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Extracellular microfibrils; contextual platforms for TGF β and BMP signaling

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Abstract

The extracellular matrix plays a key role in organ formation and tissue homeostasis. Recent studies have revealed that fibrillin assemblies (microfibrils) both confer tissue integrity and regulate signaling events that instruct cell performance and that perturbation of either function manifests in disease. These analyses have also indicated that fibrillin assemblies impart contextual specificity to TGF β and BMP signaling. Moreover, correlative evidence suggests functional coupling between cell-directed assembly of microfibrils and targeting of TGF β and BMP complexes to fibrillins. Hence, the emerging view is that fibrillin-rich microfibrils are molecular integrators of structural and instructive signals with TGF β s and BMPs as nodal points that convert extracellular inputs into discrete and context-dependent cellular responses.

Introduction

The interaction of bioactive ligands with the extracellular matrix (ECM) represents an important mechanism that establishes morphogen gradients in the developing embryo and that modulates instructive signals in the adult organism. In contrast to the well-established involvement of heparan sulfate proteoglycans (HSPG) in the extracellular regulation of several signaling pathways [1], a comparable role for the architectural elements of the ECM is only beginning to emerge. In *Drosophila*, genetic analyses have demonstrated that interaction between Decapentaplegic (Dpp) and collagen IV not only enhances Dpp signaling in the early embryo by promoting gradient formation, but also restricts the range of growth factor action in the ovary by sequestering Dpp complexes [2•]. Similar studies in mice have correlated mutations of fibrillin-1 with heightened TGF β signaling in Marfan syndrome (MFS; OMIM #154700), and loss of fibrillin-2 with decreased BMP7 signaling in developing limbs [3,4].

Fibrillin macro-aggregates perform two critical functions in organismal physiology; they provide a structural scaffold that imparts physical properties to connective tissue and they act as an instructive platform for soluble modulators of cell behavior. To generate morphologically and functionally diverse macro-aggregates, cells must tightly regulate the multiple protein interactions of fibrillins. Therefore, impaired microfibril biogenesis and/or cellular responses to abnormal matrices are probable contributors to dysregulated TGF β and BMP signaling in

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fibrillin-deficient states. This review highlights recent findings that provide insights into how fibrillins control endogenous TGF β and BMP signaling, and that suggest cell-mediated coupling of fibrillin microfibril nucleation at the plasma membrane with targeting of TGF β and BMP complexes to fibrillins. These findings are discussed within the context of probable disease mechanisms resulting from fibrillin mutations that impair ECM integrity and growth factor sequestration.

Formation of microfibril scaffolds

Fibrillins are large cysteine-rich glycoproteins that form supramolecular arrays (microfibrils) that incorporate or associate with a variety of proteins, including TGF β and BMP complexes, integrins, HSPGs, and insoluble elastin in elastic fibers [5•]. Assembly of fibrillins into microfibrils and microfibrils into elastic fibers are complex multistep processes that are yet to be fully delineated [5•]. Recent studies have focused on the mechanisms that control the initial polymerization of fibrillins into the characteristic beads-on-a-string microfibril structure in which individual molecules are organized in a head-to-tail arrangement and associate laterally (Fig. 1). Using recombinant polypeptides, Humbacher et al. [6••] demonstrated that the C-terminal half of fibrillin-1 drives formation of disulfide-bonded bead-like globular structures, which interact with N-terminal portion of fibrillin-1 to regulate linear assembly and inhibit microfibril formation when added to cell cultures. These investigators subsequently reported that the C-terminal globular multimers (but not fibrillin monomers) bind *in vitro* to a specific sequence of fibronectin, and that either silencing fibronectin biosynthesis or inhibiting fibronectin assembly disrupts microfibril formation (but not vice versa) [7••]. Additional analyses revealed that newly formed microfibrils localize to fibronectin fibrils, and that exogenously added fibrillin-1 can only assemble on a fibronectin network [7••]. Other investigators showed that antibody activation of β_1 integrins, which mediate cell-driven assembly of fibronectin, could not restore microfibril formation in fibronectin-null cells [8]. These observations reiterate the central role of fibronectin in organizing early ECM assembly and in maintaining cell-matrix adhesion sites [9].

