Invasive breast carcinoma cells from patients exhibit Mena<sup>INV</sup>- and macrophage-dependent transendothelial migration

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Metastasis is a complex, multistep process of cancer progression that has few treatment options. A critical event is the invasion of cancer cells into blood vessels (intravasation), through which cancer cells disseminate to distant organs. Breast cancer cells with increased abundance of Mena [an epidermal growth factor (EGF)-responsive cell migration protein] are present with macrophages at sites of intravasation, called TMEM sites (for tumor microenvironment of metastasis), in patient tumor samples. Furthermore, the density of these intravasation sites correlates with metastatic risk in patients. We found that intravasation of breast cancer cells may be prevented by blocking the signaling between cancer cells and macrophages. We obtained invasive breast ductal carcinoma cells of various subtypes by fine-needle aspiration (FNA) biopsies from patients and found that, in an in vitro transendothelial migration assay, cells that migrated through a layer of human endothelial cells were enriched for the transcript encoding Mena<sup>INV</sup>, an invasive isoform of Mena. This enhanced transendothelial migration required macrophages and occurred with all of the breast cancer subtypes. Using mouse macrophages and the human cancer cells from the FNAs, we identified paracrine and autocrine activation of colony-stimulating factor-1 receptor (CSF-1R). The paracrine or autocrine nature of the signal depended on the breast cancer cell subtype. Knocking down MenaINV or adding an antibody that blocks CSF-1R function prevented transendothelial migration. Our findings indicate that Mena<sup>INV</sup> and TMEM frequency are correlated prognostic markers and CSF-1 and Mena<sup>INV</sup> may be therapeutic targets to prevent metastasis of multiple breast cancer subtypes.

INTRODUCTION

Metastasis is a complex multistep process that involves cancer cell dissemination and, ultimately, patient death (1). The outcome of breast cancer patients with metastatic disease has not improved in the past 30 years in spite of the development of targeted therapies (2). Thus, understanding the details of the metastatic process is of paramount importance for the development of new prognostic and therapeutic targets.

Intravital imaging in animal models has revealed many aspects of metastasis (3–6), including the essential roles that macrophages play in the microenvironments in which mammary tumor cells invade, migrate, and intravasate (5, 7). In particular, intravital imaging of rodent mammary tumors shows that breast cancers contain a subpopulation of highly motile cancer cells that move alongside macrophages in streams toward blood vessels in response to paracrine chemotactic signaling (6, 8, 9). Upon reaching a blood vessel, cancer cells intravasate at sites enriched with perivascular macrophages (5).

Expression profiling of the invasive subpopulation of cancer cells obtained from primary tumors revealed changes in the expression of genes associated with motility pathways that control actin polymerization, epidermal growth factor (EGF)-directed cell movement, and invadopodium formation (10, 11). Directed migration of various cells is typically initiated by chemotactic signaling, which induces cytoskeletal rearrangements involving cofilin (12–14). Mena, a member of Ena/VASP family of actin-binding proteins, is a key mediator of cytoskeletal arrangement and functions at the convergence of the cofilin-regulated motility pathways (15, 16). Mena enhances tumor cell migration toward EGF in vivo, and in vitro by interfering with the activity of inhibitory capping proteins and increasing actin filament elongation rates, thereby promoting actin polymerization (6, 15, 17). These activities are essential for sustained directional cell movement in response to growth factors like EGF (18).

