

Activation of mitogen-activated protein kinase pathways by the granulocyte colony-stimulating factor receptor: mechanisms and functional consequences

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1. ABSTRACT

The cytokine Granulocyte Colony Stimulating Factor (G-CSF) promotes proliferation, differentiation, survival and functional maturation of cells within the neutrophilic granulocyte lineage. G-CSF binds to its cell-surface receptor (G-CSFR) causing activation via homodimerisation and subsequent phosphorylation on four tyrosine residues of the receptor intracellular domain. This initiates a range of intracellular signalling events including the activation of Mitogen-Activated Protein Kinase (MAPK) pathways. G-CSF stimulates activation of the ERK 1/2 pathway, as well as the stress-activated JNK and p38 pathways, and the less-characterised ERK5/Big MAPK 1 pathway. Receptor mutagenesis studies have aided in the identification of regions of the G-CSFR that mediate specific activation of these MAPK pathways. In addition, the activation of individual MAPK pathways appears to contribute to distinct biological outcomes. Thus, MAPK activation may be an important mediator of the actions of G-CSF.

2. INTRODUCTION

When cells are exposed to environmental stimuli such as cytokines, growth factors or hormones, responses are initiated by intracellular signalling pathways. These pathways relay information to various intracellular compartments to initiate changes such as alterations in gene expression. One group of signal transduction pathways known as the Mitogen-Activated Protein Kinase (MAPK) pathways are activated in response to a variety of extracellular stimuli. Several MAPK pathways have now been identified, including the extracellular signal-regulated kinase (ERK) pathway, the c-Jun N-terminal kinase (JNK) pathway, the p38 pathway and the ERK5 (Big MAPK 1) pathway (1,2,3). This review focuses on the activation of these MAPK pathways by the cytokine Granulocyte Colony Stimulating Factor (G-CSF), describing our current understanding of the mechanisms and functional consequences of MAPK activation in cells following their exposure to G-CSF.

Table 1. Mitogen-Activated Protein Kinase Pathways activated in response to G-CSF

MAPK Pathway	Cell Type	G-CSFR region	Role	Inhibitor	Reference
ERK	BaF3	646 – 739 686 – 785	proliferation	- - PD98059	21, 30, 32, 82 31
	myeloid	Y764 membrane-proximal + Box 2 ?	proliferation	U0126 U0126 PD98059	83,84 86 87
	32D	?	differentiation	U0126	98
	BaF3	Y763 Y763 686 – 715	? proliferation ?	- Tat-TIIP -	32 149 30
p38	BaF3	626 – 726 and Y763 686 – 715	proliferation	SB203580	31 30
	OCT-AML1	?	proliferation	SB203580	189
	Stromal Endothelial	?	VCAM-1 expression	SB203580	191,192
ERK5	BaF3	686 – 715 and C-terminal	proliferation, survival	-	30

Stimulation with G-CSF results in activation of several MAPK pathways, including the ERK, JNK, p38 and ERK5 pathways. Studies have utilised approaches such as G-CSF receptor mutagenesis and MAPK pathway inhibitors to delineate the regions of the G-CSFR which mediate activation, and the biological consequences of MAPK activation.

3. GRANULOCYTE COLONY-STIMULATING FACTOR AND ITS RECEPTOR ACTIVATION

The critical biological activities of G-CSF have been described over the last 25 years (4). G-CSF is the major cytokine that promotes the proliferation, maturation, and survival of cells of the neutrophilic granulocyte lineage (5,6,7). In addition, G-CSF facilitates the functional activation of mature neutrophils by enhancing cytotoxic activity and chemotaxis (8,9). The selective knockout of the gene for *G-CSF* in mice causes chronic neutropenia and impairs the response to bacterial infection. The administration of G-CSF restores these defects. G-CSF is therefore essential for maintaining normal neutrophil production during "steady-state" granulopoiesis *in vivo* and contributes to "emergency" granulopoiesis during infections (7).

These biological effects of G-CSF are mediated via a specific high-affinity receptor, G-CSFR (10,11). The G-CSFR is expressed on cells from the myeloblast to the mature neutrophil, but not on any lymphoid, erythroid or megakaryocytic lineage cells (12). Thus, the selective action of G-CSF has been attributed to this relatively restricted expression.

The G-CSFR is a transmembrane glycoprotein with an apparent molecular mass of 130 to 150 kDa, and belongs to the class I family of haemopoietic cytokine receptors (13,14). Its single polypeptide chain comprises a large extracellular ligand-binding domain, a single membrane-spanning domain and a small intracellular domain. This intracellular domain of 187 amino acids lacks intrinsic tyrosine kinase activity but is considered as the signal transduction domain of the receptor. Of importance for G-CSFR signal transduction are conserved regions called Boxes 1, 2 and 3 as well as four tyrosine (Y) residues. In the murine G-CSFR, these tyrosines are numbered Y703, Y728, Y743 and Y763, while the numbering for the human G-CSFR is Y704, Y729, Y744 and Y764 (15,16,17).

In the earliest stages of signalling by G-CSF, the G-CSFR homodimerises and its four intracellular tyrosine

residues are phosphorylated by non-receptor tyrosine kinases including Jak1, Jak2, Tyk2, Tec, Lyn, Syk and Hck (18-25). Of these, Jak1 and Lyn appear to be constitutively associated with the membrane-proximal region of the G-CSFR, while Syk, Hck and Jak2 appear to be recruited following G-CSF stimulation (24,19,21,25). Studies utilising cell lines deficient in these individual tyrosine kinases have shown they have distinct roles in G-CSF-stimulated events. Jak1, but not Jak2 or Tyk2, is essential for receptor tyrosine phosphorylation and STAT activation following G-CSF-stimulation (22), while Lyn, but not Syk, is required for proliferation (26,27). In addition, the profile of kinases activated by G-CSF in differentiating cell types differs from those activated in mature neutrophils (24,28,29). Thus, different tyrosine kinases are activated following G-CSF-stimulation depending on the stage of cellular maturation and/or the particular biological response invoked.