Earlier work had shown that fibrillins contain several heparin-binding sites, and that HSPG inhibition reduces fibrillin polymerization [10–12]. Bax et al. [13] recently implicated a syndecan/glypican HS-binding site located immediately next to the Arg-Gly-Asp (RGD) sequence of fibrillin-1 as enhancing $\alpha_5\beta_1$ -mediated focal adhesion formation. Furthermore, Cain et al [14] correlated an N-terminal heparin-binding site with supporting the linear assembly of fibrillin molecules. Collectively, these data suggest that interactions with fibronectin fibrils and HSPGs control the initial steps of microfibril biogenesis on or close to the cell surface (Fig. 1). An attractive aspect of this model is that protein self-assembly is promoted by locally concentrating interacting molecules as they are secreted into the pericellular space. Similar involvement of fibronectin and HSPGs in targeting latent TGF β complexes to nascent microfibrils (see below) raises the possibility that cells coordinate the formation of microfibril scaffolds with the sequestration of growth factors.

Targeting growth factors to microfibril scaffolds

TGF β s and BMPs specify a plethora of cellular activities, including ECM deposition and degradation, and are regulated at multiple levels, including by the storage in and release from the ECM [15••]. Control of matrix targeting of TGF β s initiates intracellularly with the covalent association between latent TGF β -binding protein (LTBP) -1, -3 or 4 and small latent complexes (SLCs), which consist of bioactive TGF β dimers non-covalently bound to their pro-domains (latency-associated protein or LAP). The resulting tripartite large latent complex (LLC) is secreted and binds to fibronectin and fibrillin assemblies through specific N- and C-terminal

LTBP sequences, respectively (Fig. 1) [16]. Genetic evidence indicates that LTBPs also have a distinct structural role in the ECM [17,18].

Cell culture experiments suggest that initial interactions between LTBPs and ECM components (and thus sorting and targeting of LLCs to the ECM) occur at the plasma membrane with direct involvement of fibronectin fibrils and HSPGs [19,20,21]. LTBPs subsequently localize to fibrillin-rich microfibrils through cell-directed reorganization of the provisional matrix (Fig. 1) [22]. Relocation of LTBPs and LLCs from fibronectin fibrils to nascent fibrillin polymers is associated with cells actively shunting ECM material from one location to another, in the absence of significant proteolytic activity [22]. Although less well understood, the mechanisms that modulate extracellular control of BMP bioavailability differ from those of TGF β because of two features. First, BMPs are directly targeted to microfibrils by non-covalent association between their pro-domains and the N-terminal region of fibrillins [23]. Second, BMP signaling can be activated through competitive displacement of the pro-domain by type II receptors [24]. However, matrix-bound BMPs may still require release from fibrillins to signal. By analogy with Dpp regulation in *Drosophila* [25], extracellular microfibrils may also sequester BMPs associated with soluble antagonists.

Release and activation of latent TGF β s from microfibril scaffolds

The prerequisite binding of TGF β s to microfibrils for proper function implies that growth factor action is modulated not only by the process of microfibril assembly, but also by the liberation and activation of ligands from the ECM [16]. Although earlier *in vitro* analyses suggested that proteases could release and activate TGF β s from the ECM, subsequent genetic studies failed to show diminished TGF β signaling in mice lacking individual proteases probably because of proteolytic redundancy in the tissue environment [25]. The finding that mice without both BMP1 and Tolloid-like 1 activity (proteases that control both ECM formation and growth factors activity) display decreased TGF β signaling supports this conclusion [26].

Unlike proteases, integrin-mediated activation of LLC is clearly a component of the extracellular control of TGF β bioavailability [27]. Integrin $\alpha_v\beta_6$ activates latent TGF β s by binding the RGD sequence of LAP- β 1 or - β 3 and by associating with the cytoskeleton through the β_6 subunit's cytoplasmic tail [28]. LTBP-mediated binding of SLC to the matrix allows $\alpha_v\beta_6$ integrin to apply force and alter the latent complex structure. Furthermore, the finding that $\alpha_v\beta_6$ integrin activates only latent TGF β s associated with LTBP-1 suggests involvement of LTBP-specific interactions with the ECM [29]. The importance of $\alpha_v\beta_6$ -mediated activation of latent TGF β s is underscored by recent studies showing that mice harboring mutations in the integrin-binding site or the LTBP-binding site of TGF β 1 phenocopy the abnormalities of *Tgfb1*-null mice [30,31]. Additionally, the demonstration that $\alpha_v\beta_5$ integrin and LTBP-1 cooperate in latent TGF β activation by myofibroblasts indicates that, to promote activation, the ECM must resist the traction applied by the integrin/cytoskeletal complex [32]. Myofibroblasts placed on compliant matrices fail to activate LLC, whereas those placed on more resistant matrices produce active TGF β s [32]. Integrin $\alpha_v\beta_8$ activates latent TGF β s through a different mechanism that may require tethering of the cell-surface protease MT1-MMP to the LLC/integrin complex, but not integrin binding to the cytoskeleton [33]. Hence, integrins $\alpha_v\beta_5$ and $\alpha_v\beta_6$ must distort LLC conformation to either free or expose TGF β s to receptors, whereas $\alpha_v\beta_8$ integrin promotes protease activation of latent complexes.