In patients, MENA expression is increased in precursor lesions of the cervix and colon, in breast lesions associated with high risk of cancer development, and in high-grade primary and metastatic breast tumors (19). Three Mena protein isoforms arising from alternative splicing are particularly important in human breast cancer: Mena<sup>classic</sup>, Mena<sup>INV</sup>, and Mena11a. Mena<sup>classic</sup> contains only the constitutive exons, whereas the two splice variants Mena<sup>INV</sup> and Mena11a contain alternatively included exons termed “INV” or “11a,” respectively. The INV (also known as “+”+) exon encodes a 19–amino acid residue inserted near the N terminus, whereas the 11a exon encodes a 21–amino acid residue inserted near the C terminus (11, 17, 20). Mena<sup>INV</sup> abundance potentiates chemotactic and invasive responses of carcinoma cells to EGF (6, 16). The observed increase in MENA expression in invasive and disseminating tumor cells reflects increased abundance of both Mena<sup>classic</sup> and Mena<sup>INV</sup>, and correlates with decreased Mena11a abundance relative to that observed in noninvasive, nonintravasating tumor cells within primary mammary tumors (17). Mena forms tetramers via a C-terminal coiled-coil sequence that is conserved in all Ena/VASP proteins, and Mena<sup>classic</sup> and Mena<sup>INV</sup> are thought to form Mena<sup>classic</sup>/Mena<sup>INV</sup> heterotetramers (11, 21).
MENA expression is found in cancer cells located at the micro-anatomical sites of cancer cell intravasation, called TMEM (tumor micro-environment of metastasis) sites (22, 23). These sites, initially observed by intravital imaging of rodent mammary tumors, have also been detected in human invasive ductal carcinomas (IDCs) by triple immunohistochemistry (IHC) (22). A TMEM site is defined as a MENA-expressing tumor cell that is in direct contact with an endothelial cell and a perivascular macrophage. Case-control studies show that the number of TMEM sites is associated with increased risk of developing distant metastases in patients with IDC of the breast (22, 23). IDC sampled by fine-needle aspiration (FNA) biopsies indicates that the relative abundance of MenaINV correlates with TMEM frequency, stability, and/or function in patients (14). Increased MenaINV abundance increases transendothelial migration (TEM) in cultured cells and promotes cell migration, streaming, intravasation, and formation of spontaneous lung metastases in orthotopic xenografts in mice (6). Other studies show that Mena knockout mice bred with PyMT (polyoma virus middle T antigen) transgenic mice develop tumors with reduced intra-vasation and metastasis and have prolonged survival (24). Thus, Menaclassic and/or MenaINV may promote metastasis by inducing TEM activity during intravasation.

Here, we tested the hypothesis that the MenaINV isoform in particular is linked to TMEM score and the associated TEM at these proposed sites of intravasation (14, 25) by measuring the TEM activity of primary tumor cells from patients using new in vitro assays.

RESULTS

MenaINV transcript expression positively correlates with the number of TMEM intravasation sites

Our previous study showed a positive correlation between MenaINV and TMEM scores in a cohort of 40 IDCs of the breast obtained from patients, indicating that relative MenaINV abundance correlates with epithelial disorganization and TMEM score in breast cancer patients (14). Here, we wanted to confirm this correlation in a larger patient cohort. We measured the abundance of transcripts encoding MenaINV and Mena11a by quantitative real-time polymerase chain reaction (qRT-PCR) in FNA samples from IDCs in a cohort of 60 patients and determined TMEM scores in formalin-fixed, paraffin-embedded (FFPE) breast cancer tissue by triple IHC from the same cohort of 60 patients (Fig. 1A). We previously demonstrated that quantification of the Mena isoforms by immunoblotting is not precise enough for correlation analysis with the TMEM score because of the lack of antibodies capable of detecting MenaINV protein present in FNA biopsies (14). Thus, the quantification of Mena isoform expression at the protein level was not performed in this study.

**Fig. 1. Correlation of Mena isoform expression to TMEM score.** (A) TMEM microanatomic cancer cell TEM sites visualized by IHC. TC, Mena-expressing tumor cells; EC, CD31-expressing vascular endothelial cells; M, CD68-expressing macrophages. Scale bars, 300 μm (left) and 50 μm (right). (B and C) Scatter plots of relative MenaINV transcript expression against TMEM score in the entire cohort of 100 IDCs (B) or by clinical subtype (C). Data were analyzed by rank-order correlation. The differences in slopes between subtypes were not statistically significant as shown by the regression model fit to the rank-transformed data. n, number of tumor cases.
Similar to our previous study on samples from 40 patients (14), the new cohort of 60 patients showed a strong positive correlation between Mena\textsuperscript{INV} score and TMEM ($r = 0.62$, $P = 10^{-6}$) and a weak negative correlation between Mena\textsubscript{11a} score and TMEM ($r = -0.17$, $P = 0.19$), as did the combined cohort of 100 patients (14) (Fig. 1B). These data support the previous finding that Mena\textsuperscript{INV} may promote intravasation of human IDCs of the breast, whereas Mena\textsubscript{11a} may suppress intravasation.

