Identification of the Receptor Tyrosine Kinase c-Met and Its Ligand, Hepatocyte Growth Factor, as Therapeutic Targets in Clear Cell Sarcoma

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Abstract

Clear cell sarcoma (CCS), a childhood tumor of the tendons and aponeuroses, is uniformly fatal once it has metastasized because of its profound therapeutic resistance. CCS is characterized by production of a chimeric transcription factor, EWS-ATF1, which is formed as the result of a disease-specific chromosomal translocation. EWS-ATF1 activates the melanocyte transcription factor MITF, which in turn activates transcription of c-Met, an oncogenic receptor tyrosine kinase recently shown to be activated in CCS. Based on this connection, we hypothesized that c-Met inhibition may offer a strategy to treat CCS, as an indirect tactic to defeat a transforming pathway downstream of EWS-ATF1. Here, we show that primary CCS and CCS-derived cell lines express c-Met, which is activated in an autocrine fashion by its ligand hepatocyte growth factor (HGF)/scatter factor in some CCS cell lines. c-Met expression is critical for CCS invasion, chemotaxis, and survival. Blocking c-Met activity with a small-molecule inhibitor (SU11274) or a neutralizing antibody to its ligand HGF (AMG 102) significantly reduced CCS cell growth in culture. Similarly, AMG 102 significantly suppressed in vivo tumor growth in an autocrine xenograft model of CCS. Collectively, these findings suggest the HGF:c-Met signaling axis as a candidate therapeutic target to improve clinical management of CCS.

Introduction

Clear cell sarcoma (CCS), an aggressive soft tissue sarcoma that typically develops in the tendons and aponeuroses of children and young adults (1, 2). A high rate of local and distant recurrence results in a 5-year overall survival of ~50% (3–5). Five-year survival decreases to 20% for metastatic disease, consistent with the profound resistance of the tumor to conventional chemotherapy and radiation therapy. Molecularily, CCS is characterized by the t(12;22) (q13;12) translocation, which results in fusion of the Ewing’s sarcoma gene EWS with the cyclic AMP (cAMP) regulated transcription factor ATF1, a member of the cAMP-responsive element binding protein (CREB) family (6–9). Gene fusion replaces the kinase-dependent regulatory region of ATF1 with the amino-terminal domain of EWS. By preserving the DNA binding and heterodimerization domains of ATF1, this chimera yields an oncoprotein capable of deregulating transcription of CRE-regulated genes (10). We have previously shown that MITF, the melanocyte master transcription factor, is a direct transcriptional target of EWS-ATF1 (11). EWS-ATF1 mimics the melanocyte stimulating hormone/CREB signaling pathway to directly and aberrantly activate MITF expression.

The MiT family regulates several targets that may be central to oncogenesis. MITF directly activates the c-Met gene through a conserved E-box element in the c-Met proximal promoter (12). c-Met is also a transcriptional target of the ASPSCR1-TFE3 fusion, as predicted by the strong homology between TFE3 and MITF (13).

The receptor tyrosine kinase c-Met normally mediates signaling from hepatocyte growth factor/scatter factor (HGF) typically expressed by stromal and mesenchymal cells. c-Met signaling has been implicated in a wide range of biological activities including proliferation, survival, and motility, all of which are frequently dysregulated in cancer. Initially identified as an oncogene when fused to the nuclear pore complex protein TPR in carcinogen-treated osteosarcoma cells (14, 15), c-Met has been implicated in the oncogenesis of a wide range of cancers including renal, gastric, and small-cell lung carcinomas, central nervous system tumors, as well
as several sarcomas\(^7\) (reviewed in refs. 16, 17). In these cancers, c-Met may be aberrantly activated by mutation, autocrine or paracrine HGF stimulation, or overexpression. Coexpression of HGF and c-Met has been noted in a number of human tumors, including carcinomas and hematopoietic malignancies, in addition to certain sarcomas including CCS (18). Activating c-Met mutations have been shown in familial and sporadic papillary renal cell carcinoma, melanoma, as well as small-cell and non–small-cell lung cancers (19–24). Mice harboring activating mutations of c-MET spontaneously develop tumors, predominantly sarcomas (25), and Ink4a/Arf-deficient mice expressing HGF develop rhabdomyosarcoma (26).

In this study, we explored the expression and function of c-Met in CCS and find that c-Met expression requires EWS-ATF1 expression. Motility and viability of CCS are dependent on signaling by the HGF/c-Met axis. Inhibition of the HGF/c-Met axis may constitute a novel biologically directed therapy for these highly metastatic and treatment-refractory cancers.

