

WJG 20th Anniversary Special Issues (14): Pancreatic cancer**c-Met signaling in the development of tumorigenesis and chemoresistance: Potential applications in pancreatic cancer**

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Abstract

Pancreatic ductal adenocarcinoma is the 4th leading cause of cancer deaths in the United States. The majority of patients are candidates only for palliative chemotherapy, which has proven largely ineffective in halting tumor progression. One proposed mechanism of chemoresistance involves signaling *via* the mesenchymal-epithelial transition factor protein (MET), a previously established pathway critical to cell proliferation and migration. Here, we review the literature to characterize the role of MET in the development of tumorigenesis, metastasis and chemoresistance, highlighting the potential of MET as a therapeutic target in pancreatic cancer. In this review, we characterize the role of c-Met in the development of tumorigenesis, metastasis and chemoresistance, highlighting the potential of c-Met as a therapeutic target in pancreatic cancer.

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Key words: Pancreatic adenocarcinoma; c-Met; Chemoresistance; Receptor tyrosine kinase

Core tip: As one of the leading causes of cancer-related deaths, pancreatic cancer remains elusive to our current therapeutic options. These modest advances in current therapies for pancreatic cancer have led to the recognition and development of targeted therapies toward tyrosine kinase receptors such as the c-Met receptor. In this review, we characterize the role of c-Met in the development of tumorigenesis, metastasis and chemoresistance, highlighting the potential of c-Met as a therapeutic target in pancreatic cancer.

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INTRODUCTION

Pancreatic cancer is the 4th leading cause of cancer deaths in the United States^[1]. Currently, surgical resection is the only treatment option with the potential of cure. However, only 17% of patients are surgical candidates upon diagnosis and surgical resection in combination with chemotherapy and radiation therapy results in a 5-year survival of approximately 23% in specialized centers focused on pancreatic cancer^[2]. While chemotherapy has the potential to delay tumor progression, innate or acquired chemoresistance and subsequent tumor resurgence is the norm^[3,4]. Biologically diverse mechanisms have been identified to be involved in the chemoresistant phenotype, ranging from genetic and epigenetic changes to microenvironmental adaptation^[4,5]. The goal of this review is to focus on the signaling of the mesenchymal-

epithelial transition factor protein (MET) in pancreatic cancer.

The mesenchymal-epithelial transition factor gene (*c-met*) encodes for a membrane-bound receptor tyrosine kinase (RTK) expressed predominantly by epithelial cells. MET is activated and signals downstream pathways following induction of phosphorylation in response to binding of its ligand, hepatocyte growth factor (HGF), also referred to as scatter factor. These ligands are secreted by cells of mesenchymal origin. The resulting HGF/MET pleiotropic signaling cascade activates mediators of cell proliferation and motility and has been heavily implicated in tumorigenesis *via* identification of amplification, activating mutation, and/or overexpression of MET in most solid organ neoplasms. Here, we review the literature to characterize the role of MET in the development of tumorigenesis, invasion, metastasis and chemoresistance, highlighting the potential of MET as a therapeutic target in pancreatic cancer.

PHYSIOLOGIC HGF-MET SIGNALING

MET activation propagates a complex system of intracellular signaling cascades that act to affect cell proliferation and migration. HGF is secreted by mesenchymal cells in close proximity to MET-expressing epithelial cells during embryogenesis or in response to tissue injury, thus functioning as a paracrine signaling mechanism that promotes cell proliferation and migration. MET is translated as a 180 kDa protein that is subsequently cleaved to form a heterodimer consisting of a short alpha (approximately 40 kDa) and long beta (approximately 140 kDa) chain of residues. The mature protein is then transported to and inserted in the plasma membrane. Upon HGF ligand binding to MET, autophosphorylation at multiple tyrosine residues within the cytoplasmic domain occurs, catalyzed by intrinsic ATPase activity. This results in changes in the tertiary structure of MET facilitating the formation of a signaling complex including GAB1 and GRB2 proteins that subsequently activates multiple downstream pathways (Figure 1). Known effector molecules of this signaling cascade include Src, mitogen-activated kinase, extracellular signal-regulated kinase 1 and 2, phosphoinositide 3-kinase (PI3K), protein kinase B (Akt), signal transducer and activator of transcription (STAT), nuclear-factor- κ B, and mammalian target of rapamycin^[6-9]. MET-mediated induction of these pathways acts to positively influence cell proliferation, migration, and survival (Figure 2). *Via* these down-stream effectors, HGF-MET signaling plays a crucial role in important physiologic processes including embryonic development, organ regeneration and wound healing.

