaction to SM1 and SM2 antibodies. Inflammatory cells were identified with antibodies to CD68 (macrophages) and CD45 (T cell; DAKO). Mouse monoclonal antibodies against human MMP-1, MMP-2, MMP-9, and MMP-13 (Oncogene Research Products), and rabbit anti-human cathepsin S and cathepsin K were used to determine the expression of collagenolytic and elastolytic enzymes. Expression of interleukin (IL)-1β (a proinflammatory cytokine that induces the expression of MMPs) was examined with goat polyclonal anti-human IL-1β (Santa Cruz Biotechnology), and cell activation was demonstrated by a monoclonal antibody to SMemb9,10 (a nonmuscle myosin also known as MHC-B). Immunohistochemistry was done using the avidin-biotin-peroxidase method after antigen retrieval. Double immunofluorescent staining7 was done to confirm coexpression of IL-1β and MMP-13 or cathepsin S. Adjacent sections treated with nonimmune IgG served as controls for antibody specificity.

TABLE 3. Antibodies Used to Characterize Myofibroblasts and Smooth Muscle Cells

<table>
<thead>
<tr>
<th>Antibody</th>
<th>Filament System</th>
<th>Antigen reaction</th>
</tr>
</thead>
<tbody>
<tr>
<td>Vimentin</td>
<td>Intermediate—mesenchymal</td>
<td>+/+−</td>
</tr>
<tr>
<td>Desmin</td>
<td>Intermediate—muscle</td>
<td>+/−−</td>
</tr>
<tr>
<td>α-Actin</td>
<td>Microfilament—actin</td>
<td>+/−+</td>
</tr>
<tr>
<td>SM1</td>
<td>Myosin heavy chain</td>
<td>−/+</td>
</tr>
<tr>
<td>SM2</td>
<td>Myosin heavy chain</td>
<td>−/+</td>
</tr>
</tbody>
</table>

SMC indicates smooth muscle cells.

In Situ Hybridization

Nonisotopic in situ hybridization for human procollagen-I mRNA was done according to the manufacturer’s instructions (InnovaGen). Sections were incubated with oligomers as follows: anti-sense: 5′-GCT CCT TCA ATC CAT CCA GAC ACA-3′, 5′-TAA CCA AAG TCA TAA CCA CCA CCG C-3′, 5′-CAT AGT CCT TGG GTG TGA G-3′; sense: 5′-TGG TCT GGA TGG ATT GAA GGG ACA GC3′, 5′-GGG GTG GTG ATT ACT TGG CTT A-3′, 5′-CTC AGA CCC AAG GAC TAT G-3′.

Quantification and Statistical Analysis

Immunohistochemical staining of MMPs and in situ hybridization for procollagen-I mRNA expression were graded as follows: 0, no appreciable staining; 1, weak in <50% of cells; 2, weak in ≥50% of cells or strong in >10% of cells; 3, strong in 10% to 50% of cells; and 4, strong in ≥50% of cells. Semiquantitative analysis was done by E.R. and an observer without the knowledge of the origin of tissue or antibodies. Valve thickness was measured using a linear eyepiece reticle (10 mm, 0.1 mm division) (Fisher Scientific) for each section in the middle portion of each leaflet and was expressed as a mean of 3 measurements. Cell density was
expressed as mean number of cells per 10 high power fields. Quantitative data were compared in both groups by Mann-Whitney’s U test. Data are presented as mean±SEM. P<0.05 was considered significant.

