

Heparan Sulfate Regulation of Progenitor Cell Fate

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Abstract Currently there is an intense effort being made to elucidate the factors that control stem and progenitor cell fate. Developments in our understanding of the FGF/FGFR pathway and its role as an effector of stem cell pluripotency have heightened expectations that a therapeutic use for stem cells will move from a possibility to a probability. Mounting evidence is revealing the molecular mechanisms by which fibroblast growth factor (FGF) signaling, together with a large number of other growth and adhesive factors, is controlled by the extracellular sugar, heparan sulfate (HS). What has resulted is a novel means of augmenting and thus regulating the growth factor control of stem and progenitor cell fate. Here, we review the numerous bioactivities of HS, and the development of strategies to implement HS-induced control of cell fate decisions. *J. Cell. Biochem.* 99: 1040–1051, 2006. © 2006 Wiley-Liss, Inc.

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The growth and survival of progenitor cells constitutes a vital step in the maintenance of tissue health and integrity. Control over these processes is exerted through the tissue *niche*, and particularly elements of its specialized extracellular matrix, which ultimately triggers a cascade of signals that regulate the uncommitted cells, including a plethora of cell survival and cell cycle progression events that shape developmental processes and ultimately morphogenesis [Aszodi et al., 2000; Gustafsson et al., 2003]. The coordination of this extracellular traffic requires a pericellular system that can rapidly adapt to the changing needs of tissue in their most dynamic phases.

Heparan sulfate proteoglycans (HSPGs) are abundant cell surface and extracellular matrix molecules that consist of a defining core protein (such as syndecan, glypican, or perlecan) to which are attached highly sulfated glycosaminoglycan (GAG) side-chains of heparan sulfate

(HS) [Bernfield et al., 1992]. Modifications of these HS chains during biosynthesis, together with core protein variability, results in the wide structural diversity of HSPGs [Carey, 1997; Perrimon and Bernfield, 2000]. Further complexity in the HSPGs arises by virtue of their cell type-specific and developmentally regulated synthesis [Bernfield et al., 1999; Perrimon and Bernfield, 2000]. Much of what we know about the function of HS chains is derived from their actions on susceptible growth factors, such as the prototypical fibroblast growth factors (FGFs).

As they become available to cells from the extracellular matrix, FGFs first bind to HS chains with relatively low affinity, but high capacity [Ornitz, 2000]; these then catalyze their binding to high-affinity, but low capacity tyrosine kinase receptors (FGFRs) [McKeehan and Kan, 1994; McKeehan et al., 1998]. Thus, the laws of mass action, together with HS diversity, create a flow of information across their transducing receptors. Despite a limited understanding of the mechanism, it has now been well established that FGF/FGFR/HSPG complexes are necessary for optimal FGF-induced mitogenesis [Rapraeger et al., 1991; Yayon et al., 1991; Krufka et al., 1996; McKeehan et al., 1998; Chang et al., 2000]. In this manner HSPGs act as reservoirs to concentrate

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growth factors close to cells, protecting them from extracellular proteases, and then shepherd them to the cell surface and cross-bind them to their receptors [Ornitz, 2000]. Binding of HS to growth factors may also be important intracellularly, as HS chains have been shown to have a relatively longer half-life than the FGFs after endocytosis, suggesting that the protective effect of HS on FGF may extend all the way to the cell nucleus, so furthering biological function [Burgess et al., 1991; Maciag and Friesel, 1995].

In a similar manner, bone morphogenic proteins (BMPs) are thought to be brought into register by HS with their threonine-serine kinase BMP receptors (BMPRs) [Paine-Saunders et al., 2000; Irie et al., 2003; Takada et al., 2003; Fisher et al., 2006]. Although hepatic growth factor [Lyon et al., 1994] and interferon- γ [Lortat-Jacob et al., 1995] display interesting variations on this pattern, this general schema probably applies to many heparin-binding species, whereby specific protein-binding sites on the rapidly turned over HS chains orchestrate the presentation of crucial factors as cells move through successive developmental phases [Nurcombe et al., 1993; Brickman et al., 1998]. Indeed, heparanase, a matrix-degrading enzyme that cleaves HS side-chains from the core proteoglycans (PGs), has been shown to liberate HS-binding protein bioactivity, as well as contributing to extracellular matrix turnover [Joyce et al., 2005].

