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Accessibility
MenaINV mediates synergistic cross-talk between signaling pathways driving chemotaxis and haptotaxis

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INTRODUCTION

Directed cell migration, a key process in metastasis, arises from the combined influence of multiple processes, including chemotaxis—the directional movement of cells to soluble cues—and haptotaxis—the migration of cells on gradients of substrate-bound factors. However, it is unclear how chemotactic and haptotactic pathways integrate with each other to drive overall cell behavior. MenaINV has been implicated in metastasis by driving chemotaxis via dysregulation of phosphatase PTP1B and more recently in haptotaxis via interaction with integrin α5β1. Here we find that MenaINV-driven haptotaxis on fibronectin (FN) gradients requires intact signaling between α5β1 integrin and the epidermal growth factor receptor (EGFR), which is influenced by PTP1B. Furthermore, we show that MenaINV-driven haptotaxis and ECM reorganization both require the Rab-coupling protein RCP, which mediates α5β1 and EGFR recycling. Finally, MenaINV promotes synergistic migratory response to combined EGF and FN in vitro and in vivo, leading to hyperinvasive phenotypes. Together our data demonstrate that MenaINV is a shared component of multiple prometastatic pathways that amplifies their combined effects, promoting synergistic cross-talk between RTKs and integrins.

ABSTRACT

Directed cell migration, a key process in metastasis, arises from the combined influence of multiple processes, including chemotaxis—the directional movement of cells to soluble cues—and haptotaxis—the migration of cells on gradients of substrate-bound factors. However, it is unclear how chemotactic and haptotactic pathways integrate with each other to drive overall cell behavior. MenaINV has been implicated in metastasis by driving chemotaxis via dysregulation of phosphatase PTP1B and more recently in haptotaxis via interaction with integrin α5β1. Here we find that MenaINV-driven haptotaxis on fibronectin (FN) gradients requires intact signaling between α5β1 integrin and the epidermal growth factor receptor (EGFR), which is influenced by PTP1B. Furthermore, we show that MenaINV-driven haptotaxis and ECM reorganization both require the Rab-coupling protein RCP, which mediates α5β1 and EGFR recycling. Finally, MenaINV promotes synergistic migratory response to combined EGF and FN in vitro and in vivo, leading to hyperinvasive phenotypes. Together our data demonstrate that MenaINV is a shared component of multiple prometastatic pathways that amplifies their combined effects, promoting synergistic cross-talk between RTKs and integrins.

Keywords: Mena, ECM, Haptotaxis, Chemotaxis, PTP1B, RCP

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Abbreviations used: ECM, extracellular matrix; EGF, epidermal growth factor; EGFR, epidermal growth factor receptor; FN, fibronectin; GF, growth factor; HGF, hepatocyte growth factor; IGF, insulin growth factor; PTP1B, inhibition of PTP1B; RCP, Rab-coupling protein; RTK, receptor tyrosine kinase; TCGA, The Cancer Genome Atlas.

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(Chan et al., 2014; Oudin et al., 2016b). The plethora of directional cues within the tumor microenvironment raises the question of how cells integrate their migration responses to these signals to metastasize efficiently.

Cells generally encounter multiple soluble and substrate-bound cues simultaneously in vivo. It is well established that the ECM binds growth factors (GFs), forming a GF reservoir that contributes to the generation of stable GF gradients (Hynes, 2009). Furthermore, ECM proteins themselves can activate receptor tyrosine kinases (RTKs), which occurs either via binding of intrinsic ECM domains such as EGF-like repeats to EGF receptor (EGFR) directly or via RTK transactivation by integrins (Kuwada and Li, 2000; Balanis and Carlin, 2012). Finally, integrins and RTKs have been shown to signal together in the context of tumor cell invasion. The mutant version of the tumor suppressor p53, which is mutated in 50% of cancers, drives invasion through enhanced Rab coupling protein (RCP)–dependent recycling of α5β1, the main receptor for FN, and several RTKs, EGFR, and Met (Caswell et al., 2008; Muller et al., 2013). Although the potential for cross-talk between ECM and GF cues has been demonstrated, its role in haptotaxis and the relationship between chemotaxis and haptotaxis remains poorly understood.