Results

Myxomatous Valves Show Altered Morphology

Figure 1 compares the histological features of normal and myxomatous valves. Analogous to aortic valves, normal mitral valves had 3 well-defined tissue layers (Figure 1A), each containing cells and characteristic ECM composition and configuration: (1) the fibrosa, which is composed predominantly of collagen fibers arranged parallel to the free edge of the leaflet, densely packed and microscopically crimped; (2) the centrally located spongiosa, which is composed of loosely arranged collagen and proteoglycans; and (3) the atrialis, which is composed of elastic fibers. In contrast, myxomatous valves showed: (1) expansion of the spongiosa by loose, amorphous ECM staining strongly positive for proteoglycans (blue/green on Movat staining); (2) diminished staining for collagen fibers (yellow); and (3) fragmentation of elastin (black). Picrosirius red staining under polarized light further demonstrated that individual collagen bundles were fragmented, coiled, disrupted, and disoriented in myxomatous leaflets; collagen fibers were almost undetectable in the spongiosa and had lower birefringence than those in normal valves. Myxomatous valves often had a layer of superficial plaque characterized by the accumulation of stellate and spindle-shaped cells, particularly on the ventricular aspect of the leaflet. Owing to both expansion of the spongiosa and plaque formation, myxomatous leaflets were significantly thicker than normal (2.27±0.1 mm versus 0.92±0.08 mm, respectively; P<0.0001; Figure 1B).

Inflammatory cells, including macrophages and T-cells, were negligible in myxomatous valves. The cell density in the spongiosa of myxomatous valves was significantly increased (approximately tripled) compared with normal (62.9±5.5 and 21.2±1.3 cells per high power field, respectively; P<0.0001; Figure 1C).
Myxomatous Valves Contain Activated Myofibroblasts

Myofibroblast-like cells accumulated in myxomatous leaflets (Figure 2). In normal valves, interstitial cells expressed vimentin (V phenotype), but not α-actin or SM1. Cells stained with α-actin and antibodies to SM1 and SM2 localized in the proximal (near annulus) and middle portions and distributed predominantly in regions adjacent to the atrial aspect of the leaflet. In myxomatous valves, in contrast, many cells in the deeper portion of the atrialis and in the spongiosa expressed vimentin and α-actin or desmin, but not SM1 or SM2, suggesting modulation of a quiescent form of interstitial cells with V phenotype in normal valves to myofibroblasts with VA or VD phenotypes11 in myxomatous valves.

Activated interstitial cells accumulated in myxomatous but not in normal valves (Figure 3). Almost all interstitial cells in myxomatous leaflets stained for SMemb, which is known to be expressed by activated mesenchymal cells9,10 whereas cells in normal leaflets were not immunoreactive to SMemb (Figure 3A). Activated (both spindle-shaped and stellate) myofibroblasts were dispersed in a random fashion in the “myxoid” stroma, which was composed mainly of proteoglycans and sparse, loosely arranged collagen fibrils (Figure 3A). In the superficial plaque, myofibroblasts strongly expressed SMemb and MMPs and had the VA phenotype (Figure 3B).

Myxomatous Valves Overexpress Proteolytic Enzymes

Interstitial cells in myxomatous valves expressed higher levels of catabolic enzymes than in normal valves, especially collagenases (MMP-1, MMP-13; Figure 4A). Semi-quantitative analysis showed that levels of MMP-1, MMP-13, MMP-2, and MMP-9 in myxomatous valves (grades 3.1±0.2, 3.3±0.13, 2.07±0.2, and 2.08±0.2, respectively) were significantly higher than those in normal (grades 1.27±0.2, 0.91±0.3, 1.18±0.2, and 1.27±0.1; P=0.0002, P=0.0001, P=0.02, and P=0.03, respectively; Figure 4B). In normal valves, sparse macrophages could be responsible for low levels of proteolytic enzymes.

Normal valves contained no cathepsin S or K or IL-1β (data not shown). In myxomatous, interstitial cells immu-
noreflective to IL-1β, MMP-13 and cathepsin K colocalized with loose collagen and fragmented elastin in areas of myxomatous degeneration (Figure 4C). Immunofluorescent double-labeling for catabolic enzymes and IL-1β also showed coexpression of MMP-13/IL-1β and cathepsin S/IL-1β by interstitial cells in the spongiosa of myxomatous valves (Figure 4D).