Molecular consequences of microfibril scaffold disruption

If ECM incorporation is essential for proper control of TGF β and BMP action, interference with matrix assembly should perturb growth factor signaling. Heterozygous mutations of fibrillin-2 result in congenital contractural arachnodactyly (CCA; OMIM # 121050), a connective tissue disorder akin to MFS, whereas heterozygous mutations of fibrillin-1 cause

the pleiotropic manifestations of MFS, which principally involve the ocular, musculoskeletal and cardiovascular systems [5•]. *Fbn1* or *Fbn2* mutant mice exhibit distinct phenotypes associated with discrete perturbations of TGF β and BMP signaling [5]. Syndactyly is the most evident phenotype of *Fbn2*-null mice and the unique trait of mice haploinsufficient for both *Fbn2* and *Bmp7* [3]. By contrast, *Fbn1* mutant mice show normal digit formation but display abnormalities in the cardiovascular, respiratory, and muscular systems secondary to heightened TGF β signaling [3,4,34–37•]. These phenotypic disparities in organs that accumulate large amounts of both fibrillin-1 and -2 imply that the mechanisms targeting TGF β and BMP complexes to microfibrils are tissue-, stage-, and fibrillin-specific.

The realization that defective fibrillin-1 assembly promotes latent TGF β activation has provided the rationale for using systemic TGF β antagonism to mitigate MFS manifestations in mice [4,34–36]. These proof-of-principle experiments have recently translated into a drug-based therapy (losartan, an angiotensin II type 1 receptor antagonist known to decrease TGF β signaling) that reduces the rate of aortic growth in children with severe and rapidly progressive MFS [32•]. As a result, a model of MFS pathogenesis has emerged whereby *FBN1* mutations preclude or decrease matrix sequestration of LLCs, rendering latent TGF β more prone to or more accessible for activation with negative consequences to cell function and tissue remodeling [35,4]. In this view, physiological levels of latent TGF β activators are sufficient to drive disease progression in MFS irrespective of whether *FBN1* mutations affect protein structure or expression (Fig. 2). In contrast to structural mutations in which phenotypic variability may reflect discrete perturbations of microfibril formation, clinical variability in MFS patients haploinsufficient or nearly haploinsufficient for *FBN1* implicates additional factors in TGF β -driven disease progression [33,40]. One possibility is that the structurally abnormal ECM promotes cellular responses that contribute to MFS pathogenesis by heightening latent TGF β activation through the action of integrins, proteases and/or other molecules (Fig. 2).

Several lines of indirect evidence support the above hypothesis. These include the aforementioned observation that loss of LTBP association with microfibrils impairs elastogenesis [17,18], the finding that interference with LLC matrix sequestration results in TGF β over-activation [41], the discovery that reduced expression of microfibril-associated fibulin-4 increases TGF β signaling and perturbs cardiovascular homeostasis [42], and the report that improper p38 MAPK signaling is an early determinant of constitutive Smad2/3 activity in *Fbn1*-null aortas [43•]. It is also noteworthy that vascular manifestations similar to those of MFS mutations are observed with mutations that affect smooth muscle cell contraction, such as β -myosin and α -actin, or the plasma membrane receptor LRP1, an integrator of PDGF and TGF β signals in the aortic wall, [44–46•]. Additional factors connected with ECM remodeling that may further exacerbate TGF β -driven aneurysm progression include a C-terminal fragment of fibrillin-1 that can displace LTBPs from microfibrils, and fibrillin-1 peptides that stimulate macrophage chemotaxis and MMP production [47,48•,49]. Consistent with the latter observation, systemic MMP inhibition improves aortic wall architecture and delays aneurysm rupture in *Fbn1* mutant mice [50,51].

Conclusions and perspectives

The studies we have described demonstrate that fibrillins play a vital role in organ formation and tissue homeostasis by imparting structural integrity to connective tissues and by modulating the activity of growth factors that regulate ECM formation and remodeling. Further investigations are required to determine the mechanistic relationships between microfibril biogenesis and TGF β and BMP targeting to fibrillins, and between fibrillin interactions with secreted and cell-surface molecules and the formation of tissue- and stage-specific macroaggregates. Likewise, additional effort is needed to delineate the pathophysiological sequence

that links fibrillin-deficient matrices with perturbed growth factor bioavailability and cell performance. Biochemical, cellular and genetic approaches, together with new technologies to monitor the dynamics of ECM interactions in real time, should instruct progress of these studies.

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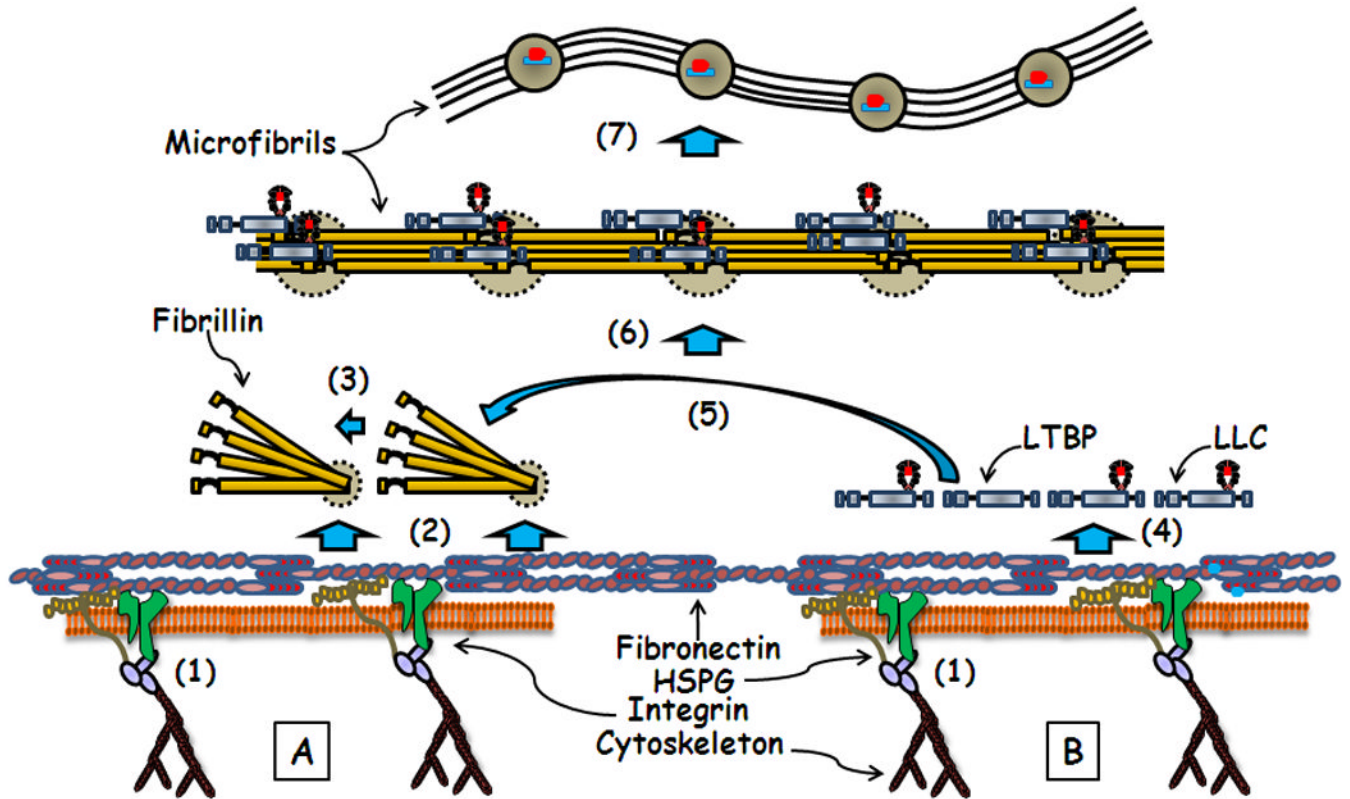


Figure 1.

Schematic representation of the fibronectin-directed, HSPG-dependent processes of microfibril assembly (A) and LTBP and LLC incorporation into the ECM (B). Relevant steps discussed in the text include (1) promotion of fibronectin fibrillogenesis by the cytoskeleton/integrin complex; (2) fibronectin and HSPG supporting C-terminal association of fibrillin monomers into bead-like structures (grey circle with dotted outline), and (3) their subsequent linear assembly into microfibrils; (4) HSPG-dependent incorporation of LTBP and LLCs onto fibronectin fibrils, and (5) their subsequent transfer to nascent microfibrils through ill-defined cellular activities. Also shown are (6) microfibrils decorated by LTBP and LLC in the overlaps (beads in (8)) between the N- and C-terminal ends of fibrillins, and (8) a schematic rendition of the beads-on-a-string microfibril structure with LLCs bound to the beads [5].