The actin-regulatory protein Mena, a member of the Ena/VASP family of proteins, regulates cell migration and has been implicated in both chemotaxis and haptotaxis (Bear and Gertler, 2009; Gertler and Condeelis, 2011). Mena is up-regulated in breast cancer, and deletion of Mena in the PyMT-MMTV genetic model of breast cancer reduces metastasis (Roussos et al., 2010). During tumor progression, Mena is alternatively spliced to produce multiple functionally distinct isoforms. MenaINV, which contains a 19–amino acid inclusion, is heterogeneously expressed in breast tumors and is associated with increased metastasis and poor clinical outcome, especially compared with expression of Mena alone (Oudin et al., 2016a,b). Mechanistically, MenaINV increases sensitivity to various GFs present within the tumor microenvironment, including EGF, hepatocyte growth factor (HGF), and insulin growth factor (IGF), by dysregulating the recruitment of the tyrosine phosphatase PTP1B to cognate receptors after ligand stimulation. Consequently, expression of MenaINV causes increased receptor phosphorylation and corresponding cell invasion in response to low levels of ligand stimulation (Hughes et al., 2015). In contrast, MenaINV, and especially MenaINV, drive metastasis through their ability to support haptotaxis on FN gradients via direct α5 integrin interaction (Gupton et al., 2012; Oudin et al., 2016b). In particular, MenaINV allows cells to haptotax at high FN concentrations similar to those present around blood vessels and in the tumor periphery via increased outside-in signaling at focal complexes (Fxs) and inside-out ECM remodeling (Oudin et al., 2016b). Given its role in regulating responses to GFs and FN, we hypothesized that MenaINV could promote α5β1-EGFR cross-talk via receptor transactivation, recycling, or synergy. Here we demonstrate that MenaINV is a shared component of the machinery that mediates both haptotactic responses to FN and chemotactic responses to EGFR.

**RESULTS**

**Mena- and MenaINV-driven haptotaxis requires EGFR signaling**

Given the established role of MenaINV in driving GF sensitization (Hughes et al., 2015) and promoting haptotaxis on FN gradients (Oudin et al., 2016b) and the emerging role of RTKs in response to ECM cues (Zhu and Clark, 2014), we asked whether MenaINV-driven haptotaxis on FN gradients requires EGFR signaling. Cultured breast tumor cells express low levels of Mena and undetectable levels of MenaINV relative to the amounts found in invasive cells collected from these tumors (Goswami et al., 2009; Oudin et al., 2016a). We generated cell lines from the p53-mutant, triple-negative breast cancer cell line MDA-MB-231, which stably express Mena or MenaINV at levels similar to the amount of Mena found in invasive tumor cells (Wang et al., 2007; ~10-fold overexpression with respect to endogenous Mena; cells referred to as 231-Control, 231-Mena, or 231-MenaINV). Previously we used a microfluidic device (Wu et al., 2012) to study cells migrating on FN gradients by time-lapse imaging, quantify the forward migration index (FMI), and assess their directional movement relative to the FN gradient (details in Supplemental Figure S1A). Given our recent findings that MenaINV enhances chemotactic response to EGF by dysregulating EGFR signaling, we wondered whether the EGFR signaling pathway might be involved in haptotaxis. Consistent with this possibility, erlotinib, an EGFR-specific kinase inhibitor, blocked Mena-driven haptotaxis on low FN gradients (125 μg/ml FN at the top of the gradient; Figure 1, A and B), whereas 231-MenaINV cells required a 10-fold higher concentration of erlotinib than 231-Mena cells to block haptotaxis completely (Figure 1A). Of interest, the effects on haptotaxis were distinct from those on cell velocity: 0.1 μM erlotinib blocked Mena-driven haptotaxis without affecting velocity, whereas higher erlotinib concentrations affected both haptotaxis and cell velocity (Figure 1B). We confirmed these findings using a second EGFR kinase inhibitor, gefitinib (Supplemental Figure S1B). To confirm the specificity of the inhibitors, we used small interfering RNA (siRNA) to transiently knock down EGFR in the cell lines (Supplemental Figure S1C). Knockdown of EGFR inhibited Mena- and MenaINV-driven haptotaxis while significantly decreasing cell velocity (Supplemental Figure S1, D and E). We previously found evidence that MenaINV expression enables haptotaxis at high FN concentrations (500 μg/ml FN at the top of the gradient; Oudin et al., 2016b). Here we found that erlotinib also inhibited MenaINV haptotaxis at high FN concentrations (Figure 1C). The overall velocity of all cells was reduced on high FN gradients, but again the effects on velocity versus directionality were distinct: 0.1 μM erlotinib blocked MenaINV-driven haptotaxis without affecting velocity (Figure 1D). We then investigated whether the haptotaxis-promoting EGFR activity on FN gradients required ligand-mediated receptor activation. Addition of mab225, which blocks EGF-dependent activation of EGFR but not its intrinsic kinase activity (Meyer et al., 2013), had no effect on haptotaxis or velocity (Figure 1, E and F), suggesting that the requirement for EGFR kinase activity revealed by sensitivity to erlotinib was not dependent on activation of EGFR by ligand. Together these data suggest that MenaINV-driven haptotaxis on low and high FN gradients requires EGFR signaling but not ligand-elicted EGFR activity.