**Mena\textsuperscript{INV} and TMEM number correlate with each other regardless of clinical subtype and tumor grade**

Because breast cancer is a heterogeneous disease, we investigated whether the Mena\textsuperscript{INV}-TMEM correlation is similar across the most common clinical subtypes and grades according to hormone receptor and HER2 expression status. We observed a very strong correlation between TMEM and Mena\textsuperscript{INV} scores in the ER\textsuperscript{PR+}/HER2– [estrogen receptor– and progesterone receptor–positive, EGF receptor 2 (also known as ErbB2 or neu)–negative] subtype (Fig. 1C). Triple-negative (TN) cases showed a strong correlation, whereas the Mena\textsuperscript{INV}-TMEM correlation in HER2+ cases was moderate. Using a regression model fit to the rank-transformed data, we observed that the differences in slopes between the tumor types were not statistically significant. Thus, although there were differences in the Spearman correlation coefficient among the clinical subtypes, this difference was not statistically significant and suggests that relative Mena\textsuperscript{INV} transcript expression correlates with intravasation-rich microenvironments in the most common clinical subtypes of breast cancer. We observed only weak correlation in 14 cases that were ER+/HER2– but lacked PR expression (table S2). This weak correlation may be due to an inadequate statistical power. However, both ER and PR signaling are very complex and involve various paracrine components. There is evidence that signaling through PR is important not only for cell proliferation and branching of breast ducts but also for extracellular matrix remodeling and angiogenesis (26). Thus, it is plausible that a lack of PR signaling affects either TMEM formation or Mena\textsuperscript{INV} transcript expression independently, resulting in observed lack of correlation.

In analyzing whether the Mena\textsuperscript{INV}-TMEM correlation was affected by tumor grade, we found that the correlation was strong in poorly and moderately differentiated tumors, and very strong in well-differentiated tumors (Fig. 2A). The regression model fit to the rank-transformed data again showed that the differences in slopes between tumor grades were not statistically significant; therefore, Mena\textsuperscript{INV}-TMEM correlation was not affected by tumor grade. Poorly differentiated IDCs grew in sheets transversed by blood vessels; moderately differentiated IDC grew in a combination...
of glands and sheets; and well-differentiated IDC typically grew in glands and cords surrounded by stroma containing blood vessels (Fig. 2B). Because of the proliferative pattern, cancer cells in well-differentiated IDC were rarely found in direct contact with perivascular macrophages, thus explaining the low TMEM score (Fig. 2A). These “TMEM-low” microenvironments in well-differentiated cases also showed low MenaINV scores, thus strongly correlating.

The data thus far indicate that relative MenaINV transcript abundance in FNA samples positively correlates with the presence of TMEM-rich microenvironments in common clinical subtypes of IDCs and across all breast tumor grades.

MenaINV and TMEM scores independently correlate with clinical and pathological parameters

Because high TMEM score correlates with metastatic outcome, and MenaINV score correlates with TMEM score, we assessed whether MenaINV and TMEM scores in our cohort independently correlate with known clinical and pathological parameters associated with prognosis. We quantified TMEM score and relative MenaINV expression in tumors of different grade, size, lymph node (LN) status, as well as hormone receptor and HER2 status (table S3). We found significant differences in TMEM score and relative MenaINV expression, independently, only between well-differentiated and poorly differentiated tumors (Fig. 2C). This is likely due to the differential cell proliferation pattern among the grades, as discussed above. There was no significant difference in either TMEM score or relative MenaINV expression among tumors of different size, LN status, or hormone receptor and HER2 expression. When we examined LN status within each clinical subtype, we observed a somewhat positive correlation of LN positivity with TMEM score and relative MenaINV expression only in ERPR+/HER2- tumors, but this did not reach statistical significance (fig. S2). These data indicate that TMEM and MenaINV scores measure aspects of tumor biology not addressed by the current clinical and pathological parameters other than tumor grade.

E-cadherin expression in tumors differs among samples according to MenaINV and TMEM scores

Tumor grade reflects mitotic count, nuclear features, and cancer cell growth pattern. Because architectural tumor growth pattern was associated with TMEM formation (Fig. 2B), we investigated whether other aspects of tumor architecture would differ among cases with low and high TMEM and MenaINV scores. Cell cohesion is one aspect of tumor biology that is not measured by current clinical and pathological parameters. The ability of tumor cells to migrate toward blood vessels, assemble TMEMs, and intravasate is believed to require the epithelial-to-mesenchymal transition (EMT) and the disruption of epithelial junctions. We previously found that discohesion of epithelial cell-cell contacts in mouse mammary tumors is associated with MenaINV score, which is associated with increased TMEM score (14). We predicted that this was also true in samples of human breast cancer. We observed significantly more cells with strong staining of cell-cell junction protein E-cadherin in cases with low TMEM and MenaINV scores than in the cases with high TMEM and MenaINV scores (Fig. 3A). Conversely, there were more cells with low E-cadherin abundance in cases with high TMEM and MenaINV scores (Fig. 3B), indicating a correlation between discohesion and the MenaINV/TMEM phenotype, as predicted.