MET is essential for embryonic development and *hgf*- or *c-met*-null embryos die *in utero*^[10]. In early embryonic development, HGF and its receptor MET are co-expressed by progenitor cells, suggesting autocrine signaling is an early homeostatic mechanism for stem cell survival^[11]. HGF-MET signaling is necessary to ensure

the growth and survival of placental trophoblast cells as well as embryonic hepatocytes. MET signaling is also necessary for the proper migration of muscle progenitor cells, development of the embryonic nervous system, and epithelial branching morphogenesis^[12,13]. Later in development, paracrine HGF-MET signaling is critical for properly orchestrating organogenesis. Assays evaluating the ability of epithelial cells to form tubules *in vitro*, a process which recapitulates organ development, demonstrate that HGF signaling induces cells to undergo an epithelial-to-mesenchymal (EMT) transition. This transition allows host cells to relocate during embryonic development. Ultimately, these cells reclaim their epithelial identity, but the EMT marks a critical event in organogenesis.^[11]

Inflammation and wound healing following injury are also highly dependent on HGF-MET signaling. HGF increases dramatically following renal or hepatic damage, inducing a diverse array of anti-apoptotic responses^[9,14,15]. In cases of chronic or repetitive injury, HGF acts to oppose fibrosis by inducing apoptosis of myofibroblasts and by antagonizing transforming growth factor- β (TGF- β)^[9,13,16]. Peptic ulcer disease represents a specific example of MET's protective effect. The loss of HGF signaling in a murine model led to decreased gastric mucosal cell proliferation and delayed healing from mucosal injury^[17]. In fact, HGF-MET signaling has been implicated as essential to the protection, regeneration, and anti-fibrotic activity of cutaneous, pulmonary, hepatic, and gastrointestinal tissues in response to injury^[13].

With respect to pancreatic endocrine physiology, the beta cell, responsible for insulin secretion, is dependent on HGF-MET signaling to hypertrophy and proliferate in response to persistent hyperglycemia^[18]. In effect, MET is essential for the hyperinsulinemia seen in Type II diabetes. *c-met* knockdown mice exhibit increased beta cell apoptosis during development and are more susceptible to streptozotocin-induced diabetes^[19]. Additionally, *c-met* knockdown mice displayed reduced beta cell expansion during pregnancy leading to an increase in gestational diabetes^[20]. Multiple investigations have confirmed that these knockdown mice have decreased glucose tolerance and reduced insulin secretion after stimulation^[21,22]. In fact, stimulation of the HGF/MET pathway has been suggested to encourage beta cell proliferation after islet cell transplantation. Thus, MET plays a critical role in pancreatic neuroendocrine cell proliferation and development.

Relatively little data is available concerning MET signaling and normal pancreatic exocrine development. A recent investigation by Anderson *et al.*^[23] examined the phenotype of a point mutation in *c-met* that impaired localization and activation of MET. Zebrafish with this mutation exhibited mislocalization of pancreatic ductal cells compared with wild-type animals. Interestingly, ductal proliferation was unaffected. Further, inhibition of MET proteindownstream signaling with PI3K and STAT inhibitors produced a similar phenotype, suggesting an essential role for MET in migration and localization of

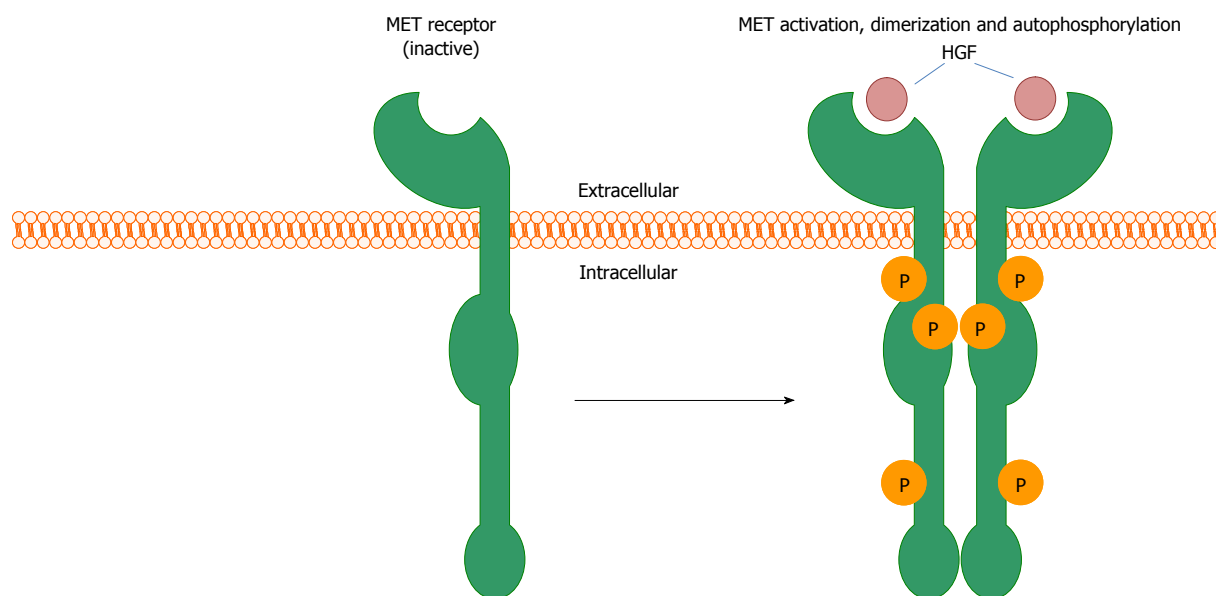


Figure 1 The mesenchymal-epithelial transition factor receptor functions as a transmembrane tyrosine kinase receptor. Ligand binding from hepatocyte growth factor (HGF)/scatter factor induces receptor dimerization and autophosphorylation of intracellular tyrosine residues, which serves as a catalytic site for the SH2 domains of numerous cytosolic signaling proteins. MET: Mesenchymal-epithelial transition factor.