The events directly following tyrosine kinase activation are also complex, but specific intracellular signalling pathways appear to contribute to the distinct target cell responses. An evaluation of these subsequent signalling events revealed activation of the Jak-STAT pathway, the Phosphatidyl inositol 3'Kinase (PI3K)-Akt pathway, and multiple Mitogen-Activated Protein kinase (MAPK) pathways (30-34). Mutagenesis of the G-CSFR itself has been useful in delineating the regions of the G-CSFR required for mediating the activation of individual MAPK signalling pathways (35,36). An overview of these findings is presented in Table 1. The MAPK pathways are the subject of this review, and are considered in more detail in the following sections.

4. AN INTRODUCTION TO MITOGEN-ACTIVATED PROTEIN KINASE PATHWAYS

The mammalian MAPK pathways have been defined by the presence of a three-tiered protein kinase module, whereby a MAPK kinase kinase (MAPKKK) phosphorylates and activates a MAPK kinase (MAPKK), which in turn phosphorylates and activates a MAPK (37) (Table 2). The MAPK pathways are evolutionarily

Table 2. Intracellular events in MAPK pathways

MAPK Pathway	ERK	JNK	p38	ERK5
Stimulus	Cytokines	Stresses	Stresses	Cytokines, hormones
Receptor	Cytokine Receptors	?	?	GCSF-R, EGF-R, NGF-R, BDNF-R, GPCRs
Adaptor/enzyme	Shc, SHP-2, Grb2, Src	Nck, Dbl, Crk, Cas, Shc, Grb2, TRAF6	Grb2, TRAF6, MyD88, IRAK	Src
Exchange factor	Sos			
Small G-protein	Ras	Rac, cdc42, Rap, Ras	Ras, Rac, cdc42, Rap	Ras
MAPKKKK		PAK, NIK, GLK, HPK, MST2, GCK	PAK, GCK	
MAPKKK	Raf-1, B-Raf, A-Raf	MEKK1, MEKK2, MEKK4, MLK2, MLK3, Tpl2, ASK, DLK, Tak1	MEKK1, MEKK2, MEKK3, MEKK4, MLK2, MLK3, ASK1, DLK, Tpl2, Tak1	MEKK2, MEKK3, Tpl2
MAPKK	MEK1, MEK2	MKK4, MKK7	MKK3, MKK4, MKK6	MEK5
MAPK	ERK1, ERK2	JNK1, JNK2, JNK3	p38 α , p38 β , p38 γ , p38 δ	ERK5
Substrates	Elk-1, p90 ^{Rsk} , Mnk, JunD	c-Jun, JunD, ATF2, Elk-1, p66ShcA, NF-Atc1, HSF-1, TAT3, Bcl. Itch, 14-3-3	MAPKAPK2, MNK1, PRAK, Tau, ATF1, ATF2, MEF2A, NFAT, Sap-2, Elk-1, Ets-1, p53	MEF2, Sap1a, CREB, c-Myc

The MAPK pathways are activated by stimuli, and are composed of a series of intracellular steps, which result in phosphorylation of protein substrates. The general organisation of a MAPK pathway is shown in (a). Some of the known stimuli, cellular receptors, signalling intermediates implicated in each level of the pathway, and substrates are summarised for the ERK 1/2 (b), JNK (c), p38 (d), and ERK5 (e) pathways.

conserved across eukaryotes and appear to be involved in critical cellular processes such as development, proliferation, differentiation, apoptosis and survival (38,39).

Several distinct MAPK pathways have been identified (reviewed in (3)). The Extracellular signal-Regulated Kinase (ERK), c-Jun N-terminal Kinase (JNK) and p38 pathways remain the best characterised, however there are other MAPKs including ERK3, ERK5, ERK7 and ERK8 (3). The ERK, JNK and p38 pathways show a number of distinctive features including their activation in response to different stimuli, their different upstream regulatory proteins, and differences in substrates and biological outcomes (40,41). Therefore, despite the overall similarities in pathway organisation, the different MAPKs are likely to play distinct, non-redundant roles. Interestingly, the tyrosine phosphorylation of cytokine receptors such as the G-CSFR initiates the activation of multiple MAPK pathways. In the following sections, we consider the ERK, JNK, p38 and ERK5 pathways in greater detail and overview their roles in signalling downstream of the G-CSFR.

5. THE EXTRACELLULAR SIGNAL-REGULATED KINASE (ERK) MITOGEN-ACTIVATED PROTEIN KINASE PATHWAY

5.1. Properties, stimuli and functions of the ERK 1/2 pathway

ERK 1 and 2 were originally identified as two serine/threonine kinases of 44 and 42kDa, respectively, activated in response to insulin stimulation (1). The ERKs have since been shown to be activated by a wide range of growth promoting stimuli including cytokines, serum, oncogenes and tumour-promoting phorbol esters (42-47), as well as a range of cellular stresses (48-51).

It is now possible to sequentially describe the intracellular events leading to ERK1/2 activation (Table

2). One of the best-studied mechanisms requires the recruitment of the adaptor protein Shc via its phosphotyrosine-binding (PTB) domain to phosphorylated tyrosine residues of cytokine or growth factor receptors (52-56). The ensuing tyrosine phosphorylation of Shc allows its subsequent recruitment of the adaptor protein Grb2 via its Src Homology 2 (SH2) domain (57). The Src Homology 3 (SH3) domain of Grb2 is bound by the exchange factor Sos and this complex allows the realisation of Sos from the cytoplasm to the membrane (58). This brings Sos into proximity with its substrate, the small G-protein Ras, which is activated through the exchange of GDP for GTP (59,60).