Further findings that cell:cell signaling molecules, such as the cellular adhesion molecules (CAMs) [Cole and Akeson, 1989], as well as almost all the extracellular matrix-resident adhesive glycoproteins [Martin et al., 1988], including laminin and fibronectin, have HS-binding sites, have similarly developed our idea of the coordinating functions of HS. The HSPGs may be acting to orientate proteins into their correct positions, whereupon liberated HS-protein complexes are released to the cell membrane to generate cell responses. Thus, the specific interactions between HSPGs and their effector proteins depend on HSPG composition, location, and 3-dimensional structure [Yanagishita and Hascall, 1992; Pye et al., 2000].

HS GLYCOSAMINOGLYCANS

PGs are composed of a core protein to which are attached sugar side-chains composed of

alternating disaccharide units of uronic acid and hexosamine (Fig. 1). The overall size of these GAG chains can vary anywhere between 20 and 150 disaccharides. The variable addition of sulfate groups at irregular intervals adds a major level of complexity to their binding behaviors [Gallagher and Turnbull, 1992; Turnbull and Gallagher, 1993; Sanderson et al., 1994; Perrimon and Bernfield, 2000]. GAG synthesis begins in the Golgi after the core protein arrives from the endoplasmic reticulum [Esko and Zhang, 1996]. Once synthesized in the Golgi, PGs are either stored in intracellular organelles transported to the cell surface, or deposited out into the ECM [Carey, 1997; Prydz and Dalen, 2000].

PGs are classified into broad categories based on the type of GAG attached to the protein. HSPGs possess core proteins which position them into basement membranes, such as collagen XVIII, perlecan, and agrin, or are attached to cell surfaces, like the families of syndecans and glypicans (GPC). HS side-chains contain alternating repeating units of glucuronic or iduronic (Ido) acid and *N*-glucosamine. The growing chain, consisting of numerous GlcA β 1,4GlcNAc α 1,4 disaccharide units, is modified by sulfotransferases and a GlcA C5 epimerase. HS sulfation can occur at 2-*O* of the uronic acid and 3-*O*, 6-*O*, and the free amine of the glucosamine. Each modification is incomplete, which leads to sequence variation on HS. Most of the binding sites that appear to interact with proteins are found in the NS and NA/NS domains, and critical sulfate group spacing creates a series of unique binding sites along any one HS chain, so determining the specificity of HS-protein interaction [Merry and Wilson, 2002]. The end result of this structural pattern is a number of high capacity, low-to-medium affinity binding pockets for particular combinations of signaling proteins closely adjacent to one another, and to the cell surface. Whether each protein has a unique HS-binding motif dedicated to it, or that motifs are created with more general binding capabilities, is still to be determined. In general, the binding of HS to heparan-binding growth factors seems to involve sulfated (S-) domains consisting of predominantly less-sulfated iduronic acid, and glucosamines with high levels of 6-*O*-sulfation. The presence of various *O*-sulfate groups in addition to *N*-sulfate groups in S-domains appears to be able to provide a relatively specific