MenaINV isoform expression is associated with TEM-competent breast carcinoma cells

On the basis of the above results and previous work indicating that MenaINV potentiates breast cancer cell intravasation, dissemination, and lung metastases in vivo (4), we hypothesized that MenaINV expression is linked to TEM. Because breast cancers with a high MenaINV/high TMEM score have less E-cadherin abundance and are less cohesive, we anticipated that a population of discohesive, breast carcinoma cells with high MenaINV scores could be obtained from patients by FNA biopsy to test this hypothesis. In addition, our previous study showed that the Mena isoform expression pattern in FNA samples reflects the cohesion or discohesion state of the cells in the tumor. In particular, smearing patterns of cells obtained by FNA from PyMT mice bearing late-stage tumors are significantly more discohesive (less aggregated) and expressed significantly more MenaINV than those from cells from early-stage tumors (14). Therefore, we collected cancer cells by FNA from 32 patients with IDC of the breast of various clinical subtypes (14) and evaluated them in an in vitro subluminal-to-luminal TEM (intravasation-directed TEM (iTEM)) assay. The luminal side of the endothelium is defined as the cell surface facing the bottom well of the iTEM
chamber containing complete medium and colony-stimulating factor-1 (CSF-1) (fig. S1A). Clinical and pathological parameters from the 32 cases used in the iTEM assay are summarized in tables S4 and S5.

Sixteen cases were examined in assays using immortalized human microvascular endothelial cell line (HMEC-1) cells to form the endothelium (fig. S3A), and 16 cases were examined using an endothelium derived from primary human umbilical vein endothelial cells (HUVECs) (Fig. 4, A to D). Similar results were obtained with these two endothelial cell populations. Before performing the iTEM assay, FNA samples were analyzed for the presence of cancer cells and macrophages by IHC for keratin and CD68 abundance, respectively (fig. S3B). In each sample, about 97% of the cells were keratin-positive cancer cells. According to intravital imaging studies, only about 2.5% of breast cancer cells are migratory (15), and of these, only about 40% have an embryonic expression pattern, including high MenaINV expression (27). Thus, we expected only about 1% of cells from the total aspirate to be iTEM-competent. The addition of macrophages significantly increased iTEM activity of tumor cells (Fig. 4A); therefore, unless otherwise noted, experiments were performed in the presence of

Fig. 4. iTEM assays using human patient IDC cells obtained from FNA biopsies. (A) Fold increase in the number of cells from ERPR+ or TN cases that crossed a HUVEC monolayer in the presence of macrophages (b) relative to the number that crossed in the absence of macrophages. Data are means ± SEM from three experiments. **P < 0.005, ***P < 0.0005, by two-tailed Student’s t tests assuming equal variances. (B) MenaINV or Mena11a transcript expression in cells that crossed the HUVEC monolayer relative to that in the loaded cell population. Data are from 16 patient cases. (C) Average MenaINV and Mena11a isoform expression in iTEM-competent cells from (B) grouped by clinical subtype. Data were not significantly different by a Student’s t test. (D) Apical z-sections from the iTEM assay. Tumor cells, green; macrophages, blue; HUVEC junctions (ZO-1), red. Squares indicate dissociating HUVEC junctions, magnified below. Right: Representative z-stacks by clinical subtype. Data are representative of each from the 16 cases in (B). (E) MenaINV and Mena11a transcript expression in iTEM-competent cells from TN human tissue transplants HT17 and HT39. Data are means ± SEM from three mice each. (F) Apical z-sections of the iTEM assay with HT17 tumor cells as in (D). Images are representative of three experiments.
macrophages. This macrophage requirement for iTEM in vitro closely resembles cancer cell invasiveness in vivo as observed by intravital imaging of mouse mammary tumors (5). In 5 of 32 cases, no cells crossed the endothelial barrier (fig. S3A). In the remaining 27 cases that showed iTEM activity, cells that crossed the endothelial layer exhibited a 3- to 15-fold greater MenaINV abundance than that in the original population of cells loaded (fig. S3A and Fig. 4B). In cells that crossed the endothelium, there was no significant difference in relative MenaINV expression between clinical subtypes (fig. 4C).