**MenaINV-driven haptokinesis requires EGFR signaling**

Having shown that EGFR signaling is required for MenaINV-driven two-dimensional (2D) haptotaxis on FN gradients, we investigated whether this pathway was also important in haptokinesis—random migration induced by ECM cues. It is well known that FN can induce migration of cells; however, it does so in a biphasic manner, with highest levels of migration at intermediate concentrations (DiMilla et al., 1993). To investigate whether MenaINV plays a role in FN haptokinesis, we examined cellular invasion in three-dimensional (3D) collagen gels containing uniform FN at different concentrations (Supplemental Figure S2A). We found that 231-Control and 231-Mena cells exhibited a biphasic response to FN concentration, with maximum invasion elicited by 50 μg/ml FN and migration returning to baseline at 125 μg/ml (Supplemental Figure S2, B and C). In contrast, 231-MenaINV cells still invaded at maximal levels at the higher concentrations.
231-Mena\textsuperscript{NV} ΔLERER cells did not display increased invasion in response to any of the FN concentrations tested (Supplemental Figure S2D). The apparent lack of invasion in the 50 μg/ml condition by 231-Mena\textsuperscript{NV} ΔLERER cells suggests that this construct may have dominant-negative effects that block the modest proinvasive activity, for example, by sequestering ligands bound to its other domains in the absence of the ability to interact with α5. Inhibition of α5β1 with blocking antibody P1D6 inhibited FN-driven invasion of 231-Mena\textsuperscript{NV} cells (Supplemental Figure S2E). In contrast, Cilengitide-mediated inhibition of αvβ3, another major FN receptor, had no effect (Supplemental Figure S2E). We then asked whether EGFR signaling was involved in Mena\textsuperscript{NV}-driven invasion into FN and found that erlotinib inhibited invasion of 231-Mena\textsuperscript{NV} cells at all FN concentrations (Figure 2B). Together these data suggest that Mena\textsuperscript{NV}-driven FN haptokinesis requires both α5β1 function and EGFR kinase activity.