Proteoglycans

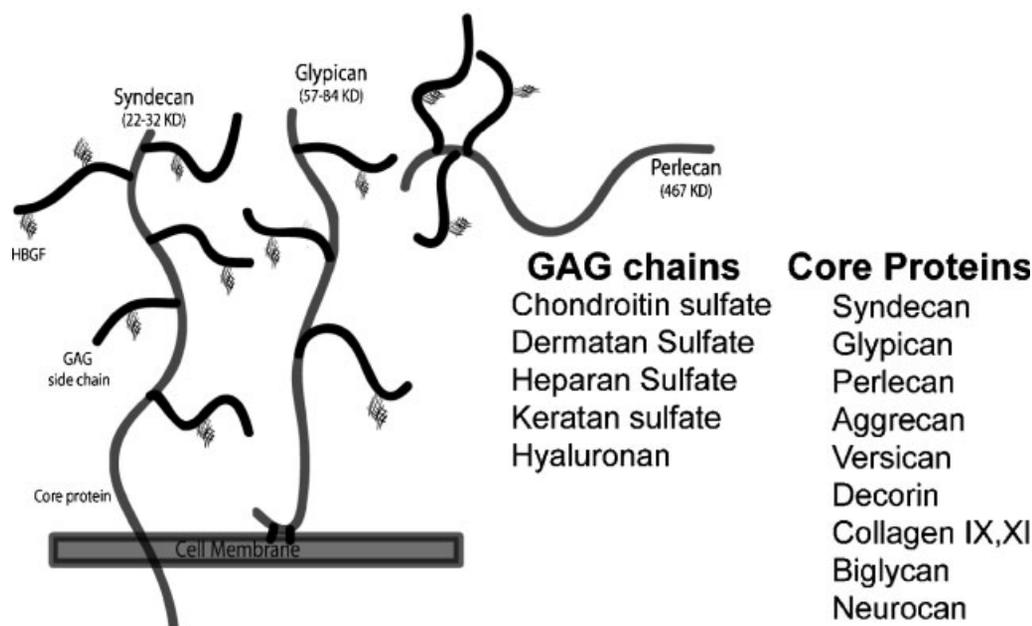


Fig. 1. Proteoglycans (PGs) are a class of heavily glycosylated proteins that have covalently linked sulfated glycosaminoglycans (GAG), (i.e., chondroitin sulfate, dermatan sulfate, heparan sulfate, keratan sulfate). There is great complexity within the proteoglycan family, which consists of numerous GAG side-chains that can potentially bind to a range of core proteins to create a diverse set of cross-linked bioactivators. HSPGs, the

most dynamic of these species, primarily consists of membrane-spanning syndecans, GPI anchored glypicans, and extracellular perlecans, with molecular weights ranging from 22 to 467 kD depending on glycosylation status. HS-GAG side-chains are responsible for binding and potentiating numerous heparan-binding growth factors (HBGFs).

affinity for different growth factors [Princivalle and de Agostini, 2002]. The use of specific heparinases and sulfatases has helped with the determination that IdoA 2-*O*-sulfate and GlcN *N*-sulfate are essential to FGF-2 binding, for example, and that only HS domains of at least deca-saccharide length or larger can stimulate mitogenic activity. In a similar fashion, and in contrast with FGF-2, it was found that a high GlcNS 6-*O*-sulfate content is required for specific HS interactions with FGF-1 and FGF-7 [Kreuger et al., 1999].

It has also been suggested that HS species can differ depending on the stage of development of the tissue [Nurcombe et al., 1993], as HS harvested from murine neuronal tissues at embryonic day 9 appears to preferentially bind FGF-2, while HS from embryonic day 11 favors FGF-1 binding; the temporal pattern of binding reflects the expression pattern of the ligand it activates. This suggested that developing cells might “fish” for the correct combination of growth factors needed to trigger the next phase of development using HS as “bait.” If this were

true, it should theoretically be possible to use the HS synthesized at different developmental stages to help determine the combination of factors needed to drive it through the next phase of maturation.

The importance of HS in mediating cell responses has also been shown with heparinase/heparitinase and sodium chlorate treatments (Fig. 2). Heparinase cleaves HS chains into inactive disaccharide and tetrasaccharide components that have been shown to inhibit FGF-2-mediated smooth muscle cell (SMC) proliferation in injured carotid arteries [Kinsella et al., 2004]. Such experiments have been part of a realization that HS domains that remain incompletely sulfated can become potent inhibitors of the interactions they would normally promote. Several *in vitro* studies have also cultured cells in media supplemented with chlorate to study the role of sulfated GAGs in different cell types [Rapraeger et al., 1991]. Sodium chlorate (NaClO₃) imparts its effects by inhibiting ATP-sulphurylase, the first enzyme in the synthesis of 3'-phosphoadenylyl