The ability of cancer cells to cross the HUVEC endothelium was studied at single-cell resolution by imaging. We observed that cancer cells from all subtypes dissociated endothelial cell-cell junctions at the sites of transmigration and that they transmigrated in close proximity to macrophages (Fig. 4D). These data indicate that macrophage-mediated iTEM activity is present in all three clinical subtypes.

Similar results were obtained using FNA-collected cancer cells from xenografts derived from two human TN breast cancer tumor tissues (Fig. 4, E and F). The tumor grafts were described previously (9). The iTEM-competent cells from both human xenografts expressed 60- to 70-fold more MenaINV abundance than did the original cell population (Fig. 4E). These data indicate that MenaINV is associated with iTEM in human IDC tissue transplants in mice and primary human breast IDCs irrespective of clinical subtype.

MenaINV promotes iTEM of tumor cells

To assess whether the expression of MenaINV has a causal or promotional role in iTEM, or is instead an acquired trait in tumor cells after iTEM, MenaINV was selectively knocked down in the TN human breast cancer cell line MDA-MB-231. The expression of the transcripts encoding Mena11a, MenaINV, or total Mena (cumulative detection of all isoforms) was quantified using qPCR after transfection with control or one of three MenaINV-targeted siRNAs (small interfering RNAs) (Fig. 5A). We observed a significant decrease in iTEM activity in cells depleted of MenaINV compared to control cells (Fig. 5B). In addition, the overexpression of green fluorescent protein (GFP)-tagged MenaINV in MDA-MB-231 cells caused a significant increase in macrophage-induced iTEM compared to cells expressing GFP alone, and this increased iTEM of GFP-MenaINV–overexpressing cells was suppressed to baseline by MenaINV knockdown (Fig. 5C). Together, these data indicate that MenaINV is required for tumor cell iTEM.

iTEM-competent cells from TN and HER2+ IDCs have increased abundance of the CSF-1 receptor

Increased CSF-1R (CSF-1 receptor) abundance in human TN mammary tumor cell lines results in a decreased reliance on macrophages for invasion and migration due to autocrine signaling (28, 29). The transmigration of cancer cells from ERPR+/HER2+ cases was associated with a higher number of macrophages located in close proximity to tumor cells compared with those in TN and HER2+ cases (Fig. 6A). Because clinical subtypes exhibit differences in the extent of tumor-associated macrophages during transmigration, and because CSF-1 is present in the bottom well of the iTEM assay, we investigated whether CSF-1R abundance in tumor cells differed among iTEM-competent cells from ERPR+/HER2+, TN, and ERPR+/HER2+ cancers. An examination of CSF-1R expression in iTEM-competent cells from these clinical subtypes as well as from TN tissue transplants revealed little or no enrichment of CSF-1R expression in iTEM-competent cells from ERPR+/HER2+ tumors; however, iTEM-competent cells from TN and ERPR+/HER2+ tumors had substantially more CSF-1R expression compared to the total FNA load (Fig. 6, B and C). These results suggest that CSF-1R–dependent autocrine signaling in TN and ERPR+/HER2+ tumors, but not in ERPR+/HER2+, accounts for the increased numbers of macrophages associated with TN and ERPR+/HER2+ tumor cells during iTEM.

