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Review

Early signaling pathways activated by c-Kit in hematopoietic cells[☆]

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Abstract

c-Kit is a receptor tyrosine kinase that binds stem cell factor (SCF). Structurally, c-Kit contains five immunoglobulin-like domains extracellularly and a catalytic domain divided into two regions by a 77 amino acid insert intracellularly. Studies in white spotting and steel mice have shown that functional SCF and c-Kit are critical in the survival and development of stem cells involved in hematopoiesis, pigmentation and reproduction. Mutations in c-Kit are associated with a variety of human diseases. Interaction of SCF with c-Kit rapidly induces receptor dimerization and increases in autophosphorylation activity. Downstream of c-Kit, multiple signal transduction components are activated, including phosphatidylinositol-3-kinase, Src family members, the JAK/STAT pathway and the Ras–Raf–MAP kinase cascade. Structure-function studies have begun to address the role of these signaling components in SCF-mediated responses. This review will focus on the biochemical mechanism of action of SCF in hematopoietic cells. Published by Elsevier Science Ltd.

Keywords: Stem cell factor; Signal transduction; Hematopoiesis; Growth factors; Cytokines

1. Introduction

Stem cell factor (SCF) is a growth factor critical in hematopoiesis as well as in the generation

of melanocytes and germ cells, reviewed in references [1–8]. SCF also plays a role in development of the interstitial cells of Cajal in the intestine and in learning functions in the hippocampal region of the brain [9–11]. Occurring physiologically in either membrane-bound or soluble form, SCF promotes viability as well as proliferation and differentiation of hematopoietic progenitor cells. In addition, SCF is potently synergistic in combination with other growth factors such as Epo, IL-3 and GM-CSF. There are several excellent reviews of SCF biology in relation to hema-

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topoiesis [2,4–6]. A comprehensive overview of SCF in relation to its various target tissues can be found in the review by Galli et al. [1]. The purpose of this review is to examine the early signaling pathways activated in response to SCF in hematopoietic cells.

SCF was cloned and characterized in 1990 [12–15]. The receptor for SCF is the product of the *Kit* proto-oncogene [16,17]. The *c-Kit* gene maps to the White spotting (*W*) locus in mice, while SCF is encoded by the Steel locus (*Sl*) [16–19]. The first descriptions of mutant *W* and *Sl* alleles were in 1927 and 1956, respectively [20]. Since that time, multiple alleles of both genes have been discovered and characterized [7,8,20]. While the absence of either SCF or *c-Kit* is lethal in utero, reductions in functional receptor, or

ligand, results in aberrations in hematopoiesis, pigmentation and reproduction.

The *Kit* gene product has been associated with several forms of cancer. The *v-Kit* oncogene was originally identified as a component of Hardy–Zuckerman strain of feline sarcoma virus [21]. In humans, a series of gain-of-function mutations in the *c-Kit* juxtamembrane region have been found in gastrointestinal stromal cell tumors [22]. *c-Kit* is also aberrantly expressed in approximately 70% of all small cell carcinomas of the lung (SCCL), as well as in breast, cervical and ovarian tumors [23–27]. Coexpression of *c-Kit* and SCF in SCCL cells generates an autocrine loop that may play a role in the etiology of these cancers. A constitutively active form of human *c-Kit* (D816 V) has been found with high frequency in

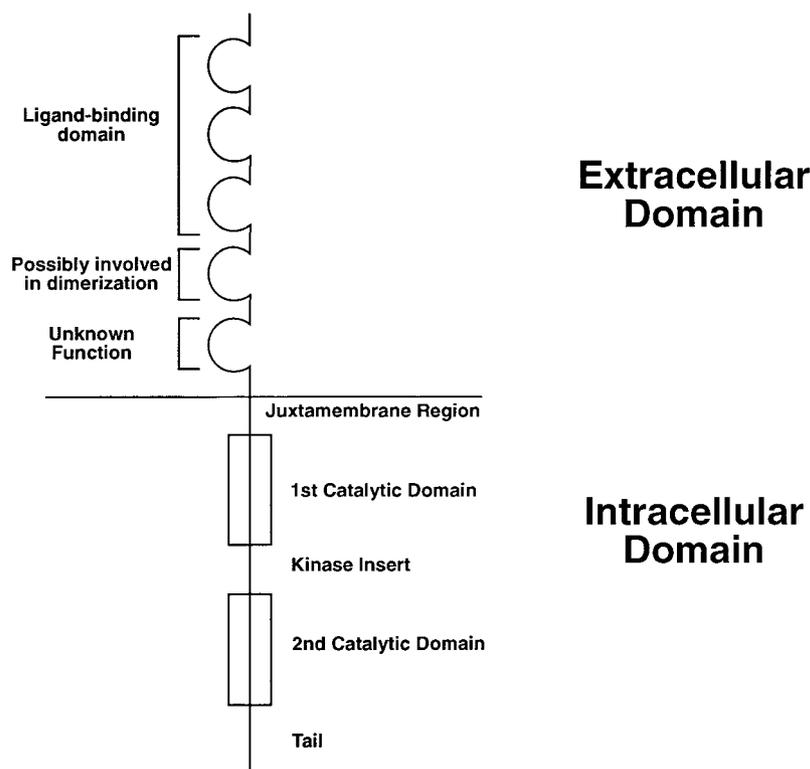


Fig. 1. Structural domains of *c-Kit*. *c-Kit* is divided into an intracellular and extracellular region. The intracellular region consists of five immunoglobulin-like domains. The first three are involved in binding SCF. The fourth may play a role in receptor dimerization and the function of the fifth immunoglobulin-like region is unknown. Intracellularly, the catalytic domain is divided into two by a kinase insert. The 30 amino acids distal to the transmembrane domain is the juxtamembrane region and the last 50 amino acids comprise the kinase tail.

patients with mastocytosis and associated hematological disorders [28]. Hematological disorders in these patients range from myelodysplasia to myeloproliferative disease. In addition, these individuals develop leukemia at high frequencies.

The important role of SCF in development of stem cells involved in hematopoiesis, pigmentation, intestinal function and reproduction, as well as its association with some forms of human disease, has led to interest in understanding its mechanism of action. This review will focus on signaling mechanisms of SCF, specifically in hematopoietic cells.

2. SCF induces receptor dimerization

c-Kit is a receptor tyrosine kinase (RTK) closely related to the receptors for platelet-derived growth factor and colony-stimulating factor-1. Structurally, the c-Kit extracellular domain can be divided into five immunoglobulin-like regions (Fig. 1). The studies of Yarden and coworkers have shown that the first three immunoglobulin-like regions bind SCF, inducing homodimerization of the receptor [29–31]. Two models for ligand-induced dimerization of c-Kit have been suggested [32–39]. The first proposes that binding of dimerized SCF initiates receptor dimerization [33,34,37]. Consistent with this, the dimeric form of SCF is more biologically active than the monomeric form [32,33]. The second model for dimerization of c-Kit proposes that SCF binding of c-Kit monomer induces conformational changes resulting in interaction of the fourth immunoglobulin-like domain between two molecules of c-Kit [39]. While a soluble form of c-Kit containing only the first three immunoglobulin-like regions is capable of dimerizing, the fourth immunoglobulin-like domain is critical for dimerization of full length, membrane-associated c-Kit.

The majority of studies examining c-Kit dimerization have been performed with recombinant proteins *in vitro* or by affinity crosslinking of cell lines engineered to express c-Kit. Recently, Broudy et al. [40] used fluorescent resonance energy transfer (FRET) to detect SCF-induced c-

Kit dimerization in both hematopoietic cell lines as well as the progeny of normal BFUe progenitor cells.

3. c-Kit autophosphorylation

The cDNA sequence of the c-Kit proto-oncogene predicted that the protein was a RTK [41,42]. Indeed, *in vitro* kinase assays of c-Kit immunoprecipitates found intrinsic tyrosine kinase activity [41,43]. The organization of the cytoplasmic domain of c-Kit is similar to that of the receptors for colony-stimulating factor-1 and platelet-derived growth factor. The catalytic domain is divided by a 77 amino acid insert (Fig. 1). The first catalytic domain contains the ATP binding region while the second catalytic domain has a number of possible autophosphorylation sites. SCF-induced dimerization of c-Kit is rapidly followed by increases in autophosphorylation activity [34–38]. While many of the early studies examining SCF-induced increases in c-Kit autophosphorylation were performed in fibroblast or endothelial cells transfected with c-Kit, identical results have been obtained in hematopoietic cell lines of multiple lineages [44–46].

SCF exists in both soluble and transmembrane forms *in vivo*. Though the soluble form has biological activity, mice expressing only soluble SCF (Steel-dickie, *Sl^d*) have abnormalities in hematopoiesis, pigmentation and reproduction [20]. Interestingly, these two forms of SCF have different effects on c-Kit kinase activity [47,48]. Increases in c-Kit autophosphorylation were maintained over 2 h after stimulation with membrane-bound SCF, while autophosphorylation in response to soluble SCF returned to basal levels in half that time. This may be due to the slower rate of c-Kit downregulation in response to membrane bound SCF [47]. Similar to soluble SCF, membrane bound SCF also dimerizes [48,49]. Although truncation of the cytoplasmic region of SCF does not impair ligand dimerization, the alteration of amino acids 238–273 in the cytoplasmic tail of SCF does reduce dimerization [49]. This mutation has been found in the *Sl^{17H}* allele and is associated with subtle defects in

hematopoiesis. Thus, dimerization of membrane bound SCF likely plays a role in maintaining normal hematopoiesis in vivo. The signaling mechanisms mediating these events remain unexplored.

Studies of *c-Kit* gene products resulting from different alleles of the White spotting (*W*) locus have demonstrated the importance of *c-Kit* kinase activity in SCF signaling. The severity of the phenotype of each of these mutants is proportional to the degree of impairment in kinase activity. One mutant with a particularly severe phenotype and concomitant reduction in kinase activity is *W*⁴². *W*⁴² results from substitution of aspartic acid 790 with asparagine of murine *c-Kit* and has a dramatic reduction in intrinsic kinase activity [50]. The molecular basis of the known *W* mutants and the corresponding phenotypes have previously been summarized [7,8,51,52].

The relationship of *c-Kit* kinase activity and cellular proliferation can further be illustrated by the factor-independent proliferation, as well as transforming abilities, of several gain-of-function mutations. The best characterized of these is the substitution of valine for aspartic acid 816 of human *c-Kit* (D816 V in human *c-Kit* and D814 V in murine *c-Kit*). This mutation has been identified in factor-independent mastocytoma lines derived from humans (HMC1), mice (P-815) and rats (RBL-2H3) [53,54]. Expression of D816 V *c-Kit* in factor-dependent cell lines results in factor-independent cell lines that produce tumors in mice [55–58]. This mutation is also found in most patients with mastocytosis with associated hematological disorders [28]. Studies of *c-Kit* activity in cells expressing the D816 V *c-Kit* mutant have found constitutive phosphorylation on tyrosine residues and increases in in vitro catalytic activity compared to wild type *c-Kit* [53–56,59]. Peptide mapping studies have suggested differences both in autophosphorylation sites and substrate specificity between wild type *c-Kit* and the D816 V *c-Kit* mutant [59]. In contrast to a number of other gain-of-function *c-Kit* mutants, activation of D816 V *c-Kit* occurs in the absence of receptor dimerization [55,60].

The *c-Kit* juxtamembrane region (amino acids 544–577) is the site of multiple mutations that constitutively activate *c-Kit*. Substitution of glycine for valine 559 of murine *c-Kit* results in constitutive dimerization and activation of *c-Kit* as well as increases in its oncogenic potential [55,57,60,61]. Deletion of seven amino acids in the juxtamembrane region also generates a constitutively active form of *c-Kit* that spontaneously dimerizes [61]. Patients with gastrointestinal stromal cell tumors have a series of mutations in the *c-Kit* juxtamembrane region that also leads to constitutive activation [22].

Lastly, the *v-Kit* oncogene has constitutive kinase activity and is transforming [21]. Structurally, it lacks the extracellular region and the 50 amino acid carboxyl terminus of *c-Kit* [42]. In addition, tyrosine 569 and valine 570 are deleted, glycine is substituted for aspartic acid 761 and a five amino acid insertion is found in the carboxyl terminus [42,62]. As expected, *v-Kit* was phosphorylated on tyrosine residues in vitro [63]. In contrast, in vivo, *v-Kit* was phosphorylated primarily on serine and threonine residues [63].

4. Phosphatidylinositol-3-kinase and *c-Kit* signaling

SCF activates multiple signaling components, however, the best characterized of these with regards to structure-function relationships is phosphatidylinositol-3-kinase (PI3 K). PI3 K is a heterodimer composed of an 85 kDa regulatory subunit and a 110 kDa catalytic subunit. The 85 kDa subunit (p85) contains several motifs implicated in protein-protein interactions. These motifs include two SH2 domains, an SH3 domain and a proline-rich domain. Increases in autophosphorylation activity of RTKs recruits p85 through the SH2 domain and localizes the 110 kDa catalytic subunit with potential substrates including phosphatidylinositol, phosphatidylinositol-4-phosphate and phosphatidylinositol-4,5-bisphosphate. Recently, phosphatidylinositol-3,4-bisphosphate, a product of PI3 K, was found

to play a role in activation of AKT, a serine–threonine kinase involved in cellular survival. Reviews of PI3 K can be found in references [64–66].

SCF induces the association of PI3 K with c-Kit as well as increases in tyrosine phosphorylation of the 85 kDa subunit. While initial studies used NIH3T3 fibroblasts transfected with a chimeric molecule containing the EGF receptor extracellular region and the c-Kit intracellular region, identical results were obtained with full length c-Kit transfected in fibroblastic cell lines as well as in hematopoietic cells [46,67,68]. Mutants lacking kinase activity do not activate PI3 K in response to SCF, while cells expressing a constitutively active c-Kit mutant have increased levels of PI3 K activity [46]. Thus, activation of PI3 K by c-Kit correlates directly with c-Kit catalytic activity.

Two proteins that associate with PI3 K after stimulation with SCF are Crkl and c-Cbl. [69,70]. Crkl is an adaptor protein that is phosphorylated on tyrosine residues in response to SCF [69,70]. In Mo7e cells, SCF induces the association of PI3 K and Crkl through the Crkl SH3 domain [70]. Stimulation with SCF also induces tyrosine phosphorylation of c-Cbl and association of c-Cbl with PI3 K [70,71]. It is likely that these proteins are involved in coupling and/or modulating SCF-induced responses mediated by PI3 K.

Studies from a number of laboratories found that PI3 K bound the kinase insert domain of c-Kit [46,72]. Tyrosine 719 of murine c-Kit (Y721 of human c-Kit) associates with the 85 kDa subunit of PI3 K and mutation to phenylalanine eliminates both the capacity of PI3 K to associate with c-Kit as well as the SCF-induced increases in PI3 K activity [73]. In contrast, the autophosphorylation activity of Y719F c-Kit is not impaired. Studies with Y719F c-Kit suggest that PI3 K has multiple roles in SCF-mediated responses and that these roles vary with cell lineage. Expression of Y719F c-Kit in murine mast cells derived from c-Kit-deficient *W^{sh}* mice, resulted in impaired adhesion, membrane ruffling and actin assembly in response to SCF [74,75]. Partial inhibition of SCF-mediated proliferation

and survival were also observed [75]. Expression of Y719F c-Kit in the murine myeloid cell line DA-1 suggests that PI3 K also plays a role in cellular trafficking of c-Kit. Although mutation of tyrosine 719 did not alter SCF-induced internalization of c-Kit, the receptor remained localized near the plasma membrane and movement through endocytic pathways was impaired [76,77]. Internalization of wild-type c-Kit was not dependent on calcium, while ligand-induced internalization of the Y719F mutant was [76]. PI3 K may also play a role in differentiation mediated by c-Kit in the myeloid progenitor cell line FDC-P1 [78]. Lastly, expression of the Y721F human c-Kit mutant in fibroblastic cell lines reduced SCF-induced activation of AKT and partially impaired the anti-apoptotic capacity of SCF [79]. Thus, similar to its role in signaling pathways of other RTKs, PI3 K is clearly involved in multiple biological responses mediated by SCF.

5. The JAK/STAT pathway and c-Kit signaling

Members of the Janus family of protein tyrosine kinases (JAKs) are activated by ligands interacting with a variety of receptors lacking intrinsic kinase activity. Among these are hematopoietic growth factors that bind receptors in the cytokine receptor superfamily. These include the erythropoietin (Epo) receptor, the granulocyte–macrophage colony-stimulating factor (GM-CSF) receptor, the interleukin 3 (IL-3) receptor as well as numerous others. Reviews relating to activation of Janus kinases by the cytokine receptor superfamily can be found in references [80,81]. Recently, animals deficient for JAK1, JAK2 and JAK3 have been described, and the phenotypes of these animals illustrate the important role of this kinase family in the development of hematopoietic lineages [82–85]. Less clear is the relationship of Janus family kinases in responses mediated by RTKs, in particular c-Kit. Studies from two groups have shown that JAK2 associated with c-Kit and that SCF induced activation of JAK2 [86,87]. Of note was the rapid and transient increase in JAK2 phos-

phorylation observed by Weiler et al. [86]. Pretreatment of cells with the protein tyrosine phosphatase inhibitor sodium vanadate reduced the rate of JAK2 dephosphorylation [88]. One protein tyrosine phosphatase that plays a role in dephosphorylation of JAK2 after stimulation by Epo is SHP1 [91]. Because SCF induces association of SHP1 with c-Kit, SHP1 may mediate the rapid dephosphorylation of JAK2 after stimulation with SCF [89,90].

One pathway activated downstream of JAK family members are signal transducers and activators of transcription (STATs). This family of transcription factors associate with phosphorylated tyrosine residues on activated receptors, are both tyrosine and serine phosphorylated, form homo- and/or heterodimers, translocate to the nucleus, bind DNA and activate transcription of a variety of genes. To date, seven STAT family members have been identified. They are STATs 1–6 with STAT5 having an *a* and *b* isoform. Comprehensive reviews of this family of transcription factors have recently been published [92,93].

SCF induces association of STAT1 with c-Kit, increases in STAT1 tyrosine phosphorylation and increases in STAT1 DNA binding activity in hematopoietic cell lines and normal progenitor cells [94]. SCF also activates STAT5 and induces serine phosphorylation of STAT3 [95,96]. Broxmeyer and coworkers [96] have suggested that STAT3 may be involved in synergistic biological responses elicited by SCF in combination with other growth factors. In contrast to these findings, several investigators have reported that SCF had no effect on JAK or STAT family members [97–101]. It remains unclear if these differences relate to technical parameters or possibly to lineage specific differences in cell lines.

While studies with antisense oligonucleotides suggest that JAK2 is required for maximal proliferation in response to SCF, experimentation with JAK2-deficient mice will provide more definitive answers on the role of JAK2 in SCF-mediated responses [86]. These animals die in utero at a similar stage of embryonic development as c-Kit or SCF-deficient mice [20,83,84].

While progenitor cells expressing c-Kit were reported at higher frequencies in the fetal livers of JAK2-deficient mice (66%) than wild-type littermates (20%), SCF-induced colony formation of JAK2-deficient fetal liver cells was reduced compared to progenitors isolated from the fetal liver of control mice [83,84]. These studies suggest a role for JAK2 in optimal responses to SCF in normal hematopoietic progenitor cells.

6. Src family members and c-Kit signaling

Src family members are involved in a wide range of cellular functions including cell adhesion, cell motility, cell cycle progression, survival, differentiation, protein trafficking and cellular architecture, reviewed in [102–104]. They interact with one or more components of most known signaling pathways. With regard to signaling through RTKs, Src family members are activated in response to numerous RTK ligands including platelet-derived growth factor (PDGF), epidermal growth factor (EGF) and colony-stimulating factor-1 (CSF-1) [105]. Little is known about Src family members in relation to SCF signaling. The Src family member Lyn is expressed at high levels in SCF-responsive cell lines and normal progenitor cells [106]. SCF induces increases in Lyn activity and association of Lyn with c-Kit. In vitro studies with GST fusion proteins have shown that Lyn binds tyrosine residues in the juxtamembrane region of c-Kit. Several lines of evidence suggest that Lyn plays a role in SCF-mediated proliferation [106]. Reduction in Lyn protein with antisense oligonucleotides inhibited SCF-induced proliferation. Similarly, PP1, a drug that inhibits Lyn activity but not c-Kit, also inhibited SCF-induced proliferation. It is probable that SCF activates other Src family members in cells lacking Lyn. The SH2 domain of c-Src coprecipitates c-Kit and treatment with the PKC inhibitor calphostin enhances this association [107]. Further, Fyn, another Src family member bound a phosphopeptide sequence corresponding to tyrosines 568 and 570 of human c-Kit [108].

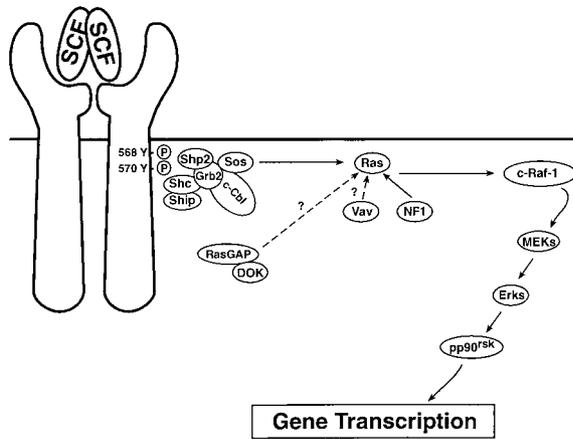


Fig. 2. SCF-induced activation of the Ras–Raf–MAP kinase cascade. Ligand-induced increases in tyrosine phosphorylation of c-Kit recruits Grb2 to the receptor complex. Grb2 may bind either directly to c-Kit or indirectly through interaction with Shc or SHP2. Because Grb2 and the nucleotide exchange factor Sos are constitutively associated, this translocation results in colocalization of Sos and Ras and subsequent activation of Ras. SCF-induced activation of Ras may also be modulated by RasGAP, Vav and NF1. Activation of Ras results in activation of the serine–threonine kinase c-Raf-1 which in turn activates the MAP kinase cascade.

One means of down-regulating the activity of Src family members is through phosphorylation of a highly conserved carboxyl-terminal tyrosine residue. Both Csk, a ubiquitously expressed tyrosine kinase, and Chk, a Csk-homologous kinase, phosphorylate Src family members at this site [109]. Chk is constitutively expressed in megakaryocytes, natural killer cells and the brain [110–113]. Chk expression is induced in activated T cells and in myeloid lineages treated with cytokines [114,115]. SCF induces increases in Chk expression that peak 8 h after stimulation and are maintained for 24 h [115]. In contrast, SCF has no effect on Csk expression [115]. Studies with phosphopeptides suggest that Chk associates with human c-Kit through phosphorylated tyrosines 568 and 570 [108]. This is of particular note since these tyrosines are in the juxtamembrane region of c-Kit and this region also associates with Lyn and Fyn [106,108]. Thus, colocalization of Chk and Src family members may be a mechanism to downregulate Src family activity after activation by SCF.

7. The Ras–Raf–MAP kinase cascade and c-Kit signaling

One signaling pathway activated in response to many growth factors is the Ras–Raf–MAP kinase cascade, reviewed in [116–118]. In brief, phosphorylated tyrosine residues on ligand-activated receptors recruit multiple SH2-containing proteins to the receptor complex and these proteins couple RTKs to activation of Ras. Included among these are Grb2, Shc, SHP2 and Grap. A Grb family member is constitutively associated with Sos, a guanine nucleotide exchange factor. Recruitment of Grb2 to the activated receptor complex, whether directly (through interaction with phosphorylated receptor) or indirectly (through interaction with receptor-associated Shc, SHP2 or other proteins) results in colocalization of Sos and Ras and subsequent increases in Ras activity. This in turn promotes the interaction of Ras with the serine–threonine kinase c-Raf-1 and activation of MEK, a MAP kinase. MEK phosphorylates MAP kinase and MAP kinase phosphorylates a number of substrates including pp90^{fsk}. In addition, this signaling pathway is regulated by numerous other proteins.

Fig. 2 summarizes what is known about SCF-induced activation of the Ras–Raf–MAP kinase cascade. Ligand-induced autophosphorylation of c-Kit induces association of Grb2, Grap, SHP2 and Shc with c-Kit [119–123]. Shc coprecipitates with a phosphopeptide sequence corresponding to tyrosines 568 and 570 in the human c-Kit juxtamembrane region. While this interaction may be indirect, the binding of SHP2, Grb2 and Grap to c-Kit is likely direct [108,119]. After association with the activated c-Kit receptor complex, both SHP2 and Shc are phosphorylated on tyrosine residues and this facilitates association with Grb2 or Grap. SCF also induces association of a 145 kDa phosphotyrosylprotein with Shc [124]. This protein has been cloned and named SHIP [125–127]. Interestingly, SHIP is an SH2-containing protein with 5′ phosphatase activity specific for inositol 1,3,4,5 tetraphosphate (I1,3,4,5-P4) and phosphatidylinositol 3,4,5, trisphosphate (PI-3,4,5-P3). Based on the phenotype of SHIP- de-

ficient mice, it appears that SHIP is a negative regulator of hematopoiesis [128].

Another protein that regulates Ras activity in response to many growth factors is RasGAP, a GTPase activating protein. Although some investigators have reported small increases in tyrosine phosphorylation of RasGAP after stimulation with SCF, many have not [45,46,68,129]. More recently, *in vitro* studies have suggested that RasGAP is capable of interacting with c-Kit, however the affinity for c-Kit is lower than that of PI3 K and phospholipase C γ (PLC γ) [130,131]. The 62 kDa GAP-associated protein, Dok, was recently cloned [132,133]. Dok is phosphorylated in response to SCF and is constitutively phosphorylated in hematopoietic cell lines transformed by p210^{bcr-abl} [134]. Although the tyrosine phosphorylated fraction of this protein associates with RasGAP, it is unclear if this interaction is involved in regulation of Ras activity or other signaling pathways.

Studies with Nf1 deficient progenitor cells have shown that this GTPase activating protein is also involved in modulating Ras activation by SCF [135]. The dose response curve for SCF-induced colony formation of Nf1 deficient progenitor cells was shifted to the left as compared to progenitors that expressed Nf1. These observations correlated with increases in MAP kinase activity in Nf1-deficient progenitors. These findings are of particular note, given the high frequencies of leukemia in both humans and mice that express reduced levels of NF1.

Vav, a 95 kDa protein expressed specifically in hematopoietic cells, may have guanine nucleotide exchange factor activity. Similar to other growth factors, SCF induces tyrosine phosphorylation of Vav, however its role in SCF-induced activation of the Ras pathway as well as other GTPases remains to be determined [136,137].

Thus, SCF-induced activation of Ras is regulated through multiple mechanisms. An immediate consequence of Ras activation is interaction with c-Raf-1 and increases in c-Raf-1 catalytic activity. Numerous laboratories have found increases in c-Raf-1 activity in response to SCF and have determined that this serine–threonine kinase is critical in SCF-mediated responses [45,67,138–140]. SCF

also induces increases in tyrosine phosphorylation and kinase activity of MEK1, MEK2 and the MAP kinases [99–101,138,141–143]. Downstream of the MAP kinases, the S6 kinase pp90^{rsk} is activated [142]. In addition to activating the classical MAP kinase pathway, SCF also activates the JNK kinase, a MAP kinase activated in response to stress [144].

8. Negative regulators of SCF signaling

Several lines of evidence suggest that SHP1, an SH2-containing protein tyrosine phosphatase specific for hematopoietic cells, is a negative regulator of c-Kit signaling. SCF induces association of the SHP1 SH2 domain with phosphorylated tyrosine 569 of murine c-Kit [89,90]. Transfection of Y569F c-Kit into BaF3 cells resulted in increases in SCF-induced proliferation [90]. Genetic evidence also suggests that SHP1 is a negative regulator of c-Kit. Motheaten mice (*me*) and motheaten viable mice lack functional SHP1 and have hyperproliferative progenitor cells [145]. To determine if the *W* locus and the *me* locus were complementary, heterozygotic *W*^v mice were crossed with heterozygotic *me* mice and backcrossed to obtain all allelic combinations of these two genes [146,147]. Expression of the *W*^v c-Kit mutant reduced the severity of the *me* phenotype and reduction in functional SHP1 also improved the *W*^v phenotype [146,147]. While the *in vivo* mast cell deficiencies found in *W*^v mice were improved in *W*^v/*me* mice, the macrocytic anemia was not. *In vitro*, SCF-mediated survival of mast cells from *W*^v/*me* mice was improved as compared to *W*^v mice, however, the *me* locus had no effect on SCF-induced proliferation of mast cells from either normal or *W*^v mice. These findings suggest lineage specificity in the role of SHP1 in SCF-mediated responses in progenitor cells and mast cells.

SHP2, another SH2-containing protein tyrosine phosphatase has also been implicated as a negative regulator of c-Kit signaling. SHP2 associates with murine c-Kit through phosphorylated tyrosine residue 567 after stimulation with SCF [90]. Expression of Y567F c-Kit in BaF3

cells results in increased sensitivity to SCF and increases in intrinsic responsiveness. As discussed previously, SHP2 also couples c-Kit to the Ras–Raf–MAP kinase cascade [123]. Studies with mice chimeric for SHP2 expression demonstrated an important role for SHP2 in erythroid and myeloid development [148]. Thus, SHP2 is likely a positive regulator of early hematopoiesis and perhaps serves as a negative regulator in more differentiated cells.

Another signaling component that negatively regulates SCF-induced proliferation is protein kinase C (PKC). Treatment of cells with SCF induces both tyrosine and serine phosphorylation of c-Kit *in vivo* [149]. *In vitro*, c-Kit is a substrate for PKC α and PKC-mediated serine phosphorylation of c-Kit had no effect on ligand binding but did reduce kinase activity [149]. Inhibition of PKC activity increased association of PI3 K with c-Kit and correlated with increases in SCF-mediated proliferation and decreases in cell motility in response to SCF. Studies using GST fusion proteins containing the SH2 domains of the 85 kDa regulatory subunit of PI3 K, Grb2, PLC γ , and Src found that calphostin, a PKC inhibitor, enhanced association with c-Kit *in vitro* [107]. These findings suggest that PKC-mediated serine phosphorylation of c-Kit reduces the capacity of multiple SH2-containing signaling components to associate with c-Kit. In contrast, inhibition of PKC had little effect on SCF-induced activation of c-Raf-1 and Erk2. Mapping studies demonstrated that serines 741 and 746 are phosphorylated by PKC both *in vivo* and *in vitro*, while serines 821 and 959 are phosphorylated *in vivo*, but not directly by PKC [150]. Mutation of serines 741 and 746 increased both c-Kit kinase activity and c-Kit-associated PI3 K activity in response to SCF. This double mutation also resulted in enhanced activation of AKT as well as increases in SCF-mediated cell survival [79]. The PKC isoform(s) mediating these responses *in vivo* have not been identified. Because these studies were performed in either endothelial cells or fibroblasts transfected with c-Kit, it will be interesting to determine the roles of PKC family members in SCF-mediated responses in hematopoietic cells.

9. Other signaling components activated by SCF

A variety of other signaling components are activated in response to SCF, although the signaling pathways these proteins are involved with, and their role in SCF-mediated responses, remain to be defined. For example, PLC γ hydrolyzes phosphatidylinositol-4,5-bisphosphate (PIP₂) into diacylglycerol (DAG) and inositol 1,4,5-trisphosphate (IP₃). SCF induces weak association between the SH2 domain of PLC γ and tyrosine 936 of human c-Kit as well as small increases in tyrosine phosphorylation of PLC γ [46,67,68,107,131,138]. Although PLC γ is a substrate for c-Kit, it is unlikely that SCF activates the classical PLC γ pathway. SCF does not induce increases in IP₃ levels and increases in DAG are likely mediated by phospholipase D [67,151,152].

Tec, a Src-like kinase related to Btk and Itk, is highly expressed in hematopoietic cells and constitutively associated with c-Kit [97]. Stimulation with SCF resulted in increases in tyrosine phosphorylation of Tec as well as increases in its catalytic activity. Recent evidence in other receptor models suggests that Tec binds phosphatidylinositol-3,4,5 trisphosphate and that this facilitates PLC γ generation of IP₃ and DAG [153]. The role of Tec in modulation of SCF signaling pathways remains to be explored.

Lastly, a 200 kDa glycoprotein associated with c-Kit after stimulation with SCF [154]. This protein was rapidly phosphorylated on tyrosine residues after stimulation with SCF but not GM-CSF or other ligands interacting with cytokine receptor superfamily members. The identity of this protein remains to be determined.

10. C-Kit signaling and cellular matrix components

Hematopoietic progenitor cells interact with both stromal cells and components of the extracellular matrix. These events, in conjunction with signals mediated by soluble and membrane-bound growth factors, are important in the regulation of hematopoiesis. Interaction of differentiated progeny, such as mast cells, with components of the

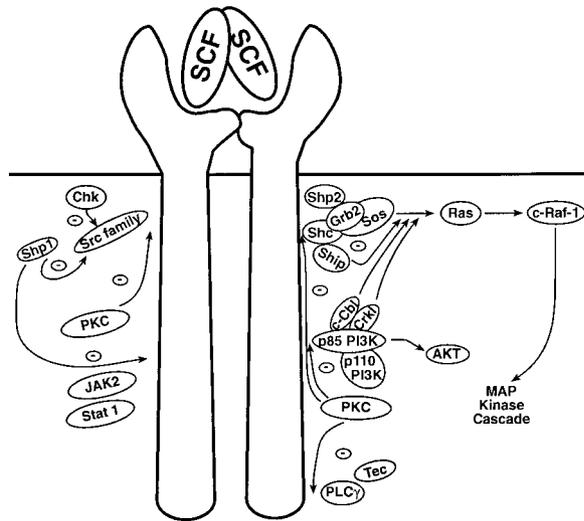


Fig. 3. Summary of the relationship between the multiple signaling pathways activated by SCF. SCF activates Src family members, PI3 K, the Ras–Raf–MAP kinase cascade and the JAK/STAT pathway. Interaction between different components of these pathways occurs at multiple points. With regard to negative regulators of these pathways, Src family members are negatively regulated by Chk and SHP1. PKC-mediated serine phosphorylation of c-Kit impairs interaction of the SH2 domain of Src, Grb2, PI3 K and PLC γ with c-Kit. Shp is a 5' inositol phosphatase that may play a role in modulating activation of Ras as well as PLC γ and AKT.

extracellular matrix is also important in their functional responses. SCF-induced adhesion occurs through multiple mechanisms. One mechanism involves interaction of membrane-bound SCF expressed on stromal cells with c-Kit expressed on progenitor cells. The absence of c-Kit kinase activity may not impair adhesion mediated by this interaction [155,156]. SCF is also involved in cellular adhesion through fibronectin receptors. SCF-induced activation of PI3 K plays an important role in mast cell adhesion to fibronectin [74]. SCF also activates, or coactivates, kinases implicated in formation of focal adhesions. Stimulation of the megakaryoblastic cell line CMK with SCF induced increases in phosphorylation of RAFTK (Related Adhesion Focal Tyrosine Kinase, also termed Pyk2 or CAK-B). This activation was dependent on PKC [157]. Stimulation of the erythroblastic cell line TF-1 with SCF had no effect on phosphorylation of FAK but did enhance integrin-

mediated activation of FAK as well as phosphorylation of paxillin [158].

11. Integrated signaling mechanisms

Although delineation of linear signaling pathways is conceptually attractive, many of the signaling components activated by SCF play roles in multiple pathways. In most cases, SCF-mediated responses result from the input of multiple, interconnected signaling pathways (summarized in Fig. 3). For example, SHP2 is likely involved in activation of the Ras–Raf–MAP kinase cascade but may also negatively regulate other signaling pathways [90,123]. Phosphorylation of c-Kit by PKC isoforms decreases interaction of c-Kit with multiple SH2-containing proteins, including the 85 kDa regulatory subunit of PI3 K, Grb2, PLC γ , and Src. SCF induces association of PI3 K with both c-Cbl and Crkl [70]. Crkl is an adaptor protein that interacts with components of multiple signaling pathways [69]. c-Cbl also associates with Grb2 and may modulate Ras activation in response to SCF [159]. Mutation of the PI3 K binding site on c-Kit expressed in murine mast cells abrogates SCF-induced PI3 K activity and partially impairs activation of Ras and c-fos and junB induction by SCF [74]. Treatment of cells with SCF also induces association of SHIP and Shc. SHIP is a 5' phosphatase recruited to signaling complexes through an SH2 domain [125,126]. Recent studies suggest that SHIP plays a role in the regulation of multiple signaling components, including PLC γ , Ras and AKT [127,153]. Thus, the biological outcome of SCF/c-Kit interaction depends on integrated signals resulting from the activation of multiple pathways.

12. C-Kit structure-function summary

SCF activates multiple signal transduction components including PI3 K, Src family members, the Ras–Raf–MAP kinase cascade and the JAK/STAT pathway. Activation of many of

Table 1
Sites on c-Kit that associate with signaling components

| Associated protein(s) | Tyrosine residue(s) (Human/Murine Sequence) | Biological function/cell line | Reference |
|-----------------------|---|--|-----------|
| Lyn | 544–577 (human) | Proliferation/Mo7e | 106 |
| Fyn | Y568, Y570 (human) | ? | 108 |
| Shc | Y568, Y570 (human) | ? | 108 |
| Shp1 | Y569 (murine) | Negative regulator of proliferation/BaF3 | 90 |
| Shp2 | Y567 (murine) | Negative regulator of proliferation/BaF3 | 90 |
| Chk | Y568, Y570 (human) | ? | 108 |
| p85 PI3 K | Y719 (murine) | Adhesion/mast cells | 74 |
| | Y719 (murine) | Partial effect on survival, proliferation/mast cells | 74 |
| | Y719 (murine) | c-Kit trafficking/DA1 cells | 76 |
| | Y721 (human) | Differentiation/FDC-P1 cells | 78 |
| | Y721 (human) | Survival/fibroblasts | 79 |
| ? | Y821 (murine) | Survival and proliferation/mast cells | 74 |
| PLCgamma | Y936 (human) | ? | 131 |

these pathways is dependent on interaction of one or more upstream signaling components with specific sites on c-Kit. Table 1 is a summary of tyrosine residues on c-Kit that interact with components of these pathways. In addition, if known, the biological consequence of mutation of each site is also shown. Fig. 4 summarizes other regions of c-Kit known to be involved in its function.

Of particular note in Table 1 are the large numbers of proteins found associated with tyrosines 568 and 570 in the human c-Kit juxtamembrane region (amino acids 544–577). This region binds Src family members, Chk, Shc, SHP1 and SHP2 [90,106,108]. To date, only one group has published mutagenesis studies of these residues. Mutation of either tyrosine 567 or 569 of murine c-Kit (corresponding to tyrosines 568 and 570 in human c-Kit) to phenylalanine and expression in BaF3 cells resulted in increased proliferation in response to SCF as compared to wild-type c-Kit [90]. It will be important to determine if similar results are obtained when these mutants are expressed in other cell lines. The effects of mutating both of these tyrosines has not been examined.

Mutations in the juxtamembrane region have also been associated with constitutively active forms of c-Kit. Substitution of valine for glycine 560 activates human c-Kit [55,57,60,61]. Murine

c-Kit lacking amino acids 573–579 is also constitutively active [61]. Gastrointestinal stromal cell tumors contain mutations in the juxtamembrane region that activate human c-Kit [22]. Thus, the juxtamembrane region is critical in regulation of c-Kit activity.

Another site on c-Kit that is well characterized in relation to SCF-mediated responses is tyrosine 721 in the kinase insert region of human c-Kit (719 of murine c-Kit). Extensive studies from Besmer and coworkers [73] have shown that the 85 kDa regulatory subunit of PI3 K binds this residue and that mutation abrogates SCF-induced activation of PI3 K. The absence of SCF-induced PI3 K activity dramatically impaired adhesion of mast cells to fibronectin as well as reduced SCF-mediated survival and proliferation [74]. In other cell lineages this region is implicated in trafficking of c-Kit as well as SCF-mediated survival, proliferation and differentiation [75–79].

Two serine residues in the kinase insert region (Serines 741 and 746 of human c-Kit) may also play a role in regulation of biological responses mediated by SCF. Mutation of these residues correlates with increases in SCF-mediated motility and decreases in proliferation in transfected endothelial cells [107].

Substitution of valine for glycine 816 in the second catalytic domain of human c-Kit results

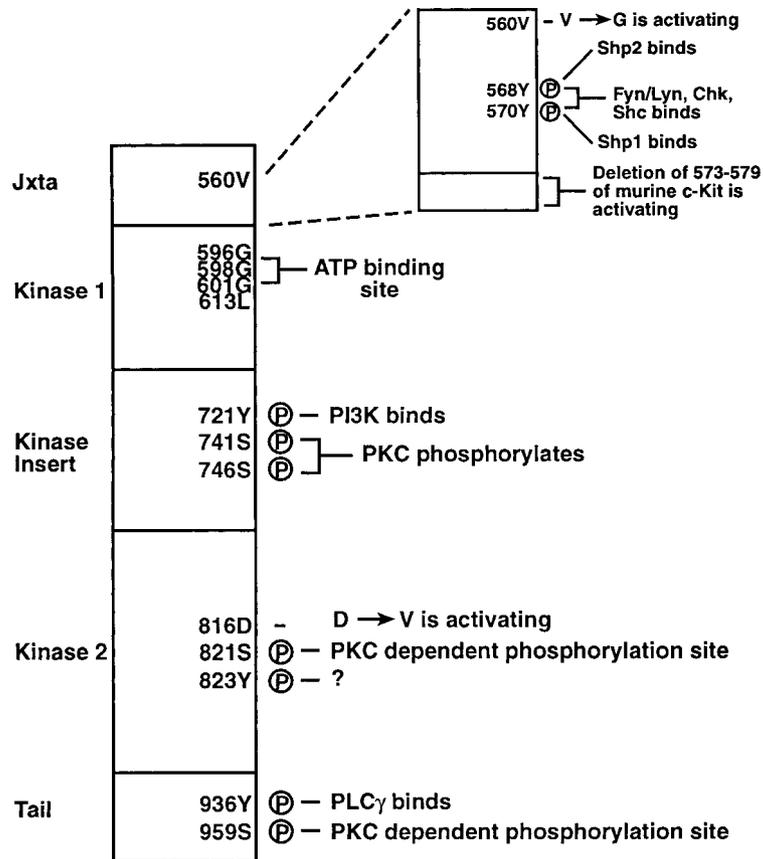


Fig. 4. Regions of human c-Kit involved in its function. The five intracellular regions of c-Kit are depicted in this cartoon. The juxtamembrane region binds multiple signaling components including SHP1, SHP2, Shc, Chk and Src family members. Several mutations have been identified within this region that result in constitutive activation of c-Kit. The first catalytic domain of c-Kit contains amino acid residues involved in binding ATP. The kinase insert contains the tyrosine that binds PI3 K as well as two serine residues phosphorylated by PKC. The second catalytic domain contains aspartic acid 816 (human c-Kit sequence). Substitution of this amino acid with valine results in a constitutively active form of c-Kit. The second catalytic domain also contains an important autophosphorylation site (tyrosine 823 of human c-Kit) as well as a serine residue that is phosphorylated in a PKC-dependent pathway. The carboxyl-tail of c-Kit has another serine residue that is phosphorylated in a PKC-dependent pathway as well as a tyrosine residue that interacts with PLC γ .

in constitutive activation [53–56,59]. Further, as discussed in previous sections, this mutation has been found in patients with a form of mastocytosis with associated hematological disorders [28]. Tyrosine 823 is another amino acid in the second catalytic domain of human c-Kit (821 of murine c-Kit) that is important for SCF-mediated survival and proliferation in mast cells [74]. The signaling component(s) that interact with this tyrosine has not yet been elucidated.

13. SCF-mediated synergy

A remarkable feature of SCF is its capacity to synergize with other hematopoietic growth factors. This is a critical because stem cells and multipotential progenitor cells respond optimally to growth factors in combination. The mechanisms mediating synergy are poorly understood. Studies from the laboratory of Keller and coworkers [160] demonstrated that synergistic responses of hematopoietic progenitor cells to combinations

of ligands binding members of the cytokine receptor superfamily correlated with the capacity of these growth factors to modulate receptor expression. In contrast, SCF synergizes with growth factors through a different mechanism. SCF does not alter the affinity, or numbers, of GM-CSF receptors in Mo7e cells, a human cell line that proliferates synergistically in response to GM-CSF in combination with SCF [138,161]. Similarly, SCF did not alter expression of IL-3 receptors in either human or murine cell lines reported to respond synergistically to this combination of growth factors [161,162]. Consistent with these findings, treatment of CD34 enriched human progenitor cells with SCF had no effect on expression of IL-6, IL-3, GM-CSF or Epo receptors [163]. Less is known about the effect of GM-CSF and IL-3 on SCF binding. However, neither IL-3 or GM-CSF effected c-Kit mRNA levels in Mo7e cells [164].

Although SCF does not modulate expression of growth factors receptors, there is evidence suggesting that c-Kit phosphorylates at least one cytokine receptor. SCF induces tyrosine phosphorylation of the Epo receptor in both HCD-57 cells, a murine erythroleukemia cell line, and purified human erythroid progenitors [100,143,165]. Conversely, Epo induces tyrosine phosphorylation of c-Kit in a human erythroleukemic cell line [40]. In HCD-57 cells, c-Kit and the Epo receptor have been reported to coimmunoprecipitate and *in vitro* studies with GST fusion proteins suggest this interaction is mediated through phosphorylated tyrosines residues in the extended box 2 region of the Epo receptor [165]. Lodish and coworkers [166] have suggested that an interaction between c-Kit and the Epo receptor occurs in normal erythroid progenitors and that this plays a role in the development of CFUe erythroid progenitors.

Another cytokine receptor phosphorylated in response to SCF is the beta chain of the IL-3 receptor. Treatment of B6SUtA1 cells with SCF induces serine and threonine phosphorylation of the B_{IL3} subunit of the IL-3 receptor [162]. Reduction in c-Kit activity with the kinase inhibitor genistein had no effect on the capacity of SCF to induce phosphorylation of B_{IL3}, while

treatment with PKC inhibitors did. Since SCF has no effect on either the affinity or numbers of IL-3 receptors, SCF-induced activation of PKC may play a role in modulating one or more IL-3 signaling pathways. The absence of synergistic increases in tyrosine phosphorylation in response to SCF and IL-3 suggests the synergistic response to these factors may involve serine/threonine kinases.

Consistent with the above findings, many reports in the literature found no correlation between early increases in protein tyrosine phosphorylation and the synergistic interactions of SCF with GM-CSF or IL-3 [45,98,138]. SCF stimulated autophosphorylation of c-Kit, but GM-CSF in combination with SCF caused no additional increase in c-Kit autophosphorylation in Mo7e cells [45]. Recently, a new megakaryoblastic cell line was described that responded to GM-CSF and SCF synergistically [167]. In contrast to studies with Mo7e cells, GM-CSF and SCF reportedly did increase autophosphorylation of c-Kit as compared to SCF alone in these cells.

The effect of SCF in combination with GM-CSF or IL-3 on specific signaling components downstream of c-Kit has also been examined. In studies of Mo7e cells, no synergistic increase in tyrosine phosphorylation of RasGAP, c-Raf-1 or MAP kinase were observed [45,138]. Similarly, in FDCP-MixA4 cells and B6 M cells, SCF and IL-3 did not induce synergistic increases in tyrosine phosphorylation of c-Raf-1, Shc, JAK2, Erk1 or Erk2 [98,101]. In contrast, the combination of SCF and IL-3 did induce synergistic increases in the kinase activity of Erk1 in both of these cell lines [98,101]. In addition, SCF and IL-3 in combination did not synergistically induce increases in the mRNA levels of the serine/threonine kinase PIM1 in B6 M cells, although costimulation of Mo7e cells with SCF and gamma interferon did [168].

Recently, the signaling pathways of Epo in combination with SCF were examined in human erythroid progenitor cells. Similar to studies of SCF in combination with GM-CSF and IL-3, no synergistic increase in tyrosine phosphorylation of either c-Kit, or the Epo receptor, were observed [143]. In contrast, synergistic increases

in phosphorylation of MEK, Erk1 and Erk2 were found and this correlated with increases in MAP kinase activity [143]. Thus, in relation to early signaling events, synergistic activation of members of the MAP kinase family in response to SCF in combination with other growth factors has been the most consistent finding.

The effects of SCF in combination with GM-CSF and IL-3 on expression of transcription factors have also been examined. As described above, SCF activates both JAK2 and STAT1 in a variety of cell lines. One group reported that while SCF activated STAT5 in mast cells, it did not activate STAT5 in the mast cell line B6 M [95,98]. Studies with B6 M cells further suggest that SCF in combination with IL-3 does not increase the tyrosine phosphorylation or DNA binding activity of STAT5 above that observed with IL-3 [98]. One intriguing study found that SCF induced serine phosphorylation of STAT3 in Mo7e cells. Also, some increases in DNA binding activity of STAT3 were observed in extracts of cells stimulated with SCF in combination with IL-9 [96].

Induction of immediate early response genes have also been examined in response to SCF in combination with other growth factors. Synergistic induction of a number of early response genes was found in Mo7e cells treated with sub-optimal concentrations of SCF with either GM-CSF or IL-3 [169]. Included among these were *c-fos*, *junB*, *egr-1* and *c-myc*. Thus, the synergistic activation of members of the MAP kinase pathway may be involved in increases in expression of some immediate early response genes. In contrast to these findings, treatment of B6 M cells with SCF and IL-3 in combination did not induce synergistic increases in expression of *c-myc* or *c-fos* [98].

In addition to possible synergistic increases in some early response genes, one group has reported activation of signaling components key to the G₁/S transition of the cell cycle that correlates with the capacity of SCF to synergize with growth factors. Enhanced phosphorylation of the Rb gene product was reported in response to SCF in combination with GM-CSF as compared to either factor alone [170]. Alterations in cellular

levels of the cyclin-dependent kinase inhibitors Cip-1 and Kip-1 also correlated with synergistic interactions of GM-CSF and SCF [170]. Further, synergistic increases in expression of the 68 kDa calmodulin binding protein (CaM-BP68), were observed in response to SCF in combination with IL-3 [171]. CaM-BP68 is involved in the G₁/S transition of the cell cycle. Thus, SCF in combination with other growth factors may induce synergistic increases in the expression or activity of signaling components associated with DNA synthesis and subsequent cell cycle progression.

14. Conclusions

In the nine years since SCF was identified as the *c-Kit* ligand, a remarkable amount has been learned about its mechanism of action. SCF activates multiple signaling pathways and these pathways lead to a variety of biological responses. While many of the early studies focused on signaling pathways activated by SCF in fibroblasts transfected with *c-Kit*, subsequent work in hematopoietic cell lines generally supports these findings. Understanding the role of these signaling pathways in SCF-mediated responses remains a more difficult task. In particular, cellular lineage is clearly critical in determining the biological outcome of different signaling pathways. Studies in hematopoietic cell lines are certainly one means to address these questions, however it is important to interpret these studies in the context of the lineage and differentiation state of the cell line. In addition, the means through which the cells were immortalized is also an important consideration. Elegant studies reconstituting mast cells from *W* mice with different *c-Kit* mutants have likely provided the most accurate information on the structure-function relationships of *c-Kit* in mast cells. It will be important to develop similar models to examine these questions in progenitor cells. Lastly, the mechanisms mediating the capacity of SCF to synergistically stimulate progenitor cells in combination with other growth factors remains an important question in the field. To date, progress in this area

has been hampered by the few numbers of cell lines available that reproducibly respond synergistically to combinations of growth factors. In addition, obtaining sufficient numbers of normal hematopoietic progenitor cells to perform signaling experiments is difficult. However challenging, insight into mechanisms of synergy could be an important key to understanding regulation of quiescent stem cells and provide insight into a fundamental question in hematopoiesis. Answers to these questions may also provide the means to mobilize these cells for use in treating disease with approaches such as gene therapy or transplantation.

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