**Mena\textsuperscript{NV} expression promotes EGFR signaling on FN**

The requirement for EGFR signaling during haptotaxis prompted us to ask whether Mena and Mena\textsuperscript{NV} drove EGFR phosphorylation in cells migrating on FN gradients. In cells haptotaxing on FN gradients, we quantified levels of EGFR phosphorylation at Y1068, but not pY1173, in human breast cancer patients after EGF stimulation (Hughes et al., 2015). First, we confirmed that expression of Mena, Mena\textsuperscript{NV}, and variants with a deletion of the LERER domain did not affect expression of EGFR (Supplemental Figure S3, A–C). Using immunofluorescence, we quantified pEGFR\textsuperscript{Y1173} levels in cells plated on gradients of FN of different concentrations. On a low FN gradient, FN concentration correlated positively and significantly with pEGFR\textsuperscript{Y1173} in 231-Mena\textsuperscript{NV} cells but not in control MDA-MB-231 cells (Figure 3, A–C). This correlation was absent when cells were treated with erlotinib (Supplemental Figure S3, D–F). However, at high FN concentration, only 231-Mena\textsuperscript{NV} cells showed a significant correlation between pEGFR\textsuperscript{Y1173} and FN (Figure 3, D–F). We then investigated whether Mena and Mena\textsuperscript{NV} mRNA expression in human breast cancer patients was associated with phosphorylation of EGFR, using The Cancer Genome Atlas (TCGA) database (Cancer Genome Atlas Network, 2012). There was a significant correlation between levels of Mena\textsuperscript{NV}, but not Mena, and levels of pY1068, but not pY1173, in human breast cancer patients from TCGA with available reverse-phase protein array data (Figure 3G). Of interest, in patients with high tumor FN mRNA levels, there was a weak but statistically significant correlation between Mena\textsuperscript{NV} and pEGFR\textsuperscript{Y1173} (Figure 3H). Together these data suggest that
Because PTP1B is known to influence signaling at focal adhesions (FXs; Burdusso et al., 2013), we hypothesized that the haptotactic effect from PTP1B was associated with altered behavior of the key FX signaling regulator paxillin. We therefore performed immunofluorescence studies on haptotaxing cells plated on a 2D FN gradient for 3 h. We measured the number of pPAX\(^{Y118}\)-positive adhesions in cells expressing different Mena isoforms plated on a 2D FN gradient. 231-Mena\(^{INV}\) cells, which haptotax toward high FN concentrations, had a significantly increased number of pPAX-positive adhesions relative to 231-Control cells (Figure 4, D and E). To test whether the haptotaxis effect of PTP1Bi is due to changes in phosphorylation of proteins in adhesions, we measured the number of pPAX\(^{Y118}\)-positive adhesions in 231-Control treated with PTP1Bi and found an increase with drug treatment (Figure 4, D and E).

Given that PTP1Bi increases EGFR phosphorylation downstream of EGF stimulation (Hughes et al., 2015), we next investigated whether Mena\(^{INV}\) could also promote FX signaling downstream of RTK activation. After EGF stimulation, 231-Mena\(^{INV}\) cells show increased FX-associated pPAX\(^{Y118}\) compared with 231-Mena (Figure 4F). In addition, PTP1Bi significantly increased pPAX\(^{Y118}\) in 231-Mena to similar levels as seen in 231-Mena\(^{INV}\) (Figure 4F). Overall these data suggest that Mena\(^{INV}\) drives PTP1B dysregulation and leads to increased FX signaling downstream of both chemotactic and haptotactic pathways.

Compared to Mena, Mena\(^{INV}\) causes more sustained FX signaling and enables haptotaxis at high FN concentrations (Oudin et al., 2016b). Therefore we asked whether PTP1Bi could drive haptotaxis of MDA-MB-231 and 231-Mena on high FN gradients and found that PTP1Bi had no effect in this context (Figure 4G). This suggests that the increase in FX signaling is not sufficient to support haptotaxis on high FN concentrations. Furthermore, we found that PTP1Bi failed to drive haptotaxis of MDA-MB-231 cells in three dimensions (Figure 4H). Taken together, these data confirm that Mena\(^{INV}\) can regulate FX signaling downstream of multiple cues and suggest that there are additional functional requirements for 3D versus 2D haptotaxis.

Knockdown of p53 and RCP, known to drive cotrafficking and recycling of \(\alpha 5\beta 1\) and EGFR, inhibits Mena\(^{INV}\)-driven haptotaxis and ECM reorganization

Whereas converging on signaling at adhesions is one way in which EGFR/\(\alpha 5\beta 1\) may contribute to motility, another way in which EGFR/\(\alpha 5\beta 1\) cross-talk could contribute to 3D invasion is via their dysregulated cotrafficking (Muller et al., 2011). Recycling of cotrafficked \(\alpha 5\beta 1\)/EGFR complexes is induced by expression of mutant p53 expression, which triggers RCP-mediated association between the two receptors, leading to increased invasion (Muller et al., 2009). Cells with mutant p53, such as the MDA-MB-231 cells used here, show increased levels of \(\alpha 5\beta 1\)/EGFR recycling and preferential targeting of the recycled complex to the pseudopods of invading cells in three dimensions. Of interest, by examining data from the TCGA breast cancer cohort, we found that breast cancer patients with mutant p53 showed significantly higher levels of Mena\(^{INV}\) than those with wild-type p53 (Figure 5A). Therefore we investigated whether dysregulated RCP-dependent recycling of \(\alpha 5\beta 1\)/EGFR might also be involved in 3D haptotaxis by asking whether expression of either mutant p53 or RCP was required for Mena\(^{INV}\)-driven 3D haptotaxis (Muller et al., 2009). First, we confirmed that there was no difference in level of total RCP or p53 expression in cells expressing Mena or
present simultaneously within the tumor microenvironment (Joyce and Pollard, 2009), we wondered how cells would respond to exposure to both cues simultaneously. We first used an in vitro chemoinvasion assay (described in Supplemental Figure S1); in this instance, collagen plus FN gels were overlaid with varying EGF concentrations. We verified the presence of gradients using fluorescent dextran of similar molecular weight to EGF (Supplemental Figure S5). Addition of a low-dose EGF gradient (0.5 nM) in the presence of 25 μg/ml FN/collagen did not affect the invasion of 231-Control or 231-Mena cells; however, these conditions evoked a 3D invasion response by 231-Mena\textsuperscript{INV} cells that was significantly greater than that observed for addition of either 0.5 nM or 25 μg/ml FN individually (\(p = 0.039\), two-way analysis of variance [ANOVA] interaction term; Figure 6A). These data suggest that Mena\textsuperscript{INV} promotes synergy between FN and EGF. We then investigated the role of the Mena–\(\alpha_{5}\beta_{1}\) interaction in this synergistic response. Of interest, deletion of the LERER region in Mena or Mena\textsuperscript{INV} did not affect protrusion of lamellipodia in response to low-dose EGF stimulation of cells.