Fig. 5. MenaINV is required for macrophage-induced iTEM in MDA-MB-231 TN breast cancer cells. (A) Transcript abundance for total Mena, Mena11a, and MenaINV in parental MDA-MB-231 cells transfected with one of three MenaINV-targeted siRNAs. (B) iTEM of MDA-MB-231 cells after MenaINV depletion in the presence or absence of macrophages (ϕ). (C) iTEM of MDA-MB-231 cells expressing GFP-tagged MenaINV alone or cotransfected with MenaINV-targeted siRNA (1). iTEM was performed in the presence of macrophages. Data in (A) to (C) are means ± SEM from three experiments. *P < 0.05, **P < 0.005, ***P < 0.0005, by two-tailed Student’s t tests assuming equal variances.
To investigate which signaling loops operate in IDC cells obtained from patients, we used an antibody specific for human CSF-1R (MAB3291) to block autocrine signaling specifically associated with the human CSF-1R present on human cancer cells, and an antibody specific for mouse CSF-1R (AFS98) to block paracrine signaling specifically associated with the mouse CSF-1R present on BAC1.2 mouse macrophages. Only inhibition of the mouse CSF-1R significantly reduced iTEM of ERPR+/HER2− cells, indicating that only the paracrine signaling mediates the transmigration activity of this breast cancer subtype. However, blockade of both the mouse and human CSF-1Rs significantly inhibited iTEM in TN and ERPR−/HER2+ cancer cells (Fig. 6D). Similar results were obtained by blocking the mouse or human CSF-1R in the TN human tissue transplants HT17 and HT39 (Fig. 6, E and F). In addition, blocking both mouse and human CSF-1R brought iTEM to baseline levels (Fig. 6F). These data indicated that TN and ERPR+/HER2− cells use both paracrine and autocrine signaling for transmigration activity.

**Primary human macrophages enhance the iTEM activity of primary human breast cancer cells**

Previous work demonstrated that several macrophage cell lines such as murine BAC1.2F5, immortalized bone marrow–derived macrophage cell line (iBMM), and RQW264.7 support iTEM in vitro (30). We wanted to assess whether primary human macrophages affected the iTEM of cancer cells in a similar fashion as do macrophage cell lines. Indeed, primary human macrophages substantially increased the iTEM activity of cells from human primary TN breast cancer xenografts HT17 and HT39 (Fig. 6A). Additionally, iTEM-competent cells showed greater MenaINV expression (Fig. 6B) and greater CSF-1R expression (Fig. 6C) than the load. Furthermore, imaging at the single-cell resolution revealed transmigration of cancer cells in close proximity to macrophages as well as the dissociation of endothelial cell-cell junctions at the sites of transmigration (Fig. 6D). Thus, primary human macrophages affect iTEM of TN primary human breast cancer cells in the same manner as do macrophage cell lines.

**DISCUSSION**

Here, we tested the hypothesis that relative MenaINV isoform expression is linked to TMEM number and the iTEM of tumor cells in human breast cancer by measuring the iTEM activity of primary tumor cells from patients. To our knowledge, this is the first study to use primary tumor cells obtained from patient breast cancers by FNA for functional iTEM assays in vitro. We found that the abundance of MenaINV, but not Mena1a, correlated positively with the number of TMEM intravasation sites in a cohort of 100 breast IDCs. Although human breast cancer is a heterogeneous disease consisting of several distinct subtypes with substantially different responses to therapy and clinical outcomes, we did not find statistically significant differences in MenaINV expression among the various subtypes. However, the correlation between MenaINV and TMEM number was stronger in TN and ERPR+/HER2− cells than in ERPR−/HER2+ cells. This suggests that the combination of MenaINV expression and TMEM number may be more predictive of iTEM activity than either alone.

To further investigate the role of MenaINV in iTEM, we used antibodies specific for human and mouse CSF-1Rs to block paracrine and autocrine signaling, respectively. Only inhibition of the mouse CSF-1R significantly reduced iTEM of ERPR+/HER2− cells, indicating that only the paracrine signaling mediates the transmigration activity of this breast cancer subtype. However, blockade of both the mouse and human CSF-1Rs significantly inhibited iTEM in TN and ERPR−/HER2+ cancer cells (Fig. 6D). Similar results were obtained by blocking the mouse or human CSF-1R in the TN human tissue transplants HT17 and HT39 (Fig. 6, E and F). In addition, blocking both mouse and human CSF-1R brought iTEM to baseline levels (Fig. 6F). These data indicated that TN and ERPR+/HER2− cells use both paracrine and autocrine signaling for transmigration activity.
In accordance with previous work, we found that, due to their growth pattern, low-grade tumors have significantly lower TMEM score than poorly differentiated cases compared to well-differentiated cases. We did not find any correlations between relative Mena isoform expression or TMEM score and LN status, tumor size, ER, PR, or HER2 status, which is also in accordance with previous studies (22, 23).

High abundance of MenaINV and high TMEM counts were both correlated with reduced E-cadherin staining in human tumors. A recent study using a human mammary epithelial cell line that had been modified to overexpress various Mena isoforms (22, 38) showed significant iTEm (6). Here, using three different MenaINV-targeted siRNAs or the overexpression of GFP-MenaINV, we demonstrated that MenaINV promotes iTEm in TN human breast cancer cell line MDA-MB-231. Thus, MenaINV not only is associated with iTEm but also functionally promotes iTEm activity in tumor cells.

It is now well recognized that tumor-associated macrophages contribute to tumor progression and metastasis, as well as to the response to anti-cancer therapies (30, 36, 37). Macrophages facilitate cancer cell intravasation in at least two ways. First, they comigrate with cancer cells using a chemotactic paracrine signaling loop consisting of macrophage-secreted EGF [which activates EGFR (EGF receptor) on cancer cells] and cancer cell–secreted CSF-1 (which activates CSF-1R on macrophage). This paracrine loop results in migratory cell streams, which efficiently move toward perivascular macrophages (8, 10, 38). Second, the direct physical contact between perivascular macrophages and cancer cells induces RhoA activity and enhances the formation of invadopodia, actin-rich matrix-degrading protrusions that are required for iTEm (7, 8, 39). Both streaming and iTEm are macrophage-dependent tumor cell behaviors that are amplified by MenaINV expression (6, 16). The claudin-low subtype of breast cancers is associated with high iTEm activity and poor clinical outcome (30, 36, 37). MenaINV promotes iTEm activity in TN human breast cancer cell line MDA-MB-231. Thus, MenaINV is likely to be a potent therapeutic target for TN breast cancer patients.
Overall, in addition to the potential for future clinical applications in prognosis and treatment of cancer, this study illustrates the value of using primary tumor cells from patients with different clinical subtypes to investigate the underlying biology behind tumor cell dissemination.

**MATERIALS AND METHODS**

**Human tissue selection and FNA biopsy procedure**

Lumpectomy and mastectomy specimens received at the Albert Einstein College of Medicine/Montefiore Medical Center, Moses and Weiller Divisions for pathological examination were used for FNA-based tissue collection under institutional review board approval. Four to five FNA aspiration biopsies per tumor were performed on grossly visible lesions using 25-gauge needles. The adequacy of the sample was assessed by the standard Diff-Quick protocol (44). Only samples composed of at least 90% malignant epithelial cells, as determined by standard pathologic characteristics (44), were used in the study. ER, PR, and HER2 receptor staining and scoring were done in accordance with United States and Canadian Academy of Pathology/American Society of Clinical Oncology (USCAP/ASCO) guidelines (45, 46).

**Intravasation TEM (iTEM)**

The iTEM assay was performed as described previously (6) and briefly described here with modifications. The Transwell was prepared so that tumor cell TEM was in the intravasation direction [from subluminal side to luminal side of the endothelium (fig. S1A)]. We define this as the iTEM assay. To prepare the endothelial monolayer, the underside of each Transwell was coated with 50 μl of Matrigel (2.5 μg/ml; Invitrogen). About 100,000 HUVEC cells were plated on the Matrigel-coated underside of the Transwells. For HMEC-1 experiments, 200,000 human microvascular endothelial cells (HMEC-1) were plated. Transwells were then flipped onto a 24-well plate containing 200 μl of α-MEM (minimum essential medium) supplemented with 10% fetal bovine serum (FBS) + 3000 U of CSF-1 and incubated until the endothelium formed impermeable monolayers. Permeability of both monolayers was tested as described previously by diffusion of 70 kD of Texas Red dextran (fig. S1, C and D) (Molecular Devices SpectraMax M5 plate reader) and by electrical resistance (World Precision Instruments) (fig. S1, E and F) (39), which demonstrated that the monolayer was impermeable at 48 hours after plating of the HUVECs and HMECs; therefore, Transwells were used at this time point. HUVEC cells generated less permeable monolayers than HMECs; therefore, after the initial experiments, HUVECs were used exclusively. Once impermeable by these criteria, the Transwell assay was used for iTEM studies. All the assays were run in the presence of BAC1.2F5 murine macrophage cell line because it was demonstrated using cancer cell lines that iTEM of tumor cells is efficient only in the presence of macrophages (Fig. 4A) (6). Although it was shown previously that several other types of macrophages including immortalized bone marrow–derived macrophage cell line (iBMM) and the RQW264.7 support iTEM in vitro (39), we chose to do most of the work with BAC1.2F5 cell line, because it generated the most consistent and robust iTEM (39).

We confirmed major findings using primary human macrophages. Peripheral blood mononuclear cells (PBMCs) from anonymous donors were isolated from the Leuko Pak obtained from blood bank. To purify PBMCs, we used density gradient centrifugation, followed by clearance of the remaining red blood cells using hypotonic lysis. The PBMCs were then differentiated into macrophages by adherence in the presence of recombinant human CSF-1 and used a week after isolation.

Macrophages and FNA-obtained tumor cells were labeled with cell tracker dyes. Then, 15,000 macrophages and 37,500 tumor cells were

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**Fig. 8. Model of MenaINV and macrophage-mediated tumor cell invasion and TEM.** Item-competent human breast cancer cells from all clinically relevant subtypes display MenaINV high/Mena11a low isoform expression and perivascular macrophages promote endothelial transmigration at TMEM sites (outlined). Item in ER+/HER2 cells is promoted by paracrine CSF-1–CSF-1R signaling, whereas Item in HER2+ and TN cells is promoted by both paracrine and autocrine CSF-1–CSF-1R signaling. R, receptor.
added to the upper chamber in 200 μl of Dulbecco’s modified Eagle’s medium (DMEM)/F12 supplemented with 0.5% FBS. After 18 hours of transmigration, the medium was removed from the top of the Transwell, and the migrated cells were scraped from the bottom of the plate and immediately subjected to qRT-PCR analysis.

For ZO-1 immunostaining, the Transwells were fixed in 4% paraformaldehyde, permeabilized with 1% Triton X-100, and stained with an anti-ZO-1 (Invitrogen). Transwells were imaged using a Leica SP5 confocal microscope using a 60× 1.4 numerical aperture objective and processed using ImageJ (National Institutes of Health (NIH)) and IMARIS programs. Quantitation was performed by counting the number of macrophages and tumor cells that had crossed the endothelium within the same field of view (60×, 10 random fields) and represented it as a ratio.

**Human tissue transplants**

The TN human tissue transplants HT17 and HT39 were previously described (9). Briefly, the tumor originated from human patient samples and have since only been propagated in SCID (severe combined immunodeficient) mice. Tumors were harvested once they reached 1- to 1.2-cm diameter. Cells were obtained by FNA from human tumors grown in mice, and experiments were carried out in the same manner as was done with direct patient samples. All procedures were conducted in accordance with the NIH regulations and approved by the Albert Einstein College of Medicine animal use committee.

**CSF-1R blocking experiments**

Inhibition of the mouse or human CSF-1R was done using the following species-specific blocking antibodies: monoclonal rat anti-mouse CSF-1R (AF598) or monoclonal mouse anti-human CSF-1R (MAB3291; R&D Systems) (47) at final concentrations of 50 μg/ml. Transwells were prepared as described above, and blocking antibody or control immunoglobulin G (IgG) was added to the top well containing tumor cells and macrophages.

**Quantitative real-time polymerase chain reaction**

qRT-PCR for Mena splice variants was performed as described previously (15). Briefly, the data analysis was conducted using the ΔΔCt method, in which all MENA Ct values in the carcinoma samples were first normalized to GAPDH. A subsequently generated Mena score indicated the relative amount of Mena isoforms in the IDCs compared to the average fold change of Mena isoforms detected in five fibroadenomas, using the ΔΔCt values for each sample. The data are referred to as either the Mena score or the relative Mena expression. qRTPCR for Mena splice variants in the iTEM assay was also conducted using the ΔΔCt method, in which all MENA Ct values in TEM-competent cells were first normalized to GAPDH. Subsequently, relative isoform levels were estimated by comparing the normalized Ct values of Mena isoforms in the cells that crossed the endothelium to the GAPDH-normalized Ct values of Mena isoforms present in the starting sample. qRTPCR analyses were performed with a SYBR Green kit (Qiagen) and analyzed with ABI 7300 sequence detector and associated software (Applied Biosystems). Primers detecting transcripts encoding MenaINV and Mena11a are described in table S1.

**Tissue selection for TEMEM staining and scoring**

At the time of routine microscopic examination of the lesions on which FNA biopsies had been performed, an appropriate area containing invasive cancer suitable for TEMEM analysis was identified by low-power scanning using the following criteria: high density of tumor, adequacy of tumor, lack of necrosis or inflammation, and lack of artifