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Mechanisms of Hepatic Fibrogenesis

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Abstract

Multiple etiologies of liver disease lead to liver fibrosis through integrated signaling networks that regulate the deposition of extracellular matrix. This cascade of responses drives the activation of hepatic stellate cell (HSC) into a myofibroblast like phenotype that is contractile, proliferative and fibrogenic. Collagen and other extracellular matrix (ECM) components are deposited as the liver generates a wound healing response to encapsulate injury. Sustained fibrogenesis leads to cirrhosis, characterized by a distortion of the liver parenchyma and vascular architecture. Uncovering the intricate mechanisms that underlie liver fibrogenesis forms the basis for efforts to develop targeted therapies to reverse the fibrotic response and improve the outcomes of patients with chronic liver disease.

Keywords

Stellate cell; fibrogenesis; tyrosine kinase; growth factors; immune cells; adipokines

Introduction

Liver fibrosis is a reversible wound-healing response to either acute or chronic cellular injury that reflects a balance between liver repair and scar formation. During acute injury, the changes in liver architecture are transient and reversible. With chronic injury, there is progressive substitution of the liver parenchyma by scar tissue. Despite ongoing injury, the liver has a remarkable regenerative capacity, and, as a result, patients often progress slowly to cirrhosis over decades.

A key discovery in understanding fibrosis has been that the hepatic stellate cell (HSC) is the primary effector cell, orchestrating the deposition of ECM in normal and fibrotic liver. HSCs are resident perisinusoidal cells in the subendothelial space between hepatocytes and sinusoidal endothelial cells. They are strategically positioned to intimately interact with hepatocytes, endothelial cells, and nerve endings through their numerous processes extending across the space of Disse [1–3]. Additionally, the HSC plays a pivotal role in activating the immune response through secretion of cytokines and chemokines and

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Conflict of Interest

None

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interacting with immune cells. HSC also contributes to angiogenesis and the regulation of oxidant stress [4].

Activation of the HSC into a myofibroblast like phenotype can be provoked by a range of chronic injuries to the liver, amongst which are viral hepatitis, toxins, [non-] alcoholic steatohepatitis and autoimmune disorders [5]. Activation consists of two major phases, initiation [also called a “preinflammatory stage”] and perpetuation, followed by a resolution phase if the injury subsides [6]. Initiation refers to early changes in gene expression and phenotype that render the cells responsive to other cytokines and stimuli shortly after injury occurs (Figure 1). The initial paracrine stimulation, including exposure to lipid peroxides and products of damaged hepatocytes and signals from Kupffer and endothelial cells, drive early activation, as well as changes in surrounding extracellular matrix. Once the cell is primed for activation, perpetuation results from the effects of these stimuli on maintaining an activated phenotype and generating fibrosis. Sustained activation involves at least seven discrete changes in cell behavior: proliferation, chemotaxis, fibrogenesis, contractility, matrix degradation, retinoid loss, and WBC chemoattractant/cytokine release. The net effect of these changes is to increase accumulation of extracellular matrix. During this phase there is a release of proinflammatory, profibrogenic and promitogenic stimuli that act in an autocrine and paracrine manner. Resolution of fibrosis refers to pathways that cause either HSC apoptosis, senescence, or quiescence [7] (Figure 1).

Fibrosis progression and regression require specific signaling pathways; thus, understanding how they interact and evolve with injury can contribute to efforts to reverse fibrosis. Complex, well-orchestrated intracellular events lead to HSC survival and growth during progressive fibrosis, while permitting their regulated clearance during resolution of fibrosis. This review will focus on key pathways and gene regulation that leads to activation of HSCs and emerging mechanisms of fibrogenesis that have provided new targets for therapy.

Key pathways of HSC activation

Growth factor signaling

HSCs are an important source of growth factors in the liver, but also respond to these factors, emphasizing the importance of tightly regulated autocrine control of growth factor activity within the pericellular milieu.

PDGF signaling is among the best characterized pathways of HSC activation[8]. PDGF binds its receptors, the receptor subunits dimerize with subsequent phosphorylation of the tyrosine residues in the intracellular domain. This leads to Ras-MAPK pathway activation, signaling through the PI3K-AKT/PKB pathway and mobilization of intracellular calcium ions to activate PKC family members [9] (Figure 2). All these events ultimately lead to cellular proliferation. Rapid induction of β -PDGF receptor, which is a hallmark of early HSC activation, is followed by development of a contractile, fibrogenic phenotype that correlates with the degree of fibrosis and inflammation [10,11]. PDGF is the most potent mitogen towards HSCs, and its antagonism therefore has potential as an anti-fibrotic strategy [12]. In fact, pharmacological inhibition of the PDGFR- β chain in pre-clinical disease models has already shown promise as an anti-fibrotic [13,14]. Sorafenib, a multiple receptor tyrosine kinase inhibitor targeting the PDGF receptor and the Raf/ERK signaling pathway, is effective in advanced HCC patients, and additionally displays anti-fibrotic activity in animal models of fibrosis [14].

Other signaling pathways converge on Akt activation, including c-Jun N-terminal kinase (JNK) phosphorylation and activation (Figure 2). JNK inhibition or genetic deletion in mice

displays a reduction in liver fibrosis, as well as decreased PDGF and TGF β signaling, implicating JNK inhibition as a potential target for drug development [15].

Transforming growth factor α (TGF α) and epidermal growth factor (EGF) are two potent epithelial growth factors that are secreted by, and also stimulate proliferation of HSCs [16,17]. Release of these growth factors is also important for paracrine stimulation of hepatocyte proliferation during liver regeneration [16,18]. Receptors for VEGF are also induced during HSC activation which contribute to enhanced mitogenesis in response to VEGF. The critical role of VEGF in angiogenesis, combined with its mitogenicity towards HSCs, establish HSCs as one of the cellular determinants of hepatic angiogenesis. Other HSC mitogenic pathways include those downstream of thrombin [19,20], keratinocyte growth factor [21], and bFGF [22] (Figure 2).

Following the response to growth factors, the HSC remodels the ECM into one rich in fibril-forming collagens, particularly types I and III. The ECM components in turn act in a positive feedback loop by releasing additional matrix-bound growth factors resulting from increased protease activity, as well as increasing liver stiffness, both of which propagate HSC migration and contraction [23].

Fibrogenic Signaling Pathways

HSCs generate fibrosis not only by increasing cell number, but also by increasing matrix production per cell. In the normal liver, the basement membrane-like matrix of the space of Disse is comprised primarily of collagens IV and VI, which is progressively replaced by collagens I and III and cellular fibronectin during fibrogenesis [24].

TGF β 1 is derived from both paracrine and autocrine sources, and is the most potent fibrogenic cytokine in liver [25,26]. TGF β 1 is stored as an inactivated protein bound to a latency-associated peptide. Once activated, TGF β 1 signals via its cognate receptors to Smad proteins, which lead to induction of collagen production [25] (figure 2). Quiescent HSCs are induced by TGF β 1 to transdifferentiate into myofibroblasts that secrete extracellular matrix. Whereas hepatocyte apoptosis and necrosis stimulate HSC fibrogenesis, TGF β 1 may sustain hepatocyte mass and regulate growth during regeneration [26]. Therefore antagonizing TGF β 1 therapeutically, will be challenging, since some of its action, for example its anti-inflammatory and growth regulatory roles, are important to sustain normal liver homeostasis [27].

Leptin, a key adipokine, has been implicated fibrogenesis through a number of pathways (detailed in adipokines, below). Downstream effects of leptin signaling during liver injury include increased release of TGF- β 1 from Kupffer cells. In contrast, leptin deficiency may reduce fibrogenesis by decreasing the activity of norepinephrine. Reduced activity of norepinephrine, in turn, leads to decreased activity of natural killer cells, and thereby attenuates the release of additional profibrogenic cytokines and reduced ECM production [28].