Active Ras then initiates signaling via the three-tier kinase cascade in the cytosol. Thus, Ras-GTP recruits and activates the MAPKKK Raf, which phosphorylates the MAPKKs MEK1 and/or MEK2 on two serine residues (61). The activated MEKs are dual-specificity kinases that phosphorylate ERK 1/2 on both the threonine and tyrosine residues of the Thr-Glu-Tyr motif within their activation loop sequences (62). The active ERKs can then phosphorylate substrates in the cytosol, such as p90^{Rsk}, or translocate to the nucleus and phosphorylate transcription factors such as Elk-1 (63-65). To date, more than 50 substrates for ERK1 or 2 have been identified (66). This emphasises the diversity of actions that ERKs are likely to play in intracellular signalling events.

The biological effects of ERK 1/2 activation include enhanced proliferation or oncogenic transformation, the suppression of apoptosis, and enhanced differentiation. In the haemopoietic system, the ERKs are critical in the processes regulated by multiple cytokines involved in normal hemopoiesis (67). A number of upstream activators of ERK are also known to be potent oncogenes. For example, the overexpression of constitutively active MEK1 transformed fibroblasts, whereas transformation by Ras or v-Src oncogenes could be reverted by a dominant negative MEK1 (68).

Furthermore, Raf has been identified as an oncogene, and its constitutive activation promotes transformation (69). Activating Ras mutations have a frequency of around 30% in myeloid leukaemia (70), although the Ras-Raf-ERK pathway is not the only Ras-induced pathway involved in cellular transformation (71). Thus, activation of the ERK 1/2 pathway is common in human neoplasia, both in solid tumors (72-75) and in haemopoietic malignancies (76,77).

The targeted disruption of the ERK1 and ERK2 genes in mice has revealed some redundant but also some specific, non-redundant functions. ERK1 (p44) knockout mice are viable and fertile, but exhibit defects in thymocyte proliferation and maturation, suggesting a specific role in thymocyte development (78). In contrast, knockout of ERK2 (p42) is embryonic lethal between days 6.5 and 11.5, due to a lack of mesoderm differentiation and increased apoptosis, and the prevention of placental angiogenesis (79-81). This supports a role for ERK 1/2 in developmental processes involving proliferation, survival and differentiation *in vivo* in a number of systems including the haemopoietic compartment.

5.2. Activation of the ERK 1/2 Pathway in Response to G-CSF

G-CSF stimulation activates the ERK 1/2 pathway in G-CSFR-expressing cells such as myeloid cell types, or in cells transfected to stably express the G-CSFR, such as the proB cell line BaF3 (21,31,82-87). Therefore, ERK activation is not merely a consequence of activation of overexpressed G-CSFRs. The functional consequences of ERK activation have been investigated in the BaF3 cell system. These cells are normally dependent on IL-3 for both proliferation and survival (88), but following their transfection with the G-CSFR they also proliferated in response to G-CSF (89). The presence of G-CSF promoted survival in the absence of IL-3, whilst its withdrawal initiated apoptotic cell death (90). This highlights that important biological events follow G-CSFR activation.

Early studies utilised the BaF3 cell system to identify the regions of the G-CSFR mediating ERK activation. Mutant forms of the G-CSFR were expressed and signalling events compared to those initiated by the wild-type receptor. Initial studies showed that truncation of the G-CSFR at residue 646, but not 739, abolished ERK activation as well as cell proliferation. This suggested the requirement for the membrane proximal 57 amino acids for signaling to the ERK 1/2 pathway (82,21). This analysis has been further refined utilising individual point mutations of the intracellular tyrosine residues (i.e. $\Psi \rightarrow F$ mutants of the G-CSFR). Interestingly and perhaps unexpectedly, this analysis revealed that ERK activation in BaF3 cells did not require any specific intracellular tyrosine residues. However, Ras activation was required and this was mediated by the membrane-proximal region (32). Studies in the myeloid cell line LGM-1 also revealed a role for the membrane-proximal region including Box 2 of the G-CSFR in mediating Jak2 and ERK activation (86). In contrast, in primary myeloid cells, ERK activation appeared to be mediated, at least partly, by Y764 (83,84), as both a Y764F and Y-Null G-CSFR failed to stimulate

ERK 1/2 phosphorylation (83). Therefore, multiple regions of the G-CSFR signal transducing domain appear to be involved in ERK 1/2 activation, and there may be cell-type-specific differences in the regions required for this activation.

G-CSFR mutagenesis studies have also provided some information on the possible roles played by ERK activation. In BaF3 cells, G-CSFR mutagenesis indicated ERK 1/2 activation correlated with proliferation (21,31,82). However, this analysis has been refined with the more recent availability of specific protein kinase inhibitors. The judicious use of these inhibitors has allowed the role of post-receptor signalling events to be investigated. PD 98059 is a flavone compound that prevents the activation of ERK (91,92). Its use has confirmed the role of ERK 1/2 in BaF3 cell proliferative responses (31), and further implicated ERK 1/2 in proliferation signalling in both myeloid cell lines and primary cells (86,84).

The modulation of ERK 1/2 activation may be an important mechanism by which cytokines, such as G-CSF, control the balance between proliferation and differentiation. A study utilising the human myeloid MPD cell line as a model of G-CSF-induced neutrophil progenitor growth and maturation showed that treatment with PD 98059 alone decreased proliferation, while stimulation with G-CSF in the presence of inhibitor increased neutrophilic differentiation (87). Conversely, over-expression of a constitutively-active MEK mutant increased cell proliferation at the expense of differentiation (87). This is consistent with a role for G-CSF-stimulated ERK 1/2 activation in proliferation. It further suggests that in the absence of ERK 1/2 activation, G-CSF signalling directs neutrophilic differentiation.

In evaluating this balance between neutrophil proliferation and differentiation, a study in MPD neutrophil progenitors was conducted (85). While ERK 1/2 was activated in progenitors by both G-CSF and Granulocyte Macrophage Colony Stimulating Factor (GM-CSF), the ability for G-CSF to activate ERK 1/2 was lost both in differentiated MPD cells and isolated mature human neutrophils. In addition, G-CSF signalling to other signalling proteins such as STAT3 and Ras was retained. Interestingly, the broad phosphatase inhibitor pervanadate restored the ability of G-CSF to activate ERK 1/2, and the use of the SHP-1 specific inhibitor, sodium stibogluconate, implicated SHP-1 as a phosphatase involved in inhibiting ERK 1/2 activation (85). When these studies (87, 85) are considered together, a model may be proposed whereby G-CSF-mediated activation of ERK 1/2 is important for neutrophil progenitor proliferation, and the expansion of the immature granulocytic pool. G-CSF may initiate differentiation by activating SHP-1, which inhibits ERK 1/2 activation and proliferation, thus permitting terminal differentiation. This regulation of ERK 1/2 activation may allow optimal neutrophil production in response to G-CSF. Physiologically, this regulation may be exerted by co-stimulatory cytokines, such as GM-CSF.

Despite the attractiveness of this model, there are discrepancies in the conclusions drawn on the activation of ERK 1/2 by G-CSF and its subsequent roles. G-CSF did not activate ERK 1/2 in mature neutrophils isolated from the peripheral blood of human donors (85,87), whereas others have consistently shown G-CSF-stimulation of these cells resulting in ERK 1/2 phosphorylation (93-97). As both protocols isolate neutrophils from peripheral blood by dextran sedimentation followed by centrifugation in a Ficoll gradient, and hypotonic lysis of contaminating erythrocytes, the reasons for such consistent discrepancies remain unclear.

ERK dependent effects in G-CSF signalling have also been observed in isolated human neutrophils (94). Thus, G-CSF treatment of these mature neutrophils enhanced phosphorylation of ERK 1/2, actin depolymerisation and concomitant morphological changes, and impaired chemotaxis (94). Treatment with the MEK inhibitor, PD 98059, but not the p38 inhibitor, SB 203580, completely prevented actin rearrangement in response to G-CSF (94). This model suggests that G-CSF may utilise the ERK 1/2 pathway to modulate specific functions of mature neutrophils.

There are numerous studies in lymphoid and myeloid cell types which suggest a role for the ERK 1/2 pathway in G-CSF-stimulated proliferation. In addition, a role for ERK 1/2 in differentiation of 32D cells in response to G-CSF has been reported (98). Pre-treatment with a MEK1/2 inhibitor, U0126, reduced granulocytic differentiation of 32D cells 9 days after G-CSF-stimulation from 64.9% to 22.1%. Similarly, U0126 pre-treatment also potently inhibited granulocytic differentiation of the myeloid cell line HL-60 following stimulation with retinoic acid (31.8% reduced to 2.2%), suggesting the MEK/ERK 1/2 pathway regulates granulocytic differentiation of myeloid cells in response to distinct stimuli (98). Future studies assessing the effect of U0126 on the cytokine-stimulated differentiation of primary myeloid cells will be useful in evaluating the role of the MEK/ERK 1/2 pathway in granulocytic differentiation.

6. THE C-JUN N-TERMINAL KINASE (JNK) MITOGEN-ACTIVATED PROTEIN KINASE PATHWAY

6.1. Properties, stimuli and functions of the JNK pathway

JNK was first described in 1990 as a 54kDa serine/threonine kinase activated following intraperitoneal injection of rats with the protein synthesis inhibitor cycloheximide (99). Two kinases of 46 and 55kDa were subsequently purified with the N-terminal activation domain of c-Jun, and thus named JNK 1 and 2 (100). Ten JNK isoforms have since been identified, which result from alternative splicing of three related genes, *JNK1*, *JNK2* and *JNK3* (101-103). *JNK1* and *JNK2* are ubiquitously expressed, while *JNK3* expression is restricted to the brain, heart and testes (104). The JNKs are

primarily activated in response to stresses such as UV irradiation, heat shock, osmotic shock, oxidative stress and protein synthesis inhibitors, or the proinflammatory cytokines Tumour Necrosis Factor (TNF)- α and IL-1 (102,105-107). Haemopoietic cytokines such as G-CSF and IL-3 are also potent activators of the JNK pathway (32,108-111).

The JNK pathway displays similar organisation to the ERK 1/2 pathway. However, the JNK pathway is more complex, with numerous proteins potentially involved at each level (Table 2). As a consequence, the upstream events in the JNK pathway have remained poorly characterised (112,113). More than twelve different mammalian MAPKKs activate the JNK pathway following their overexpression (40,114). The events leading to MAPKKK activation by stresses or cytokines, may involve various adaptor molecules (115,116), small G proteins (117) and Ste20 protein kinases (118,119). Activation of one or more MAPKKK leads to activation of MAPKKs. Two MAPKKs, MKK4 and MKK7, have been identified which directly phosphorylate both JNK1 and JNK2 on threonine and tyrosine residues of the Thr-Pro-Tyr motif within their activation loops (120,121). While there is evidence to suggest that MKK4 and MKK7 co-operate to achieve JNK activation (122), these kinases may also be differentially activated in response to cytokine or stress stimuli (123-125). Active JNK translocates to the nucleus where it phosphorylates various transcription factors including c-Jun, and activating transcription factor 2 (ATF2) (126-128). JNK also has a range of non-nuclear substrates including the Bcl family members (129), the E3 ligase Itch (130) and the 14-3-3 family of adaptor proteins (131) and thus is likely to mediate a variety of cellular responses.