Collagen-I mRNA Expression Is Similar in Myxomatous and Normal Valves

In situ hybridization using oligomers specific for human procollagen-I detected mRNA expression by interstitial cells in both normal and myxomatous valves (Figure 5A). Semiquantitative grading of procollagen-I mRNA expression showed no significant difference between normal (3.1±0.3) and myxomatous valves (3.4±0.25; $P=NS$; Figure 5B).

Discussion

This study showed that myxomatous valves have significant thickening and highly abnormal layered architecture and ECM components and that interstitial cells in myxomatous leaflets (1) exhibited features of activated myofibroblasts, (2) expressed elevated levels of proteolytic enzymes, (3) retained the ability to express interstitial collagen, and (4) significantly increased in number in the spongiosa. These results suggest that dysregulation of matrix metabolism modulates the abnormalities in collagen and other ECM components in this pathological condition.

Valvular Functional Architecture

Heart valves have a complex, layered architecture and highly specialized, functionally adapted cells and ECM. The ECM elements accommodate repetitive changes in shape and dimension throughout the cardiac cycle; interstitial cells synthesize the ECM and mediate its ongoing repair and remodeling, thereby providing durability. Each of the valvular layers is enriched in a specific ECM component and has a distinct function. These features have been demonstrated predominantly in the aortic valves. Although less work has been done to understand structure-function correlations in the normal mitral valve, the general architecture and roles of the layers are likely analogous to those of the aortic valve. In the normal aortic...
defective ECM and altered layered architecture. Indeed, a recent study demonstrated dramatic defects in the mechanical properties of myxomatous leaflets and chordae; myxomatous leaflets were more extensible and half as strong as normal valve tissue, which suggested that the abnormal stresses engendered by progressive stretching of enlarged leaflets and inherent weakness are synergistic in valve degeneration, possibly following as well as preceding valve repair.15

**Interstitial Valvular Cells**

The physiological role of valvular cells in the maintenance and remodeling of ECM in normal valves and their dysregulation in disease are poorly understood. The resting interstitial cell population of normal cardiac valves is predominantly fibroblast-like. These cells synthesize collagen, elastin, and proteoglycans. However, smooth muscle cells and myofibroblasts have also been cultured from heart valves.16–18 Myofibroblasts may well represent an intermediate state between fibroblasts and smooth muscle cells. Detection of myofibroblasts is difficult because of their heterogeneity and absence of particular immunohistochemical markers. Characterization of myofibroblasts is based on antibody reaction to 2 filament systems of cells composed of (1) actin (a component of the microfilaments) and (2) vimentin, desmin, and laminin (members of the intermediate filament system).9 In the present study, interstitial cells in normal valves expressed vimentin, but not α-actin or desmin, although other investigators have often observed α-actin–positive cells cultured from cardiac valves and characterized them as myofibroblasts.16–18 In control valve specimens, only smooth muscle cells displayed α-actin and SM1. Interestingly, in myxomatous leaflets, many cells in deep atrialis and spongiosa expressed vimentin, as well as α-actin or desmin but not SM1, suggesting that under pathological conditions interstitial cells may express features of VA or VD phenotypes of myofibroblasts.

The expression of MMPs, cathepsins, and IL-1β in myxomatous lesions and associated superficial plaques suggest activation of valvular cells. Activation of myofibroblasts was confirmed by SMemb, which is predominantly expressed by activated mesenchymal cells.9,10 Stellate myofibroblasts (large cells with long cytoplasmic extensions) were found in loose myxomatous stroma. These cells can be a local source of multiple cytokines and catabolic enzymes that affect cell proliferation, activation, and ECM accumulation. They can be found in restenotic lesions after angioplasty or stenting,19 suggesting similar mechanisms of myofibroblast activation, differentiation, proliferation, and ECM degradation.