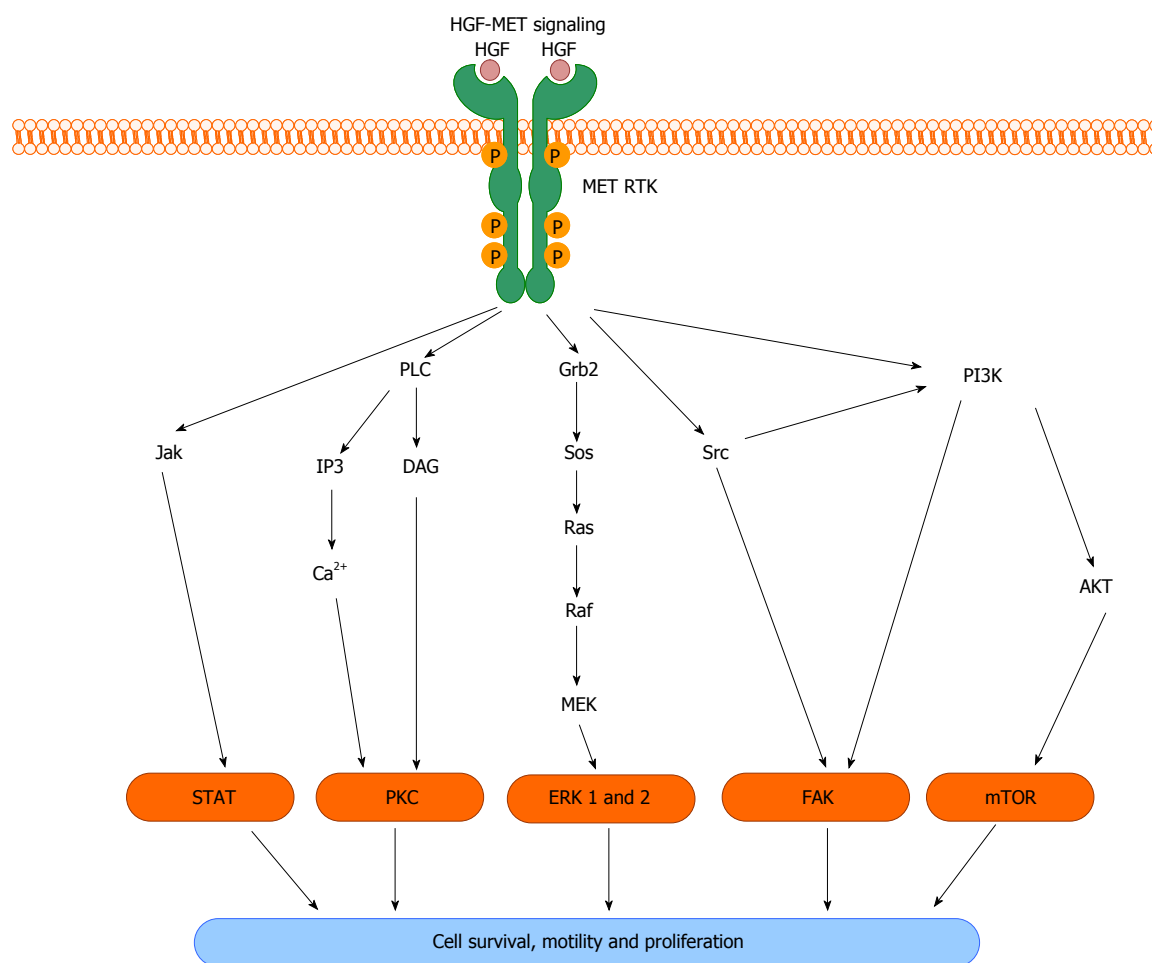


Figure 2 Hepatocyte growth factor activation of the mesenchymal-epithelial transition tyrosine kinase receptor induces a pleiotropic response involving a host of intracellular signaling to induce cell survival, migration and proliferation. HGF: Hepatocyte growth factor; MET: Mesenchymal-epithelial transition factor; RTK: Receptor tyrosine kinase; JAK: Janus kinase; STAT: Signal transducer and activator of transcription; PLC: Phospholipase C; IP3: Inositol triphosphate; DAG: Diacylglycerol; Ca²⁺: Calcium; PKC: Protein kinase C; Grb2: Growth factor receptor-bound protein 2; Sos: Son of sevenless homolog; Ras: Harvey rat sarcoma viral oncogene homolog; Raf: Rapidly accelerating fibrosarcoma; MEK: Mitogen activated protein kinase kinase; ERK: Extracellular-signal-regulated kinase; FAK: Focal adhesion kinase; PI3K: Phosphoinositide 3-kinase; AKT: Protein kinase B; mTOR: Mammalian target of rapamycin.

embryonic pancreatic ductal cells.

In summary, physiologic HGF-MET signaling is essential for appropriate embryonic development and organ repair. The function of the HGF/MET pathway observed in multiple organ systems appears to drive cell proliferation and mobility. Unfortunately, dysregulation of this pathway clearly could result in tumor initiation and/or progression. Amplification, mutation or overexpression of *c-met* become deleterious, contributing to malignant transformation and metastasis. Activating and sustaining HGF-MET signaling in this pathologic context drives tumor progression and is responsible, at least in part, to the development of chemoresistance.

PATHOLOGIC HGF-MET SIGNALING IN CANCER

Excessive MET activity is a feature of many cancers, although inciting mechanisms appear to be tumor-specific^[24]. *c-met* received early attention as a proto-oncogene when activating mutant alleles were implicated in cases of hereditary papillary renal cell carcinoma^[25]. The resulting MET receptor was constitutively activated, undergoing spontaneous ligand-independent phosphorylation^[11]. In an analysis of seven families with hereditary papillary renal carcinoma, four displayed activating *c-met* mutations, all of which were located in the tyrosine kinase domain of the MET protein^[25]. Sporadic *c-met* mutations have also been described in gastric carcinomas, glioblastomas, and squamous cell carcinomas of the head and neck^[11,12,26]. Furthermore, aberrant positive feedback systems involving autocrine and paracrine signaling in the HGF-MET axis contribute to tumorigenic phenotypes in melanomas, osteosarcomas, breast cancer and gliomas^[26]. One retrospective histopathologic analysis observed MET overexpression in 87% of renal cell carcinoma specimens^[27]. Additionally, a strong correlation between MET expression and the esophageal metaplasia-dysplasia-adenocarcinoma continuum has been shown in surgical specimens from patients with esophageal adenocarcinoma^[28]. In fact, *c-met* amplification occurs in approximately 9% of esophageal cancers^[29]. These investigations provide compelling evidence that c-Met is a potent oncogene.

The association between MET activity and neoplastic progression has been investigated in animal models. Hypoxia-induced tumor cell invasion is dependent upon upregulated MET signaling, suggesting another mechanism driving growth and metastasis^[30,31]. Overexpression of wild-type MET in hepatocytes led to spontaneous hepatocellular carcinoma development that regressed upon MET inactivation^[30,32]. Thus, overexpression of non-mutated MET is sufficient to induce tumor development. Moreover, inhibition of MET caused established tumors to regress, suggesting that MET signaling is necessary for tumor growth and maintenance. Subsequent animal models have proposed that the frequency of many carcinomas and lymphomas is greatly increased by MET overexpression^[33]. Non-neoplastic cell lines forced to constitutively

express HGF or MET become highly tumorigenic when implanted *in vivo*^[34,35]. Therefore, while MET activity may not be the inciting mechanism in the formation of many cancers, overexpression in pre-clinical models appears to confer a more aggressive phenotype.

In fact, MET expression has been correlated with more aggressive disease and worse clinical outcomes in many cancers. In NSCLC, MET overexpression correlates with an unfavorable prognosis and has been implicated as a primary mechanism of resistance to epidermal growth factor receptor (EGFR) inhibitor therapy^[36,37]. In hepatocellular carcinoma the expression level of MET is directly correlated to metastatic behavior and inversely correlated to the level of tumor differentiation and patient survival^[38-41]. In a prospective cohort analysis of 554 patients with renal cell carcinoma, a particular single nucleotide polymorphism (SNP) in *c-met* was associated with a decline in median recurrence-free survival from 50 to 19 mo^[42]. While the functional outcome of this SNP remains to be elucidated, an activating point mutation is highly suspected. Likewise, MET overexpression is a HER2/neu-independent prognostic marker for node-positive breast cancer, signifying increased tumor aggressiveness^[43]. MET expression significantly correlated with the depth of invasion and regional lymph node metastasis in colorectal cancer^[44]. Thus, the list of solid organ neoplasms for which upregulation of HGF-MET signaling portends a more aggressive phenotype is extensive^[45,46]. Taken together, this data demonstrates that dysregulation of the HGF-MET pathway contributes to tumor progression. This data also has implications regarding the status of the HGF-MET pathway on the effectiveness of certain biologic therapies, a concept we will expand upon later.

Concerning pancreatic adenocarcinoma, evidence is accumulating that correlates dysregulated MET activity with an aggressive phenotype. In a recent investigation thirty-six pancreatic tumor samples were analyzed and MET expression levels were directly proportional to tumor grade^[47]. Similar histopathologic analyses showed an approximate five to seven-fold increase in MET protein expression levels in pancreatic cancer compared to normal pancreas samples^[48,49]. Histopathologic evaluation of our own resected patient population support these findings (Figure 3). A larger collection of pancreatic tumor specimens subsequently confirmed increased MET protein expression compared with normal controls and MET protein overexpression significantly correlated with increased TNM stage^[50]. In fact, secreted HGF protein from surrounding stromal tissue has been correlated with MET overexpression in patients with pancreatic cancer and associated with worsened overall survival^[51]. Given the known pathophysiologic actions of MET in cancer and a well-demonstrated overexpression pattern in pancreatic adenocarcinoma, inhibition would seem a logical therapeutic avenue.

Unfortunately, targeting MET alone as a therapeutic strategy appears to be overly optimistic. Despite con-

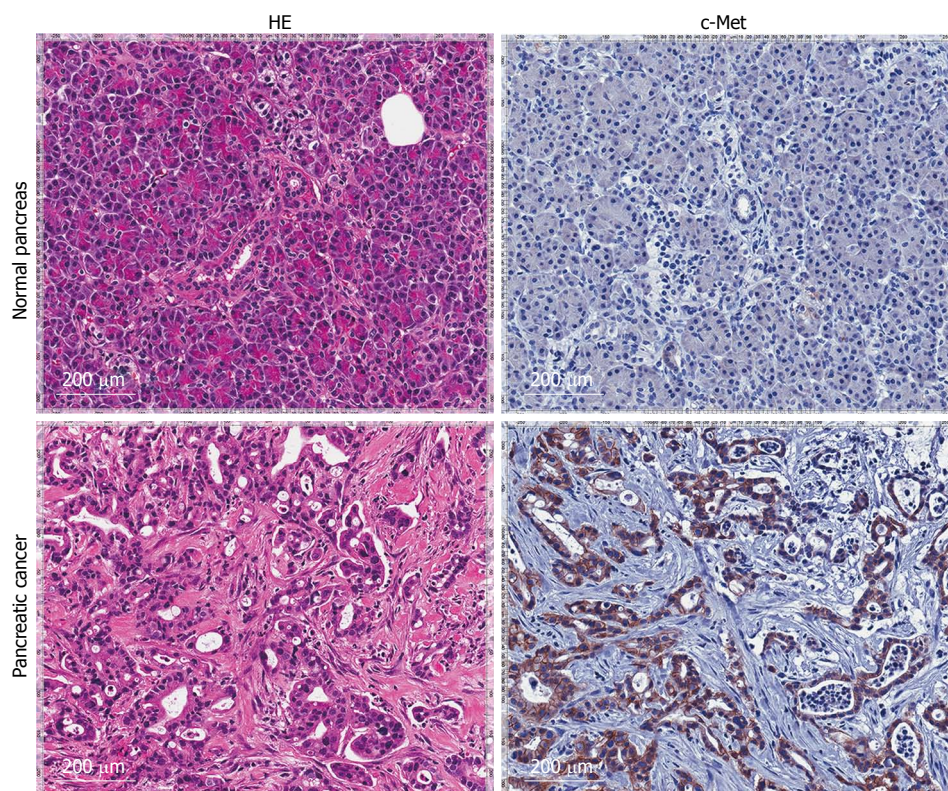


Figure 3 Immunoperoxidase staining. Immunoperoxidase staining of formalin fixed, paraffin embedded human pancreatic specimens demonstrate over expression of c-Met receptor in pancreatic cancer patients when compared to adjacent normal pancreatic tissue controls (right panel). HE staining demonstrate histological confirmation of diseased (pancreatic cancer) or normal tissue (left panel).

vincing evidence of primarily MET-induced tumors, a growing body of evidence supports secondary MET involvement in a synergistic crosstalk with other RTKs such as EGFR, vascular endothelial growth factor receptor and insulin-like growth factor-1 receptor (IGF-1R) to promote malignant cell migration, invasion, and chemoresistance^[52-55]. In hepatocellular carcinoma cells, EGFR co-immunoprecipitates with MET and activated EGFR leads to ligand-independent activation of the MET pathway^[36]. MET and IGF-1R synergistically promote migration and invasion in pancreatic adenocarcinoma. Down-regulation of MET *via* adenoviral infection with a MET ribozyme abrogated the effects of IGF-1, suggesting co-dependence of IGF-1R and MET in directing tumor invasion and migration^[56]. These complex, multifactorial interactions among RTKs play a key role in growth and maintenance of a variety of tumor types and are under intense scrutiny for potential therapeutic value or mechanisms of therapeutic resistance. These discoveries will be essential to the evolving reality of personalized cancer treatment strategies.

MET AND TUMOR METASTASIS

The microenvironment of a tumor may be as instrumental to the progression of disease as the tumor itself. In fact, stromal support in the form of angiogenesis, mitogenic signaling and cytoskeletal attachments are necessary for tumors to grow and metastasize *in vivo*. As previously

mentioned, HGF secretion by stromal cells mediates MET activity in a paracrine manner. Additionally, HGF-MET signaling encourages angiogenesis by inducing VEGF expression by cancer cells^[57,58]. However, neovascularization alone is not sufficient for metastasis to occur.

Recall that in embryonic development and tissue repair, MET plays an essential, physiologic role in cellular migration and subsequent organogenesis. Unfortunately, overexpression of MET and its subsequent downstream pathways, including PI3K and Src, similarly enable growth and invasion of malignant cell populations. An initial step in tumor migration involves clearing a path through the extracellular matrix (ECM). This is accomplished primarily by the actions of secreted matrix metalloproteinases (MMPs), which digest surrounding ECM. Not surprisingly, MMPs have been shown to be upregulated by MET signaling^[24].

Cells must also respond to chemotactic factors in the ECM for effective migration. As previously mentioned, an EMT endows epithelial cells with certain properties of mesenchymal cells that enable migration. Furthermore, it has recently been proposed that the EMT may be coupled with a transition to a more stem-cell-like state, suggesting further importance of the EMT to metastasis and tumor progression^[59]. In embryogenesis, MET controls the EMT necessary to enable myogenic progenitor cell migration^[9]. Additionally, EMT is further driven by Wnt signaling, a pathway that is also stimulated by MET *via* glycogen synthase kinase 3- β ^[60]. The mechanism by

Table 1 Cancer stem cell markers are listed with previously described functions

CSC marker	Proposed function
CD44	ECM binding, organization of actin cytoskeleton, modulation of mitogenic signaling ^[112]
CD24	P-Selectin binding, cell migration ^[113]
ESA	Mediation of epithelial intercellular adhesion ^[114]
CD133	Activation of Wnt signaling and angiogenesis ^[115,116]
CXCR4	Receptor of SDF-1, hematopoietic stem cell homing, invasion ^[117]
MET	Receptor of HGF, promotes cell growth, proliferation, migration ^[11]
u-PA	ECM degradation, cell migration ^[118]

Note the pattern of migratory functions associated with cancer stem cell (CSC) markers. ECM: Extracellular matrix; ESA: Epithelial specific antigen; CXCR4: Chemokine receptor type 4; SDF-1: Stromal cell-derived factor 1; MET: Mesenchymal-epithelial transition factor; HGF: Hepatocyte growth factor; u-PA: Urokinase-type plasminogen activator.

which MET governs the EMT directly in tumor metastases remains to be elucidated.

Finally, malignant cells must take up residence in a distant organ as a metastatic focus. Remarkably, HGF-MET signaling plays a role both in cellular dissociation within the primary tumor and cellular re-association within the metastatic niche^[24]. HGF triggers destabilization of adherens junctions within the primary tumor through FAK-mediated integrin signaling^[61]. As tumor cells invade and metastasize, failure of proper interaction with foreign microenvironments leads to programmed cell death. HGF-MET signaling upregulates cytoskeleton adhesion receptors and enables tumor cells to effectively engage their new surroundings and elude apoptosis, thereby facilitating metastatic development^[24]. Thus, in addition to fostering primary tumor growth, MET appears to act at multiple regulatory points in the development of metastatic disease.

MET AND CANCER STEM CELLS

A growing body of evidence suggests that a hierarchy exists in cancer cell populations, a notion initially discovered in hematopoietic malignancies. Cancer stem cells (CSCs) actually comprise a small minority of tumor cells but appear to be the only group capable of unlimited self-renewal and formation of xenografts. Interestingly, these cells appear to have a limited potential for further differentiation^[62,63]. CSC populations have subsequently been identified in a variety of solid organ neoplasms including brain, breast, melanoma, pancreas, prostate and colon. While CSC identification is specific to each tumor type, common themes include cell surface markers such as CD24, CD44, CD133, epithelial surface antigen (ESA), chemokine receptor type 4, and urokinase plasminogen activator (Table 1)^[64-72]. Importantly, in pancreatic cancer stem cell (PCSC) populations, MET overexpression conferred an equally tumorigenic phenotype to CD44⁺/CD24⁺/ESA⁺ cells^[73]. Restated, MET overexpression alone may sustain a pan-

creatic cancer stem cell phenotype.

Conversely, MET overexpression may prompt cancer cells to dedifferentiate into CSCs. MET activation in prostate cancer cells induces a stem-like phenotype and endows cells with more invasive potential^[74]. In head and neck squamous cell carcinoma, cells overexpressing MET can recapitulate the heterogeneity of parental tumors *in vivo* and exhibit increased self-renewal, invasion, and metastasis^[75]. In glioblastomas, overexpression of MET leads to a stem-like phenotype resistant to terminal differentiation signals^[76]. Regardless of the origin of CSCs, MET overexpression is associated with a stem-cell-like phenotype in a wide range of cancers.

MET AND CHEMORESISTANCE

Chemoresistance is an important factor contributing to the high mortality rate of most cancers and is germane to treatment failure in pancreatic cancer. With few exceptions, tumor metastasis precludes surgical therapy and leaves chemotherapy as the only therapeutic option. In borderline cases, neoadjuvant chemotherapy protocols may offer opportunities for attempts at a surgical resection. After surgery, adjuvant chemotherapy protocols are beneficial in avoiding recurrence, especially in more aggressive tumor types. Unfortunately, the development of chemoresistance is a real oncologic dilemma. In the face of chemoresistant tumor populations, no effective treatments exist. Therefore, understanding the molecular regulators of chemoresistance has major implications in therapeutic intervention. Several lines of evidence converge to suggest that MET overexpression may confer a chemoresistant phenotype.

We have outlined the close relationship between MET and CSCs. In fact, CSCs have been shown to be largely responsible for chemoresistant phenotypes in glioblastomas, hematopoietic, pancreatic and colorectal cancers^[77-83]. Mechanisms range from reducing drug delivery to repairing cytotoxic injury and ultimately result in tumor cell repopulation^[77-83]. Furthermore, a higher proportion of cells bearing CSC markers has been associated with poor outcomes in glioblastomas, breast and pancreatic cancer^[84-86]. Thus, investigative directions have become particularly focused on identifying factors that drive and sustain CSCs. Given the significance of HGF-MET signaling in PCSC populations, the role of MET in this process would seem to be particularly relevant in pancreatic cancer.

The activation of the HGF-MET axis has been directly implicated in acquiring and maintaining chemoresistance in several tumor cell populations (Table 2). HGF stimulation protects NSCLC cells from cisplatin toxicity, in part mediated by downregulation of apoptosis-inducing factor^[87]. *c-met* amplification is associated with NSCLC resistance to the EGFR inhibitor Gefitinib *via* modulation of the PI3K pathway^[88]. Multiple investigations have revealed that MET inhibition sensitizes ovarian carcinoma to carboplatin plus paclitaxel, whereas MET over-

Table 2 Mechanisms of hepatocyte growth factor-mesenchymal-epithelial transition factor induced chemoresistance in different cancer types

Cancer type	Chemotherapy	Mechanism of HGF-MET signaling in chemoresistance
Multiple myeloma	Bortezomib	MET overexpression: Apoptotic resistance <i>via</i> PI3K-Akt activation ^[92]
Glioblastoma	Radiation, cisplatin, camptothecin, adriamycin, and taxol groups	Addition of HGF: Anti-apoptotic effects <i>via</i> PI3K-Akt dependent pathways ^[91]
Rhabdomyosarcoma	Vincristine/etoposide, radiation	Addition of HGF: Enhanced migration, MMP secretion, PI3K-Akt activation ^[119]
Non-small cell lung carcinoma	Cisplatin	Addition of HGF: Downregulation of apoptosis-inducing factor (AIF) ^[87]
Non-small cell lung carcinoma	Erlotinib	<i>c-met</i> amplification: Activation of EGFR, preservation of PI3K-Akt activation ^[88]
Gastric adenocarcinoma	Adriamycin	Addition of HGF: Anti-apoptotic effects <i>via</i> PI3K-Akt upregulation ^[93]
Pancreatic adenocarcinoma	Gemcitabine	MET overexpression: Anti-apoptotic effects <i>via</i> PI3K-Akt activation, induction of EMT-like changes ^[94,95]
Ovarian adenocarcinoma	Carboplatin/paclitaxel	MET overexpression: Apoptotic resistance <i>via</i> PI3K-Akt activation ^[89,90]

MET: Mesenchymal-epithelial transition factor; PI3K: Phosphoinositide 3-kinase; Akt: Protein kinase B; HGF: Hepatocyte growth factor; MMP: Matrix metalloproteinase; EGFR: Epidermal growth factor receptor; EMT: Epithelial-mesenchymal transition.

expression imparts chemoresistance^[89,90]. Furthermore, stimulation of the HGF-MET pathway confers protection against chemotherapeutic agents by upregulation of PI3K/Akt signaling in multiple myeloma, glioblastoma and gastric adenocarcinoma^[91-93]. Our group has found that pharmacologic MET inhibition using a small molecule inhibitor sensitizes esophageal adenocarcinoma cells to pyrimidine analog chemotherapy (unpublished data). Additionally, preclinical studies have demonstrated that overexpression of MET has also been associated with EMT-like changes in acquired-gemcitabine-resistant pancreatic cancer cells^[94]. These findings are not surprising as pancreatic cancer is known for rapid acquisition of chemoresistant behavior and also MET overexpression. Additionally, MET inhibition in pancreatic adenocarcinoma leads to gemcitabine sensitization^[95]. Although consisting largely of *in vitro* data, these investigations demonstrate a strong correlation between MET overexpression and chemoresistance in a variety of malignancies.

The mechanism by which MET overexpression confers chemoresistance in pancreatic cancer likely involves the mesenchymal support network. Tumors most heavily invested with stroma are often those most refractory to chemotherapy^[4]. Stroma is the predominant source of HGF, suggesting MET activation is, at least in part, a result of paracrine signaling. In breast cancer, HGF-MET signaling augments tumor cell adhesion to ECM components by upregulating integrin synthesis and inducing conformational changes that activate integrins^[24,96]. This integrin-mediated adhesion is actually a mechanism by which tumor cells can oppose the cytotoxic effect of chemotherapy^[97]. Indeed, studies have shown that integrin expression, specifically $\alpha\beta$, is upregulated in cases of relapsed leukemia. This finding suggests that increased integrin expression may contribute to generating minimal residual disease, defined as tumor cell persistence following therapy^[4]. Further investigation is necessary to characterize the mechanism by which MET-driven integrin upregulation imparts chemoresistance and whether this principle is applicable to other tumor types. However, disruption of the HGF-MET axis may result in biochemical dissociation from the protective mesenchymal environment, thereby imparting sensitivity to cytotoxic therapies.