The activation of JNK has been associated with diverse and often apparently contradictory cellular responses (132,133). These include proliferation, differentiation, survival, and apoptosis. Initially, the biological role of JNK was studied in various cell lines by overexpression of JNK, its upstream activators, and dominant negative kinases. More recently, the production of *JNK1*, *JNK2* and *JNK3* knockout mice has allowed more detailed study of JNK functions *in vitro* and *in vivo*.

JNK activation in response to cytokines results in varying biological outcomes in haemopoietic cells. Several studies suggest a role for JNK in proliferation or survival. The proliferation of FD-EPO cells following erythropoietin stimulation required JNK activation, while the transformation and survival of B lymphoblasts by the Bcr-Abl oncogene correlated with constitutive JNK activity (134-136). In addition, constitutive JNK activation is implicated in the progression of adult T-cell leukaemia following transformation by Human T cell Leukaemia virus type I (137). The treatment of FL5.12 lymphocytic cells with the quinone reductase inhibitor, dicumarol, suppressed JNK activation and survival following IGF-1 exposure, suggesting a link between JNK and survival (138). Similarly, thymocytes defective in JNK activation appeared more sensitive to FasL and TNF α -induced

apoptosis (139,140). Conversely, the activation of JNK and p38 following IL-7 withdrawal contributed to thymocyte apoptotic cell death (141). Thus it would appear that the biological effect of JNK activation is influenced by both the stimuli and cellular context.

The duration of JNK activation may also be important in determining cell fate. For example, treatment of Jurkat T-cells with phorbol 12-myristate 13-acetate (PMA) resulted in transient JNK activation and T-cell activation. However, γ -irradiation caused the persistent activation of JNK, but not ERK or p38, and induced apoptosis (142). Furthermore, the constitutive activation of JNK1 promoted apoptosis, while a dominant negative mutant of MEKK1 or JNK1 prevented cell death (142). Similarly, overexpression of wild-type or constitutively active ASK1, a MAPKKK upstream of JNK and p38, resulted in sustained activation of overexpressed JNK and p38 following oxidative stress, and induced apoptosis through mitochondrial-dependent caspase activation (143-145). Thus, transient JNK activation, like that occurring following cytokine stimulation, may promote cellular proliferation and survival. Sustained activation may result in the induction of apoptosis. The mediators of these different cellular outcomes remain to be identified.

When the *JNK* genes were individually disrupted, mice were viable, but had defects in immune responses and apoptosis. Both *JNK1* and *JNK2* appeared to regulate proliferation, maturation and survival in T lymphocytes (146,147). In contrast, the combined disruption of *JNK1* and *JNK2* genes caused early embryonic lethality, and a severe dysregulation of apoptosis in specific areas of the brain (148). Thus JNK appears to be required for aspects of haemopoietic and neuronal development.

6.2. Activation of the JNK Pathway in Response to G-CSF

While the JNK pathway has generally been considered a stress-activated pathway, haemopoietic cytokines including G-CSF also activate JNK (32,108). The requirement of the individual tyrosines of the G-CSFR for JNK activation was assessed in the BaF3 model cell system (32). The replacement of the three membrane proximal tyrosines of the G-CSFR individually did not affect JNK activation. However, loss of the membrane distal tyrosine, Y763, completely abrogated the activation of JNK in BaF3 cells (32, 149). This indicated a requirement for Y763 G-CSFR in the initiation of the JNK pathway following G-CSF-stimulation. Subsequently, the SH2 domain-containing adaptor proteins Shc, Grb2 and 3BP2, were identified as potential binding partners for Y763 of the G-CSFR utilising peptide-binding assays (149). The mutation of the Y763 G-CSFR interaction motif selectively prevented the binding of the Shc and Grb2 SH2 domains, yet JNK activation by G-CSF was retained, suggesting the direct binding of Shc or Grb2 to Y763 was not required. Thus the activation of the JNK pathway by Y763 of the G-CSFR appears to be mediated via interaction with other signalling intermediates (149). The identification of 3BP2 as potentially interacting with

Y763 G-CSFR is of interest, as it has not been implicated in cytokine receptor signal transduction or MAPK signalling pathways specifically to date. 3BP2 is a 60kDa protein widely expressed in haemopoietic cells, and contains an N-terminal Pleckstrin Homology (PH) domain, a central proline-rich region, and a C-terminal SH2 domain (150). 3BP2 also contains 2 serine and 3 tyrosine phosphorylation sites, which bind 14-3-3 chaperone proteins and the SH2 domain-containing proteins Lyn, Vav and Phospholipase C- γ , respectively (151-153). Thus, 3BP2 may potentially interact with a large number of partners in a phosphorylation-dependent manner. As such, 3BP2 could aid in the assembly of a protein complex at the plasma membrane that leads to JNK activation (149).

While several studies have reported the absolute requirement for Y763 of the G-CSFR for JNK activation (32,149), conflicting observations have been made utilising various G-CSFR truncation mutants (30). When JNK was immunoprecipitated from G-CSF-stimulated BaF3 cell lysates expressing a Δ 715 truncated G-CSFR (thus containing only Y704), its activity as judged by substrate phosphorylation was retained. However, truncation of the G-CSFR at amino acid 685 reduced phosphorylation (30). This suggested that the membrane proximal region of residues 686 to 715, rather than Y763 G-CSFR, was required for JNK activity of the G-CSFR. Although different methods were used, both studies quantitated JNK activity by phosphorylation of known *in vitro* JNK substrates, and therefore should have made similar observations. Interestingly, the same region of 686 to 715 of the G-CSFR was also shown to be required for ERK2 and p38 activation (30). Thus, the specific region of the G-CSFR required for G-CSF-stimulated JNK activation remains to be completely defined.

The biological role of cytokine-stimulated JNK activation has been investigated in BaF3 cells using G-CSFR mutants in which the membrane distal tyrosine was replaced (Y763F) (32). The proliferation of the Y763F G-CSFR mutant in G-CSF was comparable to that of the wild-type receptor, suggesting that JNK activation was not required for proliferation (32). However, the comparison of a G-CSFR mutant containing no intracellular tyrosines, which failed to proliferate, with a mutant containing only Y763, revealed that Y763 of the G-CSFR did contribute to transduction of a proliferative signal in response to G-CSF (149). As Y763 mediated JNK activation, the potential involvement of JNK was investigated further utilising a specific JNK-directed inhibitor. A JNK peptide inhibitor based on the JNK Binding Domain (residues 153 - 163) of the scaffold JIP-1, termed 'truncated Inhibitor of JNK-based on JIP-1' (TI-JIP), selectively bound JNK and inhibited JNK activity towards substrates including c-Jun *in vitro* (154). The addition of a cell permeable derivative of TI-JIP prevented the remaining proliferation of Y763 Only G-CSFR-expressing BaF3 cells following culture in G-CSF (149). This suggested that JNK activation initiated by Y763 G-CSFR promoted proliferation (149). Another JNK inhibitor with a distinct mechanism of action would

be of use in confirming a role for JNK in G-CSF-stimulated proliferation. Whilst SP600125 has been increasingly used in a number of *in vitro* studies in non-haemopoietic systems, its specificity has been questioned (156,157) and it will remain to be seen whether other inhibitors such as AS601245 (158,159) will be more useful in such studies.

7. THE p38 MITOGEN-ACTIVATED PROTEIN KINASE PATHWAY

7.1. Properties, stimuli and functions of the p38 pathway

p38 was discovered in 1993 as a protein that was rapidly tyrosine phosphorylated in response to the endotoxin, lipopolysaccharide (LPS) (160). Its subsequent cloning in 1994 revealed a protein of 43kDa, containing a Thr-Gly-Tyr dual phosphorylation motif, sharing homology with the other MAPK family members and acting as a serine/threonine kinase (161). The p38 subfamily is now known to be composed of four isoforms (p38 α , p38 β , p38 γ and p38 δ) with p38 α and p38 β being ubiquitously expressed. Along with the JNKs, the p38s are also referred to as SAPKs, due to their activation in response to cellular stresses, such as hyperosmolarity, UV and γ -irradiation, heat shock and proinflammatory cytokines (161-163). The p38s may also be activated by cytokines including GM-CSF and IL-3 (164).

While JNKs and p38s become activated in response to similar types of cellular stresses, the activation cascades appear to be distinct (Table 2). The MAPKKKs, MLK3, ASK1, MEKK4 and TAK1, have been implicated in mediating the upstream activation of both the JNK and p38 pathways (165). However, the pathways diverge at the level of the MAPKKs, where MKK4 activates JNK, but not p38 *in vivo* (62), while MKK3 and MKK6 activate p38 and not JNK (166,167). Substrates of the p38s include the kinases MAPKAPK2, MNK1 and PRAK, and the transcription factors ATF2, ELK-1, p53 and NFAT (reviewed in (123)).

Targeted inactivation of p38 α in mice results in embryonic death due to a placental defect (168-170), thus providing little insight into the function of this p38 in the adult. Studies using cell lines have suggested an important role for p38s in cellular processes including apoptosis, proliferation, differentiation, inflammation and tumour suppression (see (171) for review). In haemopoietic cells, p38 has been implicated in macrophage and neutrophil functional responses, such as granular exocytosis, chemotaxis adherence and apoptosis (172). p38 also positively regulates the biosynthesis of TNF- α and IL-1 β by monocytes and macrophages (173,174). These proinflammatory cytokines are involved in the pathogenesis of rheumatoid arthritis, endotoxin-induced shock, inflammatory bowel disease and osteoporosis (175,176).

The increasing availability of small molecule inhibitors of the p38s have provided alternative means for evaluating the physiological roles of MAPK activation.

The pyridinyl imidazole compound SB 203580 inhibits p38 α MAPK activity *in vitro* through competition at the ATP-binding site (177). Pre-incubation with SB203580 prevented the activation of MAPKAP kinase-2 by arsenite and the endotoxin LPS, establishing MAPKAP kinase-2 as a physiological substrate for p38 α (178). Pyridinyl imidazoles have been shown to inhibit LPS-stimulated IL-1 and TNF- α biosynthesis in human monocytes (160,179) and to have therapeutic activity in inflammatory disease models (180). The potential application of SB 203580 and related compounds as anti-inflammatory therapies has led to the more recent development of other p38 inhibitors. RWJ 67657 is an orally-active pyridinyl imidazole inhibitor of p38 α and p38 β , with improved potency and selectivity over SB 203580 *in vitro* (181). RWJ 67657 is currently in clinical trials, and has shown potential in preventing endotoxin-induced renal damage (182).

Diaryl urea compounds have also now been described as a new class of p38 inhibitors. BIRB796 has little structural similarity to the pyridinyl imidazoles, and inhibits all p38 isoforms, by stabilizing a kinase conformation that is incompatible with ATP binding (183,184). BIRB796 reduced both LPS-stimulated TNF production and arthritis severity in a mouse model (184). BIRB796 also displayed anti-inflammatory effects in a trial of human endotoxemia and entered phase IIb/III clinical trials for the treatment of rheumatoid arthritis (184-187). Many of the commercially available kinase inhibitors are active against more than one kinase (156,188), therefore there is the potential that the observed effects in *in vitro* cell assays may be due to inhibition of unrelated kinases. Thus, the availability of several p38 inhibitors with distinct mechanisms of action will be useful to further elucidate the physiological roles of the p38s.