Materials and Methods

**Cell culture.** Human CCS cell lines DTC1 (10), SU-CCS-1 (27), and CCS292 (11) were cultured in RPMI with 15% fetal

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\(^7\) http://www.vai.org/met
bovine serum (FBS), penicillin, and streptomycin. Detection of EWS-ATF1 expression confirmed the CCS identity of these cells. HEK293 and HT1080 cells were cultured in RPMI or α-MEM supplemented with nonessential amino acids, 10% FBS, penicillin, and streptomycin, respectively. pLKO.1 expressing c-Met shRNA (Sigma) was used to prepare vesicular stomatitis virus-G pseudotyped lentivirus by transfection of HEK293 cells with Transit-LT1 (Mirus) as described (28). CCS cells were virally transduced as described (11). ATF1-directed ON-TARGETplus siRNA or control nontargeting pool (Dharmacon) was transfected using RNAiMAX (Invitrogen). Cells were treated with a fully human monoclonal anti-HGF antibody (AMG 102, Amgen). SU11274 (Calbiochem) was dissolved in DMSO and applied to the cells at the concentrations indicated. Control (vehicle)-treated cells were treated with DMSO only. Viability and proliferation were determined by direct cell counting or WST-1 assay (Roche). For invasion assays, 5 × 10^4 cells were plated in serum-free medium in the upper well of an invasion chamber (Matrigel, BD). Normal growth medium or CCS292-conditioned medium was placed in the lower chamber. After 24 to 48 h, membranes were removed, treated with 1% paraformaldehyde followed by 0.1% Triton X-100, and stained with rhodamine-conjugated phalloidin or 4',6-diamidino-2-phenylindole (DAPI). Membranes were imaged on a Zeiss Axiovert 200 and photographed with a Zeiss AxioCam using OpenLab Imaging software.

**Immunoblotting.** c-Met expression (C-12, Santa Cruz Biotechnology) and phosphorylation (3126, Cell Signaling Technology), mitogen-activated protein kinase (MAPK) pathway activity (7180 or 5302, Cell Signaling Technology), and ATF1 expression (25C10G, Santa Cruz Biotechnology) were monitored by immunoblots as described (12). HGF secretion was assessed by ELISA (R&D Systems).

**Xenograft studies.** CCS292 cells (1 × 10^6) were injected s.c. into the flanks of forty 4- to 6-wk-old male NCR nude mice (Charles River). Mice were housed in sterilized cages on a 12-h light/12-h dark cycle and fed *ad libitum*. Groups of 10 mice were treated with 1 mg of AMG 102 or isotype-matched control antibody (human IgG2) injected i.p. in 100 μL of PBS twice per week. Tumor volumes were measured twice per week with digital calipers. Statistical differences were assayed by repeated measures ANOVA followed by Scheffe post hoc test. Studies were done under Dana-Farber Cancer Institute Animal Care and Use Committee protocol 02-030.

**Results**

To evaluate if c-Met signaling may play a role in CCS, we analyzed available RNA microarray data derived from primary human CCS (*n* = 4), a CCS-derived cell line (*n* = 1), and other soft tissue sarcomas (*n* = 47; ref. 18). As a group, mean expression of both c-Met and HGF was significantly higher in CCS as compared with other soft tissue sarcomas (Fig. 1A; *P* < 0.0001 and *P* < 0.0225, respectively), although higher HGF expression is particularly notable in certain CCS samples. Immunohistochemical evidence of c-Met expression in primary human CCS has been previously reported (29, 30).

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**Figure 2.** CCS cells express biologically active HGF. A, secretion of HGF was quantified by ELISA of conditioned media derived from CCS cell lines CCS292, DTC1, and SU-CCS-1 cultured for 18 h, as well as fresh full-serum growth medium (*Medium*). B, CCS292 and DTC1 cells (5 × 10^4) were placed in the upper well of a Matrigel-coated invasion chamber in serum-free medium with either full-serum growth medium (−) or CCS-conditioned medium (+) in the lower well. After 2 d, cells were fixed, stained with DAPI. Membranes were imaged on a Zeiss Axiovert 200 and photographed with a Zeiss AxioCam using OpenLab Imaging software.
We examined CCS-derived cell lines and found that c-Met was expressed and phosphorylated on tyrosine residues in the kinase domain (1234/1235) in two of the three lines during normal growth (data not shown). To test for direct regulation of c-Met by MITF in CCS cells, we knocked down MITF expression using lentivirally delivered shRNA and direct siRNA transfection. Despite decreased MITF expression, c-Met levels were unchanged (data not shown). We then examined the effect of EWS-ATF1 knockdown using a series of ATF1 siRNAs (Fig. 1B). siRNAs that recognize the region of ATF1 preserved in the EWS-ATF1 fusion nearly completely eliminated c-Met expression in CCS292 cells, whereas those that target exclusively wild-type ATF1 had no effect on c-Met levels (Fig. 1C). All siRNAs greatly decreased ATF1 expression (Supplementary Fig. S1A).