Connective tissue growth factor (CTGF/CCN2) is a growth factor-modulator protein secreted from HSCs in the setting of hyperglycemia, hyperinsulinemia and ethanol-induced liver injury [29,30]. It is a major fibrogenic signal whose activity can be both TGF β -dependent when produced in hepatocytes, and TGF β -independent when derived from HSCs [31]. CTGF may be a useful serum biomarker for fibrosis severity, as it is significantly correlated with fibrosis in patients with HCV in one study [32].

Chemokine Pathways

Chemokines are a class of small chemotactic molecules with cytokine-like functions, which are well known to orchestrate inflammatory responses within different organs [33]. Multiple effector cells in liver fibrosis are potential targets and sources of chemokines, each expressing a different combination of receptors and ligands. For example, HSCs express several receptors including CXCR3, CCR5, and CCR7, and secrete numerous chemokines, including CCL2, CCL3, CCL5, CXCL1, CXCL8, CXCL9 and CXCL10 [34]. Specific functions of these chemokines are being actively explored both to understand the pathophysiology of fibrosis, as well as to unearth new therapeutic targets.

In general, chemokines promote the migration of fibrogenic cells to the site of injury, thereby enhancing fibrogenesis through increased cell number and amplified inflammation. Notably, CCR5, whose ligand, RANTES, is induced by NF κ B signaling, and stimulates HSC migration and proliferation [35]. In mouse models of fibrosis (CCl₄ and bile duct ligation), CCR1- and CCR5-deficient mice displayed substantially reduced hepatic fibrosis and macrophage infiltration [36]. Genetic deletion of platelet-derived CXCL4 in mice also significantly reduces inflammation and reduces fibrosis [37]. In contrast, CXCL9, through its cognate receptor CXCR3, is anti-fibrotic [38]. It is therefore important to define the role of each chemokine independently and in combination, to better understand their overall impact on fibrosis progression and regression.

Adipokine Pathways

Adipokines are polypeptides secreted by adipose tissue in a regulated manner. While some of these molecules are expressed only by adipocytes, resident and infiltrating macrophages and components of the vascular stroma also contribute to the expression of others. Adipokines also contribute to the hepatic manifestations of obesity and are increasingly recognized as key mediators of fibrogenesis, especially in the setting of NAFLD (Non-Alcoholic Fatty Liver Disease) [39].

Leptin, a circulating adipogenic hormone, promotes stellate cell fibrogenesis and enhances TIMP-1 expression, which is associated with increased leptin signaling [40,41]. It exerts its action through the leptin receptor (OB-R), which leads to stimulation of Janus kinase (Jak)-signal transduction and activates the Jak-signal transduction and activator of transcription (STAT) transcription signaling pathway [42] (Figure 2). Leptin has a pro-fibrotic action partially through suppression of peroxisome proliferator-activated receptor- γ (PPAR γ), an anti-fibrogenic nuclear receptor that can reverse HSC activation and maintain HSC quiescence [43]. Leptin levels in circulating blood are proportionate to adipose mass, and enhanced leptin has been clearly tied to HSC fibrogenesis. Sources are likely to be both endocrine and autocrine, and its activity is amplified due to enhanced signaling through the leptin receptor, the expression of which is up-regulated during HSC activation [44]. Concurrently, down-regulation of adiponectin in obesity, a counter-regulatory hormone, might amplify the fibrogenic activity of leptin [45]. Adiponectin expressed is reduced in hepatic fibrosis, and mice lacking adiponectin have enhanced fibrosis after toxic liver injury [46].