**Role and Mechanisms of Matrix Remodelling in Myxomatous Mitral Valve Degeneration**

Members of a family of enzymes that includes interstitial collagenases and gelatinases, MMPs are involved in the matrix breakdown in normal and pathological conditions such as atherosclerosis6–7 and aortic aneurysms.13 Interstitial collagenases mediate the initial step of collagen

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**Figure 5.** In situ detection of collagen synthesis. A, Procollagen-I mRNA expression by interstitial cells in normal and myxomatous valves detected by in situ hybridization using antisense oligomers specific for human procollagen-I (red reaction product). No signal was detected with sense probes used as negative control. Bar=50 μm. Magnification ×400. B, Semiquantitative analysis for procollagen-I mRNA expression showed no significant difference between normal and myxomatous valves. Bars represent SEM.

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**Myxomatous Valve Degeneration**

The pathogenesis of the connective-tissue abnormalities causing floppy mitral valve remains uncertain. In some cases, there is an identified genetic/congenital defect in connective tissue (ie, Marfan syndrome).13 Moreover, a genetic defect has been postulated for idiopathic/isolated mitral valve prolapse.14 Other cases likely result from either acquired abnormalities of valvular connective tissue geometry, composition, or context (ie, ischemic papillary muscle dysfunction and functional mitral regurgitation in heart failure).

In the present study of myxomatous valves from patients without known contributory systemic illness or cardiac disorder, interstitial cells expressed considerable collagenolytic enzymes but maintained collagen synthesis. These observations suggest that the abnormalities of collagen result primarily from excessive collagenolytic activity rather than decreased collagen synthesis. The deranged mechanical properties of myxomatous valves result from...
degradation by breakdown of the native helix of the fibrillar collagen network (type I is most abundant, comprising ~70% of the total collagen in valves). These fragments then become accessible to the other proteases, such as gelatinases, which further catabolize collagen. Cathepsins S and K are also involved in ECM remodeling, particularly elastin. Cathepsin K, the most potent elastase yet described, also has collagenolytic activity. Several lines of evidence suggest that resident cells mediate ECM degradation in many degenerative diseases. Stimulation of these cells in some way elicits soluble extracellular messengers that, in turn, induce resident cells to initiate matrix degradation. For example, cardiac catabolic factor, which is derived from porcine heart valves, stimulates collagen and proteoglycan degradation in vitro. It has properties similar to those of catabolin, a cytokine first detected in porcine synovium and considered a form of porcine IL-1. Previous studies have shown that cultured smooth muscle cells exposed to IL-1β release MMP-2, MMP-9, and cathepsins S and K.

The present study indicates that resident valvular cells contribute to matrix destruction and remodeling in myxomatous valves. Interstitial valvular cells were the major source of the significantly increased expression of proteolytic enzymes, such as MMPs, that mediate ECM degradation and were significantly increased in number compared with normal valves, suggesting cell proliferation. Our study also demonstrated the presence of interstitial cells immunoreactive for cathepsins S and K and strongly expressing IL-1β in the myxomatous valves. Moreover, IL-1β co-localized with MMP-13 and cathepsin S. These observations suggest that interstitial cells induced by IL-1β could mediate the expression of catabolic enzymes and modulate the development of the defective ECM by enzymatic breakdown of the connective tissue first described by Caulfield et al. in myxomatous valves.

The present study provides new insight into mechanisms by which ongoing and progressive matrix degeneration may contribute to a common clinical pathway. These data clearly establish that interstitial cells express excessive catabolic enzymes in valves with myxomatous degeneration. However, it remains to be determined whether high proteolytic activity and cell activation in the mitral leaflets are causal or whether regurgitation and abnormal mechanical stress induce matrix remodeling as a reactive mechanism. Nevertheless, these observations on diseased human tissues cannot definitely resolve the nature of the primary stimulus to myxomatous degeneration. Our data implicate a progression of cell/tissue level to clinical events, which is summarized schematically in Figure 6. They also suggest a mechanism by which progressive deterioration of myxomatous tissue could occur after otherwise successful valve repair surgery.

Conclusions

Taken together, these results suggest that the altered layered architecture of the leaflet and structural abnormalities of connective tissue components, as well as excessive levels of collagenolytic and elastolytic enzymes expressed by activated interstitial cells, could cause the leaflet functional abnormalities of myxomatous valves in patients with mitral regurgitation.

Acknowledgments

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References


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