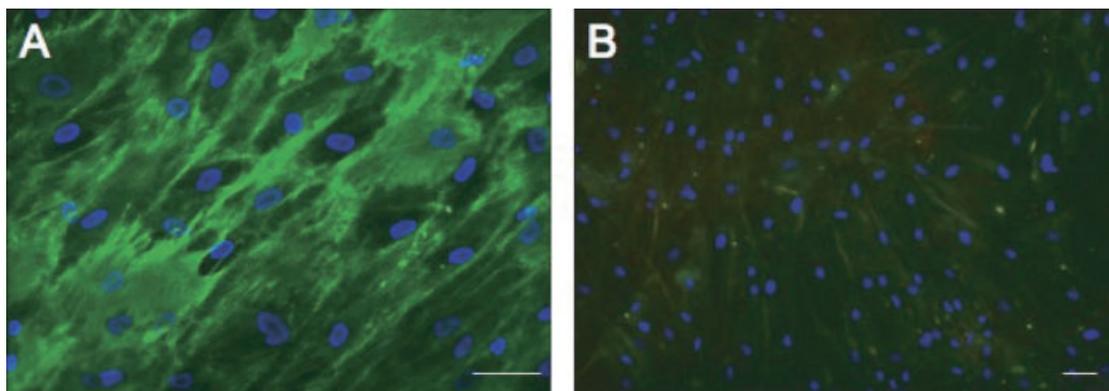


Fig. 2. Mesenchymal progenitor cell cultures express abundant heparan sulfate (HS) when expanded *ex vivo*, as revealed by staining with the HS-specific 10E4 antibody (the monoclonal antibody 10E4, recognizes an epitope that contains *N*-unsubstituted glucosamine, is commonly used to trace HSPGs) (A). This binding is lost when cultures are pre-treated with heparanase, a matrix-degrading enzyme that cleaves HS side-chains from the core protein (B). Cell nuclei have been stained with DAPI. Scale bar = 10 μ m. [Color figure can be viewed in the online issue, which is available at www.interscience.wiley.com.]

5'-phosphosulfate (PAPS), a high-energy sulfate donor in biological reactions [Klaassen and Boles, 1997]. The mitogenic response of cells to FGF-2 is inhibited when cells are cultured in the presence of 30 mM NaClO₃; *N*-sulfation of HS is unaffected by treatment with NaClO₃, whereas significant reductions in 2-*O* and 6-*O* sulfation are observed [Safaiyan et al., 1999]; such data have helped established the idea that HS does not only bind a ligand for delivery to its cognate receptor, but must also itself bind to the receptor, in reactions that involve 6-*O*-sulfate moieties [Guimond and Turnbull, 1999], in order for signal transduction to initiate [McKeehan et al., 1998].

Thus, although the exact roles of HS in the signaling complex have been reasonably well characterized, it is yet to be definitively established that this trimeric model extends to all the other HS-dependent systems. What is known is that defects in HS can cause the complete loss of FGF, Hedgehog, and Wingless/Wnt signaling pathways and lead to severe abnormality, including bone abnormality, during embryonic development [Paine-Saunders et al., 2000; Koziel et al., 2004; Shimo et al., 2004; Song et al., 2005; Yabe et al., 2005]. HS, of course, binds multiple species of not only growth factors, cytokines and chemokines, but also morphogens, such as Wnt and Sonic Hedgehog [Dhoot et al., 2001], most of the large glycoproteins in the ECM [Perrimon and Bernfield, 2000], let alone a suite of proteases and synthetic enzymes. The role of HS thus may be to allow extremely precise and specific molecular interactions to occur at the

right times and places during maturation and regeneration. As such, PGs, and HS in particular, have been styled as catalysts of molecular encounter [Lander, 1998]. Certainly the heterogeneity seen in HS chains during development may reflect the multiple interactions being regulated at each developmental stage [Nurcombe et al., 1993]. One advantage of such tripartite systems is that a particular responsiveness (i.e., intracellular signaling) is not selected by levels of a growth factor or its receptors but by the targeting of a growth factor to a particular receptor by a specific motif on the HS chain [Chang et al., 2000].

NOVEL CONTROL OF GROWTH FACTOR SIGNALING

Among the HS-binding factors known to be important to progenitor cells are a suite of mitogens that include the PDGFs, the VEGFs, the FGFs, BMPs 2, 4, and 7, their receptors, as well as TGF- β 1, collagen I, laminin, and fibronectin, together with cell-cell mediators, such as the CAMs and cadherins [Ruoslahti and Yamaguchi, 1991; San Antonio et al., 1994; Perrimon and Bernfield, 2000; Ornitz and Marie, 2002] (Table I). Among this list, members of the FGF family play a major role in maintaining human embryonic stem (hES) cell self-renewal and pluripotency [Amit et al., 2000; Xu et al., 2005]. The FGF family presently encompasses more than 20 members, of which the prototype members are FGF-1 and FGF-2 that bind to four related receptor tyrosine

**TABLE I. Heparan Sulfate and Heparin-Binding Proteins (Incomplete List)
[Yayon et al., 1991; Rapraeger, 1995]**

Mitogens/morphogens/chemokines	FGF-1, FGF-2, FGF-3, FGF-4, FGF-5, FGF-6, FGF-7, FGF-8, FGF-9, HGF, VEGFs, activins BMPs, TGF- β s, PDGFs, HB-GAM, pleiotropins, GM-CSF, interferon- γ , NT4/5, GDNF, Wnts Hedgehogs
Adhesive glycoproteins	Fibronectin, vitronectin, laminin, collagens, thrombospondin, tenascin, vonWillebrand factor, NCAM, N-cadherin
Enzymes	Lipoprotein lipase, hepatic lipase, phospholipase, apolipoprotein B, apolipoprotein E
Serine protease inhibitors	Antithrombin III, heparin cofactor II, protease nexins
Other factors	Superoxide dimustase, elastase, platelet factor 4, N-CAM, transcription factors, DNA topoisomerase, RNA polymerase, tumor necrosis factor stc

kinases (FGFR-1–4) coded by four distinct genes expressed in most cell types [Naski and Ornitz, 1998]. Over the past 10 years, we have been able to confirm seminal findings [Rapraeger et al., 1991; Yayon et al., 1991; Kan et al., 1993; Nurcombe et al., 1993; Brickman et al., 1995; Joseph et al., 1996; Boilly et al., 2000] that FGF interactions with cellular receptors are dependent on HS [Colin et al., 1999].

While not directly responsible for signal transduction, HSPGs have been shown to internalize with FGF from the cell surface, thus suggesting the bioavailability of FGF to FGFRs may be under the control of a dual role of HSPGs, those of immobilization and internalization [Colin et al., 1999]. FGF-specific HS chains have been isolated from embryonic mouse neuroepithelial cells that have potentiating effects specifically for FGF-1 and FGF-2 [Nurcombe et al., 1993, 2000], a differential mechanism that has now been confirmed in fibroblasts, macrophages, and cancer cells [Bernfield et al., 1999]. Furthermore, we used cross-linking to show that specific combination of FGF and HS preparations cause an increase in specific FGFR isoform activity [Nurcombe et al., 2000] and thus effect phenotypic change.

HS AND DEVELOPMENT

During embryonic development, the BMPs are known to exert control over crucial events including mesoderm formation, neural patterning, skeletal development, and limb formation. Tellingly, BMPs were originally isolated using heparin affinity columns, and thus the involvement of HS in the control of BMP-mediated developmental processes, including BMP signaling, has long been suspected [Sampath et al., 1990]. More recently, it has been shown in *Xenopus* embryos that HS/heparin chains are capable of binding to BMP-4 and restricting its

expression pattern [Ohkawara et al., 2002]. As well as its agonistic effects on BMP, HS is also known to bind to BMP antagonists, such as noggin, a secreted polypeptide that inhibits the functions of BMPs, resulting in modification of BMP activity [Paine-Saunders et al., 2002]. In addition, mutations of the *Drosophila* gene *dally*, which encodes a *Drosophila* glypican, show abnormalities in the modulation of Decapentaplegic (Dpp), a member of the *Drosophila* TGF- β /BMP superfamily, resulting in altered morphogenesis [Jackson et al., 1997]. Recent genetic studies also support the idea that HS chains are involved in regulating multiple signaling pathways crucial to developmental processes [Nakato and Kimata, 2002]. For example, *Drosophila* mutants with defects in the genes *sulfateless* and *sugarless*, which encode for HS N-deacetylase/N-sulfotransferase and UDP-glucose dehydrogenase respectively, show abnormalities in Wingless-mediated dorsal/ventral patterning [Lin and Perrimon, 1999]. Another *Drosophila* mutant, with a defect in HS copolymerase (*tout velu*), exhibits abnormal Hedgehog diffusion [Bellaiche et al., 1998]. Furthermore, combined genetic deficiencies for GPC-3 and BMP-4 result in abnormal skeletal development [Paine-Saunders et al., 2000]. GPC-3 deficiency also abrogates BMP-2 and BMP-7-dependent ureteric bud morphogenesis in embryonic kidney explants [Grisaru et al., 2001]. Thus, HS orchestrates the molecular context of BMP bioactivity.