Neuroendocrine Pathways

The fibrogenic function of HSCs is also influenced by neurochemical and neurotrophic factors that may be exploitable for targeted therapy. Upon chronic liver injury, the local neuroendocrine system is up-regulated, and activated HSCs express specific receptors, most prominently those regulating cannabinoid signaling [47]. Activated stellate cells are additionally a key source of the endogenous cannabinoid, 2-AG, which drives increased CB1 receptor signalling [48] (Figure 2). Stimulation of the CB1 receptor is profibrogenic,

whereas the CB2 receptor is anti-fibrotic and hepatoprotective. CB1 receptor may also mediate steatosis, since daily cannabis use is a risk factor for steatosis and fibrosis in HCV. In fact, a peripheral CB1R antagonist that does not enter the CNS (where both receptors are also highly expressed), leads to improvement in fatty liver in an animal model [49]. Efforts are being expanded based on pre-clinical models to either antagonize CB1 or agonize CB2 for therapeutic use [50,51].

Other neurotrophic or hormonal mediators also contribute to fibrosis. Opioid signaling increases proliferation and collagen production in HSCs [52]. Serotonin has a pro-fibrotic effect that synergizes with PDGF signaling [53]. Thyroid hormones enhance activation of HSC through increased p75NTR and activation of Rho, thereby accelerating development of liver fibrosis [54]. These cellular pathways merit further exploration as new drug targets since there are already agonists or antagonists for them in clinical development.

Immune Interactions

The inflammatory response plays an important role in driving fibrogenesis, since persistent inflammation almost always precedes fibrosis. Activated HSCs secrete inflammatory chemokines [see above], interact directly with immune cells through expression of adhesion molecules [55], and modulate the immune system through antigen presentation [56]. Therefore, a positive feedback loop exists in which inflammatory and fibrogenic cells stimulate each other in amplifying fibrosis. Other cell types regulating progression and resolution of fibrosis include natural killer cells (NK)[57], T-cells [58], dendritic cells [59], macrophages [60], Kupffer cells [61], as well as HSCs [56] and endothelial cells [62].

Immune activation also provokes fibrosis through signaling in response to bacterial lipopolysaccharide (LPS), a ligand for the TLR4 receptor, which is expressed on both macrophages and HSCs [63,64]. In fact, signaling of HSCs in response to either LPS or endogenous TLR4 ligands (high-mobility group box 1 (HMGB1), biglycan and heparan sulfate) may be even more important to the fibrogenic response than macrophage activation (Figure 2). Downstream of TLR4, BAMBI, a transmembrane suppressor of TGF β 1, when suppressed, leads to activation of TGF β 1 [65].

In another interaction, Kupffer cell activation leads to increased NF- κ B activity and subsequent secretion of pro-inflammatory cytokines including tumor necrosis factor- α (TNF- α) and monocyte chemoattractant protein (MCP)-1, which provoke the activation of HSCs [61]. HSCs in turn respond to this stimulation by secreting macrophage colony-stimulating factor (M-CSF)[66], MCP-1 [67], IL-6 [68], CCL21 [4], RANTES, and CCR5 [35] leading to an amplified acute phase response with further activation of macrophages. TNF- α also induces neutrophil infiltration and stimulates mitochondrial oxidant production in hepatocytes, which are sensitized to undergo apoptosis. In mice deficient for both TNF receptors (types 1 and 2) fed with an MCD diet (an established model for fibrosing steatohepatitis), there is less Kupffer cell activation and reduced collagen deposition compared to wild-type mice [69], implicating TNF- α directly in Kupffer cell activation.

Oxidant stress [70] and apoptotic parenchymal cells [71] are also strong inducers of the immune system (see Oxidant stress below). Apoptotic cells resulting from liver injury may be phagocytosed by HSCs, which in turn stimulates an increase in NADPH oxidase (NOX) and cell survival [72,73]. NOX induction also provokes oxidant stress, which contributes to HSC activation. Additionally, apoptotic hepatocyte DNA can interact with Toll like receptor 9 (TLR9) expressed on HSCs. Activation of TLR9 can repress HSC migration and increase collagen production [74]. Although blocking apoptosis of hepatocytes has been an attractive anti-fibrotic pathway, clinical trials using apoptosis inhibitors have been discontinued over fears that they may promote the risk of cancer.

Natural killer (NK) cells have an anti-fibrotic activity by inhibiting and/or killing activated HSCs (Figure 1). In liver injury, NK cells induce apoptosis of HSCs through production of interferon γ [59]. Quiescent HSCs are relatively resistant to apoptotic signals but become sensitive after activation and down-regulation of their class I MHC expression [75]. Moreover, immuno-suppressed individuals with decreased levels of NK cells in the liver have increased fibrosis, possibly due to less NK cell-mediated HSC apoptosis [76]. One mechanism for NK cell-mediated HSC death requires down-regulation of iKIR, an inhibitory receptor on NK cells, and down-regulation of MHC class I on HSCs for efficient killing. In mice and human co-culture models, knockdown of iKIR with siRNAs in lymphocytes stimulates NK cells and promotes their antifibrogenic activity [59].

Lastly, HSCs interact directly with various immune cells through their expression of adhesion molecules, including intercellular adhesion molecule 1 (ICAM-1) [55,59] and vascular cell adhesion molecule 1 (VCAM-1)[77]. Expression of both adhesion molecules is increased in HSCs during injury, which is mediated by TNF α , and peaks with maximal cell infiltration. Thus, adhesion molecule induction on HSCs facilitates the recruitment of inflammatory cells to the injured liver.

Angiogenesis

Angiogenesis is a key component of the wound healing response to hepatic fibrosis and is essential for liver regeneration. Conversely, it is also implicated as a promoter of liver carcinogenesis; therefore, a fine balance of pro- and anti-angiogenic factors maintains a healthy liver [78].

The contractile phenotype of HSCs is thought to contribute to angiogenesis and portal hypertension in the cirrhotic liver [79]. HSCs are uniquely positioned in the perisinusoidal space where their long processes have a potential regulatory effect on pericapillary resistance and may help regulate intrahepatic blood flow via their contractile phenotype [80]. In fact, the contractile force generated by HSCs in response to vasoactive substances is sufficient to contract against sinusoidal pressure based on *in vitro* and *in vivo* studies [81]. Some vasoactive factors, especially endothelin-1 (ET-1) [82], constrict HSCs, whereas others, including nitric oxide and carbon monoxide (CO), promote relaxation. Interestingly, physiological concentrations of CO acts as an antioxidant, and are anti-inflammatory and anti-apoptotic. This cytoprotective effect is seen in response to cellular stress, in addition to its vasodilatory effect [83].

During progressive liver injury, there are areas of vascular disorganization that create a hypoxic milieu, which is a major stimulus to angiogenesis. Hypoxia-inducible factor-1 α (HIF-1 α) is an oxygen-sensitive transcription factor and the primary mediator of the hypoxia-induced angiogenic response. VEGF and PDGF are cytokines that drive both angiogenic and fibrogenic responses, each of which is induced in hypoxic states, in part by HIF- α [78]. HSCs are activated in response to hypoxia and play a key role in angiogenesis through interactions with endothelial cells via PDGF and VEGF signaling (Figure 2).

Endothelial cells, in addition to contributing to angiogenesis, exert paracrine effects on HSCs through nitric oxide (NO) synthase-derived NO production. Activated HSCs are more sensitive to NO-induced apoptosis, which may be a mechanism to counter-balance HSC expansion in injured livers [84].

NADPH oxidase/oxidant stress

Reactive oxygen species (ROS) are generated through lipid peroxidation, and both initiate and then perpetuate fibrosis [85]. ROS can originate from hepatocytes, macrophages, HSCs, cholangiocytes and inflammatory cells, and are enhanced by ethanol, polyunsaturated fatty

acids, and iron. In alcoholics, there is strong induction of cytochrome P450 2E1 leading increased ROS and peri-central (zone 3) injury. NADPH oxidase (NOX) mediates liver injury and fibrosis through generation of oxidant stress and activation of HSCs, Kupffer cells and macrophages. NOX also contributes to angiotensin signaling [86]. Curtailing oxidative stress as a therapeutic option in patients with liver fibrosis is still under investigation. In a phase II clinical trial of the mitochondria-targeted anti-oxidant mitoquinone there was significantly decreased plasma ALT and AST in patients with chronic HCV infection, suggesting that the drug may decrease necroinflammation in the liver in these patients. A possible mechanisms includes induction of the antioxidant transcription factor Nrf2 [87,88].

Ethanol metabolism leads to free fatty acid accumulation, which is an important stimulus to fibrogenesis. Free fatty acids which promote oxidant stress, are indirect activators of HSCs in culture [89]. In ethanol-fed mice, resveratrol improved mortality, transaminase levels and liver lesions [90]. However, cell culture experiments revealed activation of HSCs when treated with resveratrol under free fatty acid-rich conditions, contradicting the beneficial effects seen in obese patients [91].

Gene regulation during HSC activation

Regulated changes in gene expression are required for HSC activation, which reflect the convergence of several intracellular signaling cascades on regulatory regions of key molecular signals. Mechanisms of gene regulation include not only direct modulation of transcription factor activity, but also epigenetic regulation through promoter methylation, mRNA stabilization, and microRNA interactions. Additionally, post-translational regulation of transcription factors with modifications including phosphorylation, SUMOylation, prenylation, acetylation, and glucosylation, add another layer of complexity to gene regulation [92]. Collectively, these regulatory changes control the fibrogenic and proliferative state of the HSC.

Transcription Factors

Although countless transient changes in gene transcription occur after activation of HSCs, the prominent transcriptional targets include: type I collagen [alpha 1 and alpha 2 chains], α -SMA, TGF β 1, TGF β receptors, MMP-2, and TIMPs 1 & 2 [93–95]. Among the transcription factors that activate these downstream targets are Ets-1, Mef2, CREB, Egr-1, Vitamin D receptor, Foxf1, JunD, and C/EBP β [96]. LIM homeobox gene 2 (Lhx2) knockout mice embryos develop a spontaneous and progressive hepatic fibrosis, so is considered to be an anti-fibrotic transcription factor [97]. Forkhead box gene, group O (FoxO1) inhibits proliferation of HSCs, and is inactivated by phosphorylation downstream of PDGF and insulin signaling [97,98].

HSC express several basic helix–loop–helix (bHLH) transcription factors, which bind to a DNA hexanucleotide sequence known as the E box. Some of these factors (MyoD, SREBP-1c, c-myb and c-Myc) regulate tissue development and differentiation. HSCs also express Id proteins, which operate as dominant-negative bHLH transcriptional regulators that inhibit differentiation and promote cell proliferation; surprisingly, they display an anti-fibrotic effect when over-expressed in a thioacetamide-induced mouse model of fibrosis [92]. C/EBP α is an anti-fibrotic transcription factor that declines in expression with HSC activation. Forced over-expression of C/EBP α in HSCs not only inhibits their proliferation but also decreases other fibrogenic features of the cell [99].

Nuclear Receptors

HSCs express a diverse group of nuclear receptors, including the retinoid responsive RXR and RAR, the farnesoid X receptor (FXR), the pregnane X receptor (PXR), and peroxisome proliferators-activated nuclear receptors (PPARs) [92]. RXR and FXR dimerize after sensing bile acids to suppress collagen gene expression through the action of SHP. PXR is highly expressed on HSCs and is activated by steroids, drugs, xenobiotics and antibiotics. PXR then dimerizes with RXR to induce cytochrome p450 enzymes. PPAR γ nuclear receptor down-regulates HSC activation and reduces collagen gene expression [92].

Epigenetic Regulation

Epigenetics refers to changes in DNA methylation and associated histone modifications that influence the chromatin states and impact gene expression patterns, without affecting the sequence of the target DNA. Epigenetic regulation is a relatively new area of gene regulation, but its importance in HSC activation is already clear. HSC activation leads to global hypomethylation, reflective of the overall increase in protein synthesis needed to transdifferentiate a quiescent cell to an activated state [100]. However, induction of the molecules CBF1 and MeCP2 lead to I κ B repression through promoter methylation, which is necessary for de-repressing NF κ B activity and promoting HSC survival [94]. Therefore, although many genes need to be activated by de-methylation in fibrogenesis, there exist dominant pathways that must still be silenced in order to yield a fully activated HSC.

microRNA

MicroRNAs (miRNAs) represent a family of small non-coding RNAs controlling translation and transcription of many genes [101]. This new level of regulation has provoked the reassessment of previously well-understood pathways of disease to now consider the contribution of miRNAs. Although miRNA research has quickly expanded in the field of cancer, only recently have miRNAs been evaluated for their role in fibrogenesis.

Based on gene array analysis in mouse models of fibrosis, the miR-29-family of miRNAs is down-regulated in fibrotic livers. This down-regulation is also reported in patients with more advanced hepatic fibrosis. Mechanistically, miR-29 in HSCs is down-regulated via TGF- β , LPS, and NF- κ B. Additionally, over-expressing miR-29b in HSCs lead to a decrease in collagen production [102]. There is still a lot to be learned about miRNAs in the field of fibrosis, but with each discovery comes the exciting possibility of a new drug target for therapy.

Summary

In the past decade, dramatic advances have advanced our understanding of the cellular and molecular mechanisms underlying liver fibrogenesis. The identification of activated HSC as the major fibrogenic cell type in the injured liver, as well as revealing the intricacies of HSC initiation and perpetuation have unearthed important targets for drug development, including PDGFR, TGF- β , EGF, and VEGF. These signals conspire to generate scar through enhanced HSC proliferation, contractility, fibrogenesis, matrix degradation, and pro-inflammatory signaling.

This review has also described the prominent new mechanisms of liver fibrosis and highlighted signaling pathways that are being actively studied. There is growing appreciation for the importance of immune interactions, chemokines, adipokines, neuroendocrine factors, and oxidant stress towards fibrogenesis. Steady advances in understanding how to exploit these various pathways towards fibrosis regression is generating realistic hopes for effective anti-fibrotic therapies.

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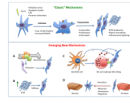


Figure 1. Stellate cell activation through “classic” mechanisms (upper panel) and emerging new mechanisms (lower panel)

The HSC is the central effector in hepatic fibrosis and undergoes activation through a two-phase process. Initial liver injury results in hepatocyte cell apoptosis with generation of apoptotic bodies, reactive oxygen species, and paracrine stimulation of HSCs. Additionally, LPS from the gut can stimulate HSCs. These initial stimuli allow the cell to become sensitized to additional activation by upregulating various receptors and is termed the initiation phase. Subsequently, it is able to secrete autocrine and paracrine growth factors, chemokines, and ECM. Maintenance of HSC activation is termed the perpetuation phase, and involves changes in HSC behavior, including proliferation, chemotaxis, fibrogenesis, and contractility. (A) Among other cell types that may contribute to ECM production, fibrocytes derived from the bone marrow are believed to transdifferentiate into myofibroblasts. (B) Mechanical stiffness of the ECM can be sensed by and activate HSCs. (C) The contribution of dendritic cells to fibrosis is complex and not yet well understood, however, they can activate NK cells. HSCs become sensitized to NK cell mediated apoptosis after cellular activation causes downregulation of their inhibitory MHC class I molecules. (D) New evidence suggests fibrosis can regress through reversion, senescence or apoptosis of HSCs.

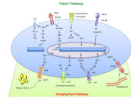


Figure 2. Current and emerging signaling pathways regulating HSC activation

PDGF signals partially through ERK activation and also through AKT via mTOR mediated protein synthesis regulation. PDGF activation also allows for influx of Ca^{2+} ions, which contributes to gene regulation. In addition to PDGF, several other growth factors can activate tyrosine receptors, which lead to Akt activation and then either mTOR or JNK activation. TGF- β recruits Smad2/3, leading to their phosphorylation and stimulation of fibrogenic gene expression. Emerging pathways of importance to fibrosis include contributions from adipokines (leptin), neuroendocrine signals (2-AG), TLR signaling, and angiogenic signals (VEGF), among others.