To test the importance of c-Met signaling in CCS, we examined cell viability after inhibiting c-Met expression. Lentivirally expressed c-Met–directed shRNA was transduced into CCS cells (Supplementary Fig. S1B). c-Met–directed shRNA greatly decreased DTC1 or CCS292 viability but had no effect on the viability of control HEK293 cells (Fig. 1D).

We then explored potential mechanisms for c-Met activation. Because activating c-Met mutations have been identified in several cancers, we fully sequenced c-Met exons encoding the juxtamembrane domain through the tyrosine kinase domain. No activating mutations were detected in any of the three CCS cell lines tested. We next tested whether c-Met activation could be mediated through an autocrine mechanism. HGF expression was analyzed by ELISA of conditioned media derived from CCS292 and DTC1, but not SU-CCS-1, cells secreting HGF into the media (Fig. 2A).

HGF is expressed as a single-chain propeptide that requires proteolytic cleavage to generate an active α/β heterodimer (31–33). To test whether HGF produced by the CCS cells is biologically active, we treated HGF-responsive melanoma cells (501mel) with conditioned media from CCS cells as well as recombinant HGF. Culture medium derived from CCS292 robustly activated c-Met in 501mel melanoma cells (Supplementary Fig. S1B and Fig. 3A). Weaker c-MET phosphorylation was noted in 501mel cells after exposure to DTC1 medium (as compared with CCS292) and likely reflects the lower levels of HGF produced by DTC1 (Supplementary Fig. S1B).

Because c-MET has been implicated in cellular motility and metastasis, we examined CCS cells for their ability to invade and if c-Met may mediate this process. CCS cells (CCS292 and DTC1) cultured in Matrigel invasion wells showed a small degree of invasion in the presence of fresh serum-containing growth medium (Fig. 2B). However, invasion and migration was greatly enhanced when CCS292 conditioned medium (which contains HGF) was placed below the membrane (Fig. 2B). Inhibition of c-MET expression significantly reduced chemotaxis (Fig. 2C and D).

The simultaneous expression of c-Met and HGF by CCS292 cells and the basal level of phospho-c-Met suggest that c-Met may be activated through an autocrine pathway. The recent identification of a fully human monoclonal anti-HGF antibody (AMG 102; ref. 34) offered an opportunity to study the effect of HGF inhibition on CCS. To show the activity of AMG 102 on CCS-derived HGF, 501mel cells were treated with CCS conditioned medium that had been pretreated with AMG 102. At all concentrations tested, AMG 102 completely blocked c-Met activation (Fig. 3A). This result confirms that c-Met activation in this melanoma cell line is mediated exclusively by HGF and not by another secreted factor in the conditioned medium.

We then tested the effect of HGF inhibition on CCS by treating CCS292 cells with increasing concentrations of AMG 102. In contrast to an isotype-matched control antibody (IgG2), AMG 102 resulted in a marked, albeit incomplete, decrease in activated c-Met (Fig. 3B). Decreased phospho-c-Met was accompanied by an increase in total c-Met, possibly reflecting a diminished rate of receptor turnover in the absence of continuous, autocrine ligand stimulation. We also examined whether AMG 102–mediated c-Met inhibition affected intracellular signaling in CCS292 cells. Both AKT and MAPK signaling were inhibited by AMG 102 treatment in a dose-dependent fashion (Fig. 3B).
Small-molecule inhibitors of c-Met provide an alternative strategy to modulate c-Met. SU11274 is an inhibitor of c-Met (35–37) with activity in both ligand-dependent and ligand-independent models. Treatment with SU11274 at concentrations reported to inhibit c-Met resulted in a dose-dependent decrease in phospho-c-Met (Fig. 4A). The inhibition of phospho-c-Met was associated with decreased downstream MAPK and AKT phosphorylation (Fig. 4A). We then examined cell proliferation and survival after SU11274 treatment. SU11274 at 1 μmol/L transiently decreased cell proliferation (Fig. 4B). However, treatment with 10 μmol/L SU11274 resulted in a sustained decrease in cell proliferation and decreased cell viability. The data using either an HGF inhibitor (AMG 102) or a c-Met kinase inhibitor (SU11274) suggest that c-Met plays a vital role in a subset of CCS and that its activity plays a dominant role in the stimulation of two pathways (phosphoinositide 3-kinase–MAPK and AKT) central to cell proliferation and survival.