7.2. Activation of p38 in response to G-CSF

The regions of the G-CSFR involved in activation of the p38 pathway in response to G-CSF have been investigated by receptor mutagenesis studies in BaF3 cells. Two distinct regions were involved in p38 activation. The membrane-proximal 100 amino acid portion was sufficient for low levels of p38 phosphorylation and MAPKAPK2 activation. However, a Y763F mutant G-CSFR showed a strong reduction in p38 and MAPKAPK2 activation following G-CSF-stimulation, showing this second region of the G-CSFR was required for maximal activation of these kinases (31). These same regions had previously been implicated in controlling low and high levels of Ras activation respectively (32). Thus, the inducible expression of a dominant negative Ras mutant protein, confirmed that p38 activation by G-CSF was dependent on Ras at least in BaF3 cells, while activation by the stress stimuli, anisomycin, was Ras-independent (31). However, reminiscent of the studies on G-CSF-mediated JNK activation in BaF3 cells (32,149), another study produced conflicting results (30). Dong and colleagues utilised G-CSFR truncation mutants to assess p38 activation in response to G-CSF. While p38 activation was retained in the Δ 715 G-CSFR truncation mutant, truncation at residue 685 abolished activation, suggesting

the region spanning residues 686 to 715 was required (30). While Rausch and Marshall utilised phospho-p38 immunoblotting and measured MAPKAPK2 phosphorylation of a substrate to show activation of these kinases, Dong and colleagues assayed p38 phosphorylation of the substrate ATF2 (30,31). Both assay techniques appear robust, therefore the reason for the discrepancies remains unclear.

As mentioned in the preceding section, SB 203580 inhibits p38 MAP kinases (173,178). In BaF3 cells, inhibition of p38 by SB 203580 halved the G-CSF-stimulated DNA synthesis in cells expressing the full length G-CSFR. Inhibition of the MEK/ERK 1/2 pathway by PD 98059 reduced G-CSF-induced DNA synthesis by a similar proportion, while a combination of both inhibitors was additive, reducing G-CSF-induced DNA synthesis by 80-90% (31). This suggests that in BaF3 cells, the ERK and p38 pathways co-operate to promote proliferation in response to G-CSF. This observation was confirmed in a leukaemic progenitor cell line (189), suggesting co-activation of the ERK and p38 pathways may be a common mechanism by which G-CSF promotes cell growth.

Interestingly, the ability to activate p38 appears to be selectively lost in mature neutrophils by G-CSF, while other cytokines, such as GM-CSF, IL-1 β and TNF α , stimulate p38 phosphorylation (94-97). Thus, the differential activation of MAPK pathways by the cytokines G-CSF, GM-CSF, IL-1 β and TNF α , may partly explain the different effects of these cytokines on neutrophil function.

Perhaps somewhat surprisingly, p38 activation by G-CSF may have specific functions in some non-haemopoietic cell types. While specific for the neutrophilic granulocyte lineage, the G-CSFR has been found on cell types within tissues that interact with haemopoietic cells, such as stromal and endothelial cells (190). Bone marrow stromal cells are important structural components of the bone marrow microenvironment, while the vascular endothelium is an interface between circulating blood components and extravascular tissues. G-CSF-stimulation of a stromal cell line or endothelial cells cultured *in vitro* resulted in activation of p38, and promoted the increased expression of adhesion molecules such as vascular cell adhesion molecule (VCAM-1). This significantly increased the adherence of isolated CD34⁺ progenitors to the stromal cell layer (191), and increased the recruitment of leukocytes to an endothelial cell monolayer (192). These effects were blocked by G-CSFR antibody, or SB 203580 (191,192). The expression of adhesion receptors, such as VCAM-1, on the surface of stromal and endothelial cells within the bone marrow, may regulate self-renewal, differentiation and release of haemopoietic progenitors into the blood stream. Thus G-CSF, by stimulating activation of the p38 pathway in non-haemopoietic cells, may enhance the homing events of progenitor cells in the bone marrow microenvironment. Conversely, the down-regulation of this MAPK

pathway may be one mechanism by which G-CSF promotes the mobilisation of CD34⁺ haemopoietic progenitors from the bone marrow to circulating blood.

8. THE ERK5 OR BIG MITOGEN-ACTIVATED PROTEIN KINASE 1 PATHWAY

8.1. Properties, stimuli and function of the ERK5 pathway

ERK5 or Big MAPK1 (BMK1), cloned in 1995 (193,194), was the fourth member of the MAPK family to be identified, and is currently one of the least studied. ERK5 shares homology with ERK 1/2, and contains a Thr-Glu-Tyr sequence as its dual phosphorylation site within its activation loop (193,194). However, with a molecular mass of approximately 100kDa, ERK5 has a large C-terminal tail distinguishing it from the other MAPKs (194). ERK5 may be activated by stresses such as hyperosmolarity and oxidative stress, in addition to the growth factors EGF, NGF and Brain-Derived Neurotrophic Factor, and agents that act via G-protein-coupled receptors (195-198). Some of the upstream components of the ERK5 pathway have been identified, and include the tyrosine kinase Src; small G-protein Ras; the MAPKKs MEKK2, MEKK3 and Tpl2, and the MAPKKs MEK5 (199,195,200). Its downstream targets include transcription factors of the myocyte enhancer factor 2 family, Sap1a and CREB (200) (Table 2). The dual-specificity phosphatases CL100 and MKP3, which were previously thought to be specific for ERK 1/2, have now been implicated in ERK5 inactivation (195).