**Mena\textsuperscript{INV} promotes synergy between EGF and FN**

Our data suggest that Mena\textsuperscript{INV} promotes directional migration downstream of \(\alpha_{5}\beta_{1}\) and RTKs. However, given that both cues are present simultaneously within the tumor microenvironment (Joyce and Pollard, 2009), we wondered how cells would respond to exposure to both cues simultaneously. We first used an in vitro chemoinvasion assay (described in Supplemental Figure S1); in this instance, collagen plus FN gels were overlaid with varying EGF concentrations. We verified the presence of gradients using fluorescent dextran of similar molecular weight to EGF (Supplemental Figure S5). Addition of a low-dose EGF gradient (0.5 nM) in the presence of 25 μg/ml FN/collagen did not affect the invasion of 231-Control or 231-Mena cells; however, these conditions evoked a 3D invasion response by 231-Mena\textsuperscript{INV} cells that was significantly greater than that observed for addition of either 0.5 nM or 25 μg/ml FN individually (\(p = 0.039\), two-way analysis of variance [ANOVA] interaction term; Figure 6A). These data suggest that Mena\textsuperscript{INV} promotes synergy between FN and EGF. We then investigated the role of the Mena–\(\alpha_{5}\) interaction in this synergistic response. Of interest, deletion of the LERER region in Mena or Mena\textsuperscript{INV} did not affect protrusion of lamellipodia in response to low-dose EGF stimulation of cells.
FIGURE 4: Inhibition of PTP1B phenocopies MenaINV. (A) FMI of MDA-MB-231, 231-Mena, and 231-MenaINV cells treated with PT1Bi (10 μM) on a low 125 μg/ml FN gradient. (B) FMI of MDA-MB-231 cells with sgRNA targeted against a control sequence or Mena treated with PT1Bi (10 μM) on a low 125 μg/ml FN gradient. (C) FMI of 231-Mena ΔLERER and 231-MenaINV ΔLERER cells treated with PT1Bi (10 μM) on a low 125 μg/ml FN gradient. (D) Representative images of 231-Control cells showing GFP (green), F-actin (blue), and pPAX118 (red) for cells plated on a low 125 μg/ml FN gradient and treated with PT1Bi (10 μM). Scale bar, 5 μm (main image), 1 μm (inset). (E) Number of pPaxY118-positive adhesions in 231-Control and 231-MenaINV cells plated on a 2D FN gradient with DMSO or PT1Bi treatment. (F) Levels of pPaxY118 in Mena-positive adhesions in 231-Mena and 231-MenaINV cells plated on collagen and Matrigel and treated with 0.25 nM EGF for 1 min. (G) FMI of MDA-MB-231, 231-Mena, and 231-MenaINV cells treated with PT1Bi (10 μM) on a high 500 μg/ml FN gradient. (H) FMI of MDA-MB-231, 231-Mena, and 231-MenaINV cells treated with PT1Bi (10 μM) in a 3D 125 μg/ml FN gradient. Haptotaxis data are pooled from at least three experiments, with at least 75 cells analyzed overall. Results show mean ± SEM; significance determined by one-way ANOVA, *p < 0.05, **p < 0.01, ***p < 0.005. See Supplemental Figure S4.
Second, we find that Mena\textsuperscript{INV} promotes synergistic responses to combined EGF and FN gradients. Of interest, phospho–mass spectrometry analysis in 231-Mena\textsuperscript{INV} cells treated with EGF revealed increased phosphorylation of multiple proteins known to be present at FXs and playing a role in responses to ECM cues, such as vinculin, paxillin, P130Cas, and FAK (focal adhesion kinase) (Hughes et al., 2015). Inhibition of PTP1B enables haptotaxis and increases FX signaling downstream of both EGF and FN. It is well established that signaling downstream of RTKs and integrins can converge on common signaling pathways, such as the Ras–mitogen-activated protein kinase pathway, the phosphoinositide 3-kinase/Akt pathway, or Rho GTPases, particularly at focal adhesions (Huttenlocher and Horwitz, 2011). However, how these pathways are coordinated to drive directional migration in response to multiple cues is poorly understood. Recent studies identified several important components of haptotactic responses that are actually not required for GF chemotaxis, including LKB1 signaling via kinases of the microtubule affinity-regulating kinase family (Chan et al., 2014). Of interest, two key cytoskeletal molecules—the Arp2/3 complex, which nucleates branched F-actin, and fascin, which supports filopodia formation through its F-actin bundling activity—are also similarly required for haptotaxis on FN gradients (Wu et al., 2012; Johnson et al., 2015) but not for chemotaxis to growth factors. Therefore, whereas some signaling pathway components are exclusively required downstream of a single directional cue, others, like Mena\textsuperscript{INV}, may play roles in multiple modes of migration.

Finally, one other well-described mechanism by which RTK/integrin cross-talk can promote invasion is through cotrafficking (Paul et al., 2015). Mutant p53 has been shown to drive p53-dependent recycling of a5β1 with EGFR and Met, a process that contributes to 3D invasion (Muller et al., 2013). We previously reported that 231-Mena\textsuperscript{INV} cells show a 30% increase in surface a5 levels (Oudin et al., 2016b) and a small but significant 10% increase in EGF recycling (Hughes et al., 2015). Knockdown of p53 and RCP, which reduces the recycling of a5β1 and EGFR (Muller et al., 2009), also blocked Mena\textsuperscript{INV}-driven 3D haptotaxis and ECM reorganization. Whether or not Mena isoforms directly contribute to receptor cotrafficking is beyond the scope of the present study and will be the topic of future investigation.

Overall our study shed light on how cell migration behavior is coordinated by diverse and often overlapping signaling pathways that are activated during local tumor cell invasion, summarized in Figure 7. We focused on EGF and FN, both of which are present in the tumor microenvironment and can elicit directional tumor cell migration. However, given that there are many other cues present in the tumor microenvironment, it is likely that additional pathways participating in GF/ECM cross-talk downstream of a variety of cues and will contribute to metastasis.

**MATERIALS AND METHODS**

**Antibody reagents, growth factors, and inhibitors**

The growth factor EGF was from Life Technologies (Carlsbad, CA). Antibodies were as follows: EGFR (555996; BD Biosciences, San Jose, CA), paxillin (610052; BD Biosciences), pPaxillin Y118 (44-722G; Life Technologies), and pEGFR1173 (Abcam, Cambridge, MA). Drugs were erlotinib (LC Labs, Woburn, MA), gefitinib (Peprotech, Rocky Hill, NJ), Cilengitide (Selleck Chemicals, Houston, TX), and PTP1B (Millipore, Burlington, MA).

**Cell culture**

MDA-MB-231 cells were obtained from the American Type Culture Collection (Manassas, VA) and cultured in DMEM with 10% serum.
We coated 96-well plates with 3% bovine serum albumin (BSA; Sigma, St. Louis, MO) at 37°C for 3 h. MDA-MB-231 cells expressing different Mena isoforms were lysed in 25 mM Tris, 150 mM NaCl, 10% glycerol, 1% NP-40, and 0.5 M EDTA with protease Mini-Complete protease inhibitors (Roche, Indianapolis, IN) and a phosphatase inhibitor cocktail (PhosSTOP; Roche) at 4°C. Protein lysates were separated by SDS–PAGE, transferred to a nitrocellulose membrane, blocked with Odyssey Blocking Buffer (Li-Cor, Lincoln, NE), and incubated in primary antibody overnight at 4°C. Proteins were detected using Li-Cor secondary antibodies. Protein level intensity was measured with ImageJ, and data were pooled from at least three different experiments.

Western blot

Standard procedures were used for protein electrophoresis, Western blotting, and immunoprecipitation. MDA-MB-231 cells expressing different Mena isoforms were lysed in 25 mM Tris, 150 mM NaCl, 10% glycerol, 1% NP-40, and 0.5 M EDTA with protease Mini-Complete protease inhibitors (Roche, Indianapolis, IN) and a phosphatase inhibitor cocktail (PhosSTOP; Roche) at 4°C. Protein lysates were separated by SDS–PAGE, transferred to a nitrocellulose membrane, blocked with Odyssey Blocking Buffer (Li-Cor, Lincoln, NE), and incubated in primary antibody overnight at 4°C. Proteins were detected using Li-Cor secondary antibodies. Protein level intensity was measured with ImageJ, and data were pooled from at least three different experiments.

FACS

MDA-MB-231 cells expressing the different isoforms were trypsinized, resuspended in medium, and then incubated with a primary antibody in phosphate-buffered saline (PBS) and 5% medium for 30 min on ice. Next the cells were incubated with a species-appropriate, Alexa 647–tagged secondary antibody and then resuspended in PBS with 10 μg/ml propidium iodide. Samples were then analyzed on a FACSCalibur machine (BD Biosciences) as previously described (Gupton et al., 2012). Cell lines engineered to stably express Mena isoforms expressed 10- to 15-fold more protein than wild-type cell line (Oudin et al., 2016b). Knockdown of p53, RCP, and EGFR was performed using previously published siRNA sequences (obtained from Dharmacon, GE Lifesciences, Lafayette, CO; Muller et al., 2009) and transient transfection with Dharmafect4.

and penicillin-streptomycin-glutamine. Retroviral packaging, infection, and fluorescence-activated cell sorting (FACS) were performed as previously described (Gupton et al., 2012). Cell lines engineered to stably express Mena isoforms expressed 10- to 15-fold more protein than wild-type cell line (Oudin et al., 2016b). Knockdown of p53, RCP, and EGFR was performed using previously published siRNA sequences (obtained from Dharmacon, GE Lifesciences, Lafayette, CO; Muller et al., 2009) and transient transfection with Dharmafect4.

Three-dimensional in vitro chemotaxis assay

We coated 96-well plates with 3% bovine serum albumin (BSA; Sigma, St. Louis, MO) at 37°C for 3 h. MDA-MB-231 cells expressing different Mena isoforms were lysed in 25 mM Tris, 150 mM NaCl, 10% glycerol, 1% NP-40, and 0.5 M EDTA with protease Mini-Complete protease inhibitors (Roche, Indianapolis, IN) and a phosphatase inhibitor cocktail (PhosSTOP; Roche) at 4°C. Protein lysates were separated by SDS–PAGE, transferred to a nitrocellulose membrane, blocked with Odyssey Blocking Buffer (Li-Cor, Lincoln, NE), and incubated in primary antibody overnight at 4°C. Proteins were detected using Li-Cor secondary antibodies. Protein level intensity was measured with ImageJ, and data were pooled from at least three different experiments.

Protrusion assay

Collagen-coated glass-bottomed dishes (MatTek, Ashland, MA) were coated with 0.2% Matrigel in serum-free medium for 30 min at 37°C. Cells were seeded sparsely overnight and then serum starved for 4 h in Leibowitz’s L-15 medium (Life Technologies) with 0.35% BSA. Differential interference contrast images were acquired every 20 s for 10 min in an environmentally controlled microscope (TE2000; Nikon) with a 20x objective and a Photometrics CoolSNAP HQ camera. Growth factor/inhibitor solutions were added after 80 s. Cell areas were traced immediately before and 9 min after stimulation using ImageJ (National Institutes of Health, Bethesda, MD). Data shown are from individual cells (at least 60 overall) pooled from at least three separate experiments.

Western blot

Standard procedures were used for protein electrophoresis, Western blotting, and immunoprecipitation. MDA-MB-231 cells expressing different Mena isoforms were lysed in 25 mM Tris, 150 mM NaCl, 10% glycerol, 1% NP-40, and 0.5 M EDTA with protease Mini-Complete protease inhibitors (Roche, Indianapolis, IN) and a phosphatase inhibitor cocktail (PhosSTOP; Roche) at 4°C. Protein lysates were separated by SDS–PAGE, transferred to a nitrocellulose membrane, blocked with Odyssey Blocking Buffer (Li-Cor, Lincoln, NE), and incubated in primary antibody overnight at 4°C. Proteins were detected using Li-Cor secondary antibodies. Protein level intensity was measured with ImageJ, and data were pooled from at least three different experiments.
The dimethyl sulfoxide (DMSO) control data for the MDA-MB-231 haptotaxis on FN gradients were in the range 0.1–0.25. Note that by the total distance migrated; typical values for MDA-MB-231 are 0.3–0.5 μm. Cells were then fixed for 20 min in 4% paraformaldehyde in PBS buffer (60 mM piperazine-N,N′-bis(ethanesulfonic acid), pH 7.0, 2.5 mM 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid, pH 7.0, 10 mM ethylene glycol tetraacetic acid, pH 8.0, 2 mM MgCl₂, and 0.12 M sucrose) and then permeabilized with 0.2% Triton X-100, blocked with 10% BSA, and incubated with primary antibodies overnight at 37°C. Z-series of images were taken on an Applied Precision DeltaVision microscope using Softworx acquisition, an Olympus 40×/1.3 NA Plan Apo objective, and a Photometrics CoolSNAP HQ camera. Images were deconvolved using DeltaVision Softworx software and objective-specific point spread function. Images were analyzed with ImageJ. Images are pooled from at least three independent experiments, with at least 10 cells per experiment.

**TCGA data analysis**

Data retrieval from TCGA was explained in Oudin et al. (2016b).

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Immunofluorescence cells are the same for Figures 1C and 4G, given that both erlotinib and PTP1B are in DMSO and experiments were carried out at once.

**Tumor formation and in vivo invasion assay**

MDA-MB-231 cells (2 million per mouse in PBS and 20% collagen) expressing different Mena isoforms were injected into the fourth right mammary fat pad of 6-wk-old female NOD-SCID mice (Taconic, Hudson, NY). The in vivo invasion assay was performed in four mice per condition as previously described, once tumors had reached 1 cm in diameter, at ~8 wk after injection (Wyckoff, 2004). Briefly, needles were held in place by a micromanipulator around a single mammary tumor of an anesthetized mouse. Needles contained a mixture of 0.5 mg/ml collagen I, EDTA with L-15 medium, and 5 mM EGF and/or 50 μg/ml FN. After 4 h of cell collection, the contents of the needles were extruded. Cells were then stained with 4′,6-diamidino-2-phenylindole and counted.

**Haptotaxis assay**

Microfluidic devices were prepared as previously described (Wu et al., 2012). For 2D haptotaxis, after bonding polydimethylsiloxane devices to MatTek dishes, the cell culture chamber was coated with 0.1 mg/ml collagen I for 1 h at 37°C, and then 250 μg/ml fluorescently labeled FN was flowed through the source channel for 1 h. Cells were then plated in the device in full serum medium and left to attach for 1 h before imaging. For 3D haptotaxis, cells were resuspended in 1 mg/ml collagen I (BD Biosciences) with 10× DMEM, 1 N NaOH, and 3 nM EGF, plated in the cell culture chamber, and left to settle for 8 h at 37°C. Fluorescently labeled FN (250 μg/ml unless otherwise specified) was then flowed through the source channel for 1 h before imaging. Cells were imaged overnight in the haptotaxis device, with images acquired every 10 min for 16 h in an environmentally controlled microscope (TE2000, Nikon) with a 20× objective and a Photometrics CoolSNAP HQ camera. Individual cells were manually tracked using the ImageJ Manual Tracking plug-in. The tracks obtained were further analyzed using the chemotaxis tool developed by ibidi in ImageJ. This analysis tool was used to extract the FMI (Supplemental Figure S1A), which is defined as the displacement of the cell in the direction of the gradient divided by the total distance migrated; typical values for MDA-MB-231 haptotaxis on FN gradients were in the range 0.1–0.25. Note that the dimethyl sulfoxide (DMSO) control data for the MDA-MB-231
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