Because HGF-stimulated c-Met activation seems to be a central activator of both survival and proliferation pathways in CCS, we examined the effect of HGF inhibition on tumor cell proliferation in culture and in vivo. We cultured CCS cell lines in the presence of the selective HGF inhibitor AMG 102. A significant decrease in proliferation was noted in two CCS lines (Fig. 5A and B). CCS292 cells, which express the most HGF, showed the most significant difference with weaker antiproliferative effects in DTC1. The difference in effect on proliferation correlates with HGF expression (Fig. 2A). For CCS292, the most appreciable inhibition occurred during the first few days of treatment with AMG 102. We then examined the effect of HGF/c-Met inhibition on the progression of CCS tumors in mice. Immunocompromised mice were implanted with CCS292 cells. The effect of AMG 102 treatment was tested using both established tumors and a minimal disease setting. In the minimal disease setting, treatment with AMG 102 was initiated immediately following tumor cell implantation, whereas in the established tumor model, tumors were allowed to develop to a size of ~250 mm³ before initiating AMG 102 treatment. Mice were treated twice per week by i.p. injection of AMG 102 or isotype-matched control antibody, and tumor size was measured. Treatment with AMG 102 resulted in significantly decreased growth in both tumor models. In the established tumor model, as a group, tumors in AMG 102–treated mice were 32% smaller (P < 0.005), whereas in the minimal disease setting, much more striking tumor growth suppression was observed (Fig. 5C and D).

**Discussion**

The search for biologically directed therapies for cancer depends on the identification of critical cellular targets in specific tumor types and/or patients. The receptor tyrosine kinase c-Met has been implicated in a growing number of diverse cancers and was shown to be a transcriptional target of the MITF transcription factor in melanocytes (12). We found that a subset of CCS highly expresses the receptor tyrosine kinase c-Met, and some of these coexpress its ligand HGF. We showed that survival/proliferation as well as invasion and chemotaxis are dependent on c-Met signaling in cellular models of CCS. We found that EWS-ATF1, the product of the pathognomonic translocation associated with CCS, is required for c-Met expression. However, because MITF is also a transcriptional target of EWS-ATF1, we cannot exclude the possibility that in conjunction with other putative pathways activated by EWS-ATF1, aberrant MITF expression contributes to c-Met expression. c-Met is activated by autocrine expression of HGF in some of these tumor cell lines. Significant expression of HGF has also been shown in primary CCS tumors, although it is unclear whether HGF was expressed by tumor or stromal cells. The HGF/c-Met axis seems to be a principal activator of intracellular signaling through both the MAPK and the AKT pathways. Given the unique importance of c-Met as a potential therapeutic target, we showed that CCS is a malignancy with susceptibility to c-Met or HGF inhibition. In the autocrine setting, represented by CCS292, blocking c-Met or HGF function decreased intracellular signaling, suggesting that c-Met is the primary regulator of...
MAPK signaling, even in cells grown in full serum. In vivo, HGF inhibition significantly decreased tumor development and growth in both established and minimal disease settings of CCS.

We examined the tumors that developed despite anti-HGF antibody treatment and found that c-Met was strongly activated in these tumors (data not shown). This result, taken together with the xenograft minimal disease finding, suggests that the antibody most potently inhibits the survival/proliferation of isolated tumor cells or very small tumors. Once the tumor becomes established, the antibody may be no longer capable of inhibiting autocrine signaling. It is possible that the local availability of antibody is insufficient to block the HGF produced by a growing tumor or that the microenvironment of a larger tumor fosters HGF signaling. However, the minimal disease model may mimic the scenario faced by clinicians with a high-risk tumor. After resection of a large primary tumor in the absence of gross metastatic disease, microscopic disease often leads to local or distant recurrences, and thus such HGF suppression may exhibit efficacy in the adjuvant setting. Targeting MITF-activated c-Met in melanoma could serve a similar therapeutic role (23).

Although it remains to be determined exactly what fraction of CCS tumors exhibit c-Met activation (by either autocrine or paracrine mechanisms), knockdown data suggest that the importance of c-Met to CCS may sometimes be independent of HGF production (i.e., ligand-independent receptor activation; ref. 38). In addition, other strategies could result in c-Met activation. For example, in vivo, activation could be mediated through paracrine mechanisms as seen in other tumor types (39). Our study suggests the potential for therapeutically targeting HGF/c-Met in CCS. Pathologic interrogation of c-Met expression and phosphorylation status in human tumors should permit selection of patients most likely to respond to HGF/c-Met–directed therapy.

Disclosure of Potential Conflicts of Interest


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References

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