Data specific to the pancreatic cancer microenvironment regarding MET signaling is forthcoming. Animal models that utilize VEGF inhibitors to impart ischemia actually result in increased tumor growth and invasion but inhibition of MET abrogates this proliferative response to hypoxia^[98]. As previously mentioned, PCSCs can be defined by comparatively high MET expression. Pharmacologic inhibition of MET in PCSC populations blocked self-renewal capacity, reduced the overall PCSC population and significantly slowed tumor growth *in vivo*^[99]. Treatment with MetMab, a monovalent antibody against MET, has shown decreased pancreatic tumor growth in orthotopic models *in vivo*^[100]. Further, recent preclinical data suggest cabozantinib, a novel small molecule MET inhibitor, overcomes gemcitabine resistance. These studies will likely lead to phase 3 clinical trials using this inhibitor in pancreatic cancer patients^[101].

Finally, the interplay between RTKs and the potential for redundancy deserves emphasis when discussing therapeutic intervention. MET and other RTKs are involved in a complex signaling network that may exist as a redundant system with controlled feedback. For example, MET induction has been associated with anti-EGFR therapy and resultant MET overexpression confers resistance to EGFR inhibitors in lung and colorectal cancer^[88,102-104]. Thus, MET inhibition may potentiate therapeutic effects aimed against other RTKs, and vice versa. In fact, effective siRNA inhibition of c-Met transcripts in NSCLC confers sensitization to gefitinib, an inhibitor of EGFR^[88]. Further, concomitant administration of EGFR and MET inhibitors eliminated NSCLC cells more effectively than either drug alone^[55,105]. Similarly, MET inhibition led to increased sensitivity of her2-positive breast cancer cells to trastuzumab^[106]. Not surprisingly, combination RTK inhibition is quickly becoming the standard in targeted oncologic chemotherapies involving MET inhibition.

CONCLUSION

In summary, *c-met* encodes a versatile RTK crucial to physiologic cell proliferation, organogenesis and wound healing. Its mechanism of action involves multiple anti-apoptotic, pro-mitogenic, and pro-motility downstream

Table 3 Mesenchymal-epithelial transition factor inhibitors are shown with specific targets and evidence of anti-tumor effect

Drug	Target(s)	Impact
Cabozantinib	MET	Induced apoptosis in gemcitabine-resistant pancreatic cancer cell lines, currently in phase I clinical trials ^[101]
Crizotinib	ALK, MET	Inhibited growth of gemcitabine resistant pancreatic cancer cell lines ^[95] , FDA approved for ALK-expressing NSCLC and myofibroblastic sarcomas
Foretinib	MET, VEGFR	Inhibited tumor growth in lung metastasis animal model but failed to show benefit in multiple phase II clinical trials ^[110,120,121]
Tivantinib	MET	Inhibited growth in multiple cancer cell lines <i>via</i> MET targeting as well as inhibition of microtubule formation ^[122]
E7050	MET, VEGFR	Inhibited growth in xenograft models of lung, gastric and pancreatic cancer ^[123]
PF-04217903	MET	Inhibited growth and metastasis of pancreatic neuroendocrine tumors ^[124]
SU11274	MET	Inhibited growth and proliferation in colon cancer cell lines ^[125]
T-1840383	MET, VEGFR	Inhibited tumor growth in a variety of murine xenograft models ^[126]

MET: Mesenchymal-epithelial transition factor; ALK: Anaplastic lymphoma kinase; NSCLC: Non-small cell lung carcinoma; VEGFR: Vascular endothelial growth factor receptor.

effectors. Unfortunately, dysregulated HGF-MET signaling is implicated in multiple oncologic mechanisms, including tumor growth, invasion and chemoresistance. Not surprisingly, clinical studies have consistently revealed MET overexpression as a negative prognostic indicator in a wide variety of malignancies.

HGF-MET signaling mediates mesenchymal-cell-mediated mitogenic support to developing tumor cell populations. MET activity enhances ECM degradation and integrin-mediated adhesion. In addition to promoting mobility and invasion, this appears to confer a protective microenvironment conducive to the development of chemoresistant clones. MET signaling is a marker of cancer stem cell populations, a recently characterized subgroup of cancer cells resistant to cytotoxic therapies.

A better understanding of tumor growth signaling pathways and chemoresistant mechanisms carries the potential of immense therapeutic value, especially in aggressive tumors such as pancreatic adenocarcinoma. Strategies include targeting chemoresistant CSCs, limiting acquired resistance with combination therapy, and developing methods of biochemically dissociating tumor cells from their mitogenic microenvironments. Each of these mechanisms has been associated with HGF-MET signaling. Not surprisingly, a series of MET inhibitors and more nonspecific RTK inhibitors are currently under investigation (Table 3)^[107-111]. The evidence presented makes a compelling case for further insights into HGF-MET signaling as a therapeutic target in pancreatic cancer.

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