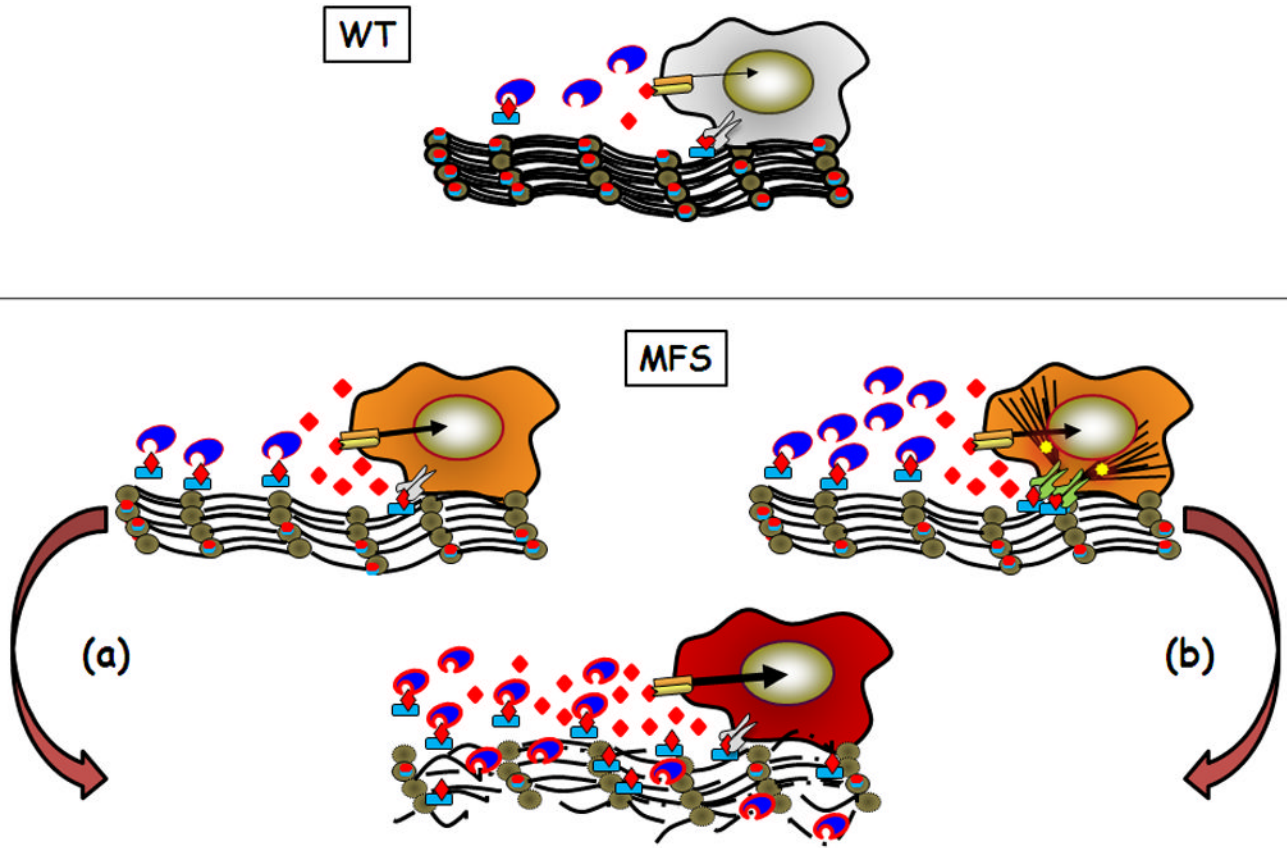


Figure 2. Model of normal regulation of TGFβ by microfibrils (WT) and perturbations associated with microfibril deficiency in Marfan syndrome (MFS). Two models of MFS pathogenesis leading to loss of tissue integrity (bottom) are shown. In the first model (a), physiological levels of activators (proteases (blue indented ovals) and integrins (grey symbols)) drive disease by increasing release of TGFβ (red diamonds) from matrix-free LLCs (blue rectangle with red diamond). In the second model (b), cells enhance TGFβ activity by producing more proteases, by increasing integrin-mediated LLC activation (also through heightened cytoskeletal tension (black lines)), and by stimulating stress-response signaling pathways (yellow stars). Although the two models focus on the onset of MFS pathogenesis, impaired LLC sequestration (model (a)) could be the immediate trigger of cellular responses to an abnormal matrix (model (b)).