Activation of the ERK5 pathway has been associated with proliferation, cell survival and differentiation. The ablation of ERK5 gene expression in mice results in embryonic lethality at E9.5 - 11.5, due to defects in cardiac development and angiogenesis (201-203). This suggests ERK5 is required for cell survival and normal development of the vascular system during embryogenesis.

8.2. Activation of the ERK5 Pathway in response to G-CSF

Despite being expressed in haemopoietic tissues including the bone marrow and spleen, there is a scarcity of studies describing the activation and function of ERK5 in haemopoietic cells. However, a role in haemopoietic cells may be implied, as ERK5 activation is also stimulated by G-CSF (30). G-CSF-stimulation strongly activated both MEK5 and ERK5 in BaF3 cells over-expressing the G-CSFR. Treatment with the tyrosine kinase inhibitor genistein prevented ERK5 activation, while ERK5 activity was enhanced by the protein kinase C-specific inhibitor GF109293X. Receptor mutagenesis showed the C-terminal region of the G-CSFR was required for ERK5 activation, with residues 686 - 715 being indispensable, and the remaining C-terminal amino acids playing an important role. The over-expression of dominant-negative and constitutively-active MEK5 mutants implicated the ERK5 pathway in proliferation, and cell survival in reduced concentrations of G-CSF (30). Thus ERK5 activation may mediate multiple biological effects of G-CSF-stimulation. Lending support to this

hypothesis, the presence of ERK5 has been reported in human neutrophils (204). The activity of MEK5 and ERK5 was stimulated by the bacterial tripeptide, formyl methionyl-leucyl-phenylalanine (fMLP), which functionally activates mature neutrophil cytotoxic actions. Thus, in addition to ERK and p38, ERK5 may also regulate neutrophil chemotactic responses (204). It therefore remains to be determined if ERK5 is activated in response to G-CSF-stimulation of physiologically relevant cell types such as neutrophils.

9. PERSPECTIVES

G-CSF can stimulate the activation of the ERK1/2, JNK, p38 and ERK5 MAPK families. The intracellular regions of the G-CSFR mediating activation of the individual MAPK pathways have been investigated predominantly using mutagenesis studies in heterologous cell systems such as the BaF3 cell line. These studies have shown the membrane-proximal region of the G-CSFR is sufficient to mediate activation of the ERK, p38 and ERK5 pathways. In contrast, the membrane-distal tyrosine residue, Y763, contributes to maximal p38 activation, and appears to be required for JNK activation in response to G-CSF. However, the regions of the G-CSFR mediating activation have not been completely defined, as discrepancies can be found in the literature, even when studies have been carried out in identical cell systems. Therefore, further studies are required to identify both the events initiated by the G-CSFR, and the subsequent downstream signalling from the G-CSFR, which culminates in MAPK activation. The increasing availability of specific inhibitors for signalling intermediates should facilitate such studies.

The activation of the MAPK pathways following stimulation with G-CSF may influence the biological outcomes in target cells. The current evidence suggests that activation of the ERK 1/2 pathway in immature or non-myeloid cell types promotes proliferation, consistent with its reported role in many non-haematopoietic cell types. As cells mature along the neutrophil lineage, the regulation of ERK 1/2 activation may be important in balancing pro-proliferation versus pro-differentiation signalling. G-CSF may also utilise the ERK 1/2 pathway to modulate the function of mature neutrophils. While the JNK, p38 and ERK5 pathways have all been implicated in proliferative responses to G-CSF in a lymphoid model system over-expressing the G-CSFR, their role in myeloid cells remains to be examined. The activation of the p38 pathway by G-CSF in stromal and endothelial cells has the potential to indirectly influence outcomes in haemopoietic cells, by modulating adhesive interactions with the haemopoietic microenvironment. Thus activation of the various MAPK pathways in response to G-CSF-stimulation appears to have diverse roles. The specific outcome is likely to be influenced by a combination of factors including the duration of MAPK activation, specific cellular context and other regulatory influences within the cell. It is apparent that further studies utilising multiple experimental approaches, including the overexpression of wild-type or mutant kinases, targeted

disruption of MAPK genes in mice, and the use of specific kinase inhibitors in physiologically relevant cell types such as mature neutrophils, will be required before the contribution of the individual MAPK pathways to G-CSF-mediated biological responses can be fully elucidated.

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Abbreviations: G-CSF: Granulocyte Colony-Stimulating Factor, G-CSFR Granulocyte Colony-Stimulating Factor Receptor, MAPK: Mitogen-Activated Protein Kinase, ERK: Extracellular Signal-Regulated Kinase, JNK: c-Jun N-terminal Kinase, Y: tyrosine, PI3K: Phosphatidylinositol 3'Kinase, MAPKKK: MAPK kinase kinase, MAPKK: MAPK kinase, PTB domain: Phosphotyrosine Binding domain, EGF: Epidermal Growth Factor, NGF: Nerve Growth Factor, FGF: Fibroblast Growth Factor, OSM: Oncostatin M, IL: interleukin, SH2: Src Homology 2, SH3: Src Homology 3, GM-CSF: Granulocyte Macrophage Colony-Stimulating Factor

Key Words: ERK 1/2, c-Jun, N-terminal, Kinase, p38, Src Homology, Oncostatin, Epidermal Growth Factor, Nerve Growth Factor, Fibroblast Growth Factor, ERK5, MAPKKK, MAPK Pathways, Granulocyte Colony Stimulating Factor, GCSF Receptor, Proliferation, Neutrophil, Function, Review

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