Antagonism between FGF and BMP signaling is a feature of development. Recently, it has been shown that introducing inhibitors of BMPs together with FGF-2 into culture medium of hES cells can facilitate the long-term maintenance of these cells in a pluripotent state [Xu et al., 2005]. Hence, the coordinated control of progenitor cell proliferation, as prescribed by the balance in FGF- and BMP-mediated signaling, imposes a primary control over subsequent

cell fate decisions. Thus, it is possible to posit that FGF-specific HS will promote the proliferation of progenitor cells, prevent their exit from the cell cycle, and contribute to maintenance of a progenitor/*naive* precursor cell identity. In contrast, it is possible to predict that BMP-specific HS should have little effect on cell proliferation, but instead would coordinate with FGF to control the initial onset of differentiation.

HS AND CELL PHENOTYPE

Until quite recently there was a consensus that the fate of adult stem cells was restricted to their tissues of origin. However, the recent spate of findings that adult stem cells could be “re-programmed” to express genes typical of differentiated cell types across all three of the mesodermal, endodermal, and ectodermal lineages when fused to cells in heterokaryons has been both informative and provocative [Brazelton et al., 2000; Mezey et al., 2000; Blau et al., 2001]. This degree of plasticity demonstrated that the differentiated state might be reversible, requiring continuous prompting to maintain the correct balance of differentiating factors needed. More recently, it has been shown that progenitor cells can assume diverse fates under physiologic conditions. Bone marrow cells can be made to yield not only all cells of the blood, but also cells bearing a liver phenotype [Petersen et al., 1999]. Muscle-derived and CNS-derived progenitor cell-like populations have also been reported that can reconstitute the blood and so rescue lethally irradiated mice [Mezey et al., 2000; Vescovi et al., 2001]. Recently, data from our lab demonstrated that adult neural progenitor-derived HS was able to apparently “transdifferentiate” primary, vimentin-expressing pre-osteoblasts into a neuronal-like phenotype that expressed MAP2 [Chipperfield et al., 2002]. When looking at progenitor cell niches, it is striking that all contain laminins, either in the form of a basal lamina (BL) in contact with the progenitor or supporting cells, or as a non-BL matrix secreted by the supporting cells, such as the bone marrow stroma [Fuchs et al., 2004]. Where laminin is expressed, HS follows.

HS and Neural Progenitors

Integrin β 1-expressing neural progenitors in both embryonic and adult cerebral cortex are in intimate contact with HS-rich BL. In the

embryonic cerebral cortex, stem cells are present in the periventricular niche [Cohen et al., 1986] whereas in the adult individual neural progenitor cells are contacted by extensions protruding from the blood vessels in the subventricular zones [Parati et al., 2004]. Several growth factors, including LIF, EGF, and FGF-2, are capable of triggering the proliferation of multipotent progenitor cells in vitro [Gage et al., 1995; Carpenter et al., 1999; Palmer et al., 1999]. The exact combination or cascade of growth factors necessary for this process seems to be largely determined by the stage of differentiation [Hogg et al., 2004]. FGF-2 appears to be crucial for the continued proliferation of cells that have reached the stage of being committed to a neural fate [Palmer et al., 1999] and different doses of this factor appear to trigger different phenotypes from the progenitor pool [Qian et al., 1998].

Developing neuroblasts project axons over long distances in order to reach their final synaptic targets. HS has been shown to alter the characteristics of neurite outgrowth from neurons in vitro [Bandtlow and Zimmermann, 2000]. The leading growth cone detects and responds to both the attractive and repulsive environmental cues that guide them; these include contact-mediated cues acting over short distances or secreted molecules acting over comparatively longer distances [Tessier-Lavigne and Goodman, 1996]. Axonal reactions depend on intracellular state of the growth cone, differential expression of receptor complexes, and cross-talk between intracellular signaling cascades. Axon guidance molecules can bind to GAG chains in vitro: netrins were originally purified using heparin affinity columns [Serafini et al., 1994], and the netrin receptor DCC also binds to GAG chains in vitro [Bennett et al., 1997]. The Slits, which also modulate neuritic branching and neuronal cell migration [Wang et al., 2005] are also HS-binding, although it is not known if their receptors, the Robos, are. The large family of Eph tyrosine kinases, receptors for the ephrins, are apparently modulated by HS [Wilkinson, 2001], and other signals which could potentially be modulated by HS include the semaphorins, a family of membrane-associated proteins, members of which are capable of mediating both repulsive and attractive cues [Raper, 2000].

Perhaps the most compelling evidence for HS involvement in the development of

neuroarchitecture is from amphibians. Addition of HS to the developing *Xenopus* optic pathway causes severe targeting errors [Walz et al., 1997], and inhibiting sulfation of endogenous HS with chlorate causes axons to bypass their target, the tectum [Irie et al., 2002]. Experiments with purified heparin saccharides show that bypass-inducing activity correlates with distinct structures, particularly those containing a combination of 2-*O*- and 6-*O*-sulfate groups. The results indicate that specific HS sequences, rather than gross structural composition, are critical for activity. In situ hybridization revealed differential staining patterns for HS synthetic enzymes in the region of the tectal synaptic targets, where HS 6-*O*-sulfotransferase is regionally expressed along the border of the projecting dorsal optic tract whereas 2-*O*-sulfotransferase is expressed more widely. It is now known that attractive guidance cues can be converted to repulsive ones by the extracellular matrix; thus, HS may similarly be involved in the modulation of synaptic targeting signals. Interestingly, along these lines, netrin-1 can be converted from an attractive signal for retinal axons to a repulsive one by laminin [Hopker et al., 1999].

HS and Hematopoietic Progenitors

In a similar manner, the microenvironment created by stromal cells has been used to establish cultured hematopoietic progenitors in the absence of exogenously added cytokines [Sutherland et al., 1989; Sutherland et al., 1991; Verfaillie, 1992; Verfaillie, 1993]. In these studies, up to 50% of the long-term culture initiating cells (LTC-IC) can be maintained for up to 8 weeks when cultured in the presence of media conditioned from stromal cells (stroma-derived soluble factors). Additional studies suggest that soluble PGs, but not glycoproteins, are responsible for this sustained growth [Gupta et al., 1996]. Furthermore, LTC-IC maintenance is largely retained after digestion of the PGs with proteinase K, but is completely abolished following treatment with nitrous acid, which digests an involvement of HSPG. Collectively, these studies implicate a role for HS in the maintenance of hematopoietic progenitors *ex vivo*. This is perhaps not surprising, considering stromal HS and hyaluronate are partly responsible for binding hematopoietic progenitors to the marrow microenvironment [Siczkowski et al., 1992; Zweegman et al., 2004].

Furthermore, HS has been shown to stimulate megakaryopoiesis [Han et al., 1996], although recent evidence suggests it may also be inhibitory by virtue of its ability to bind hematopoietic progenitors and megakaryocytopoiesis-inhibiting cytokines [Zweegman et al., 2004]. HS has also been implicated in the differentiation of the human promyelocytic leukemia cell line HL-60 [Luikart et al., 1990] through its action of modifying the activity of several growth-regulating factors, in particular the chemokines, macrophage inflammatory protein 1alpha (MIP1alpha) [Stringer et al., 2002; Stringer et al., 2003], and SDF-1 [Netelenbos et al., 2002]. In addition, loss-of-function mutations in the gene encoding the HS proteoglycan GPC-3 result in a selective impairment of the development of the common hematopoietic lineage from which monocyte/macrophages and peripheral blood mononuclear cells are derived [Viviano et al., 2005]. This was the first report of a requirement for HS, and specifically GPC-3, in the lineage-specific differentiation of these cell types *in vivo*.

HS and Mesenchymal Progenitors

Mesenchymal stem cells are maintained in a local, FGF-rich environment within the bone marrow; this ECM maintains the ability of the stem and progenitor cells to divide asymmetrically in times of quietude, but to rapidly mobilize the proliferation of daughter, transit-amplifying cells during times of rapid growth or tissue repair. This local environment, consisting of the sum of influences provided by support cells and its ECM, contributes to what has become known as the stem cell "niche" [Fuchs et al., 2004]. It has evolved to protect and perpetuate the self-renewing, undifferentiated state of its inhabitants, and to regulate the rate of production of committed progenitors [Marie et al., 2000]. Osteoblasts and adipocytes share a common mesenchymal precursor, whose lineage-specific differentiation is induced by members of the HS-activated BMP family [Irie et al., 2003]. The mechanisms mediating these two mutually exclusive commitment decisions appear to be directly controlled by discrete signaling pathways emanating from the differentially expressed subtypes of the BMP receptors BMPR1A and BMPR1B [Chen et al., 1998]; we consider it highly likely that these receptors are activated by different HS configurations.

Human adult mesenchymal stem cells (hMPC) are routinely expanded in tissue culture utilizing a medium rich in serum, conditions remarkably similar to those used to expand most adherent stromal cell types. Yet despite these culture similarities, the factors that mediate hMSC self-renewal to maintain these *naive* cells as progenitors capable of multilineage differentiation remains unclear. Recent evidence suggests that FGF signaling plays a pivotal role in maintaining the growth, survival, self-renewal, and pluripotency of hES cells [Xu et al., 2005]. The evolutionary conservation of key developmental pathways across germ lines strongly suggests that mechanisms controlling self-renewal and multipotentiality in hMSCs might well share essential features with hES cells.

Our group has previously shown how specific elements of the extracellular matrix within the stem cell *niche*, more particularly HS, can protect, hold, and present FGFs to cells, thus controlling intracellular signaling cascades and ultimately cell fate decisions. More recently, as detailed above, HS has also been shown to be required for BMP signaling, supporting the view that HS orchestrates the transition between proliferation and differentiation. Consequently, tissue-specific HS forms are plausible candidates for the augmentation of hMSC self-renewal by potentiating the FGF signaling cascade while retarding BMP signaling. Interestingly, mutations in glycosyltransferases that function as hetero-oligomers in the Golgi to add repeating GAGs to HS chains have been shown to impair chondrocyte differentiation, and perhaps the perichondrial stem cell reserve [Hecht et al., 2005].

HS and Smooth Muscle Cells

Studies on SMCs indicate that the HS species present in the artery wall can regulate the SMC phenotype. HS extracted from the artery wall of normal non-atherosclerotic arteries not only prevents SMC phenotypic change *in vitro*, but inhibits myointimal thickening when applied to balloon catheter-injured arteries in a periaortic gel [Bingley et al., 1998]. This HS is active at concentrations below that of heparin, or HS derived from other tissues. The addition of HS-degrading enzymes induces modulation of phenotype *in vitro*, while enzymes, such as trypsin and chondroitin ABC lyase, which

degrade other matrix components, have no effect [Campbell et al., 1992]. Further to this, macrophages added to SMCs in primary culture induce changes in phenotype by degrading HS [Fitzgerald et al., 1999]. This change can be prevented by addition of HS or heparin, but not other GAGs, such as chondroitin sulfate. Such phenotypic modulation is not surprising, given that interactions between negatively charged GAG chains and growth factors are essential for the differentiation of cells during development, and for the maintenance of tissue organization [Prydz and Dalen, 2000].

CONCLUSIONS

The development of an "HS approach" for the control of progenitor phenotype has become more feasible in recent years as our understanding of HS cell biology improves. HSs are particularly attractive, as they potentiate the powerful effects of growth factors on cell recruitment, proliferation, and differentiation, and do not depend on the synthesis of other cofactors or other specific activating agents. Thus, they represent a novel approach to for the control of cell phenotype.

We would anticipate that HS, by virtue of its modulation of the biological activities of the FGFs and the BMPs, offers the possibility of intervening not just in embryonic growth, and stem and progenitor cell self-renewal, but also in stem cell-dependent wound healing and regenerative medicine. Unlike other nucleic acid-based clinical approaches (e.g., virus and siRNA), therapeutic intervention may be particularly advantaged because HSs are chemically stable, naturally occurring non-toxic sugars that can be isolated as biologically active compounds from a range of mammalian species.

Realization of the potential of HS for regenerative medicine will depend, however, on a detailed understanding of their effects on cell self-renewal and differentiation, and of how these effects are linked to downstream signaling cascades. Importantly the mechanisms by which inductive signals control the identity, proliferation, and timing of differentiation of stem and progenitor cells remains poorly understood. We hope in the future to provide evidence that HS plays a central role in the coordinated control of progenitor identity, proliferation, and differentiation by regulating FGF- and BMP-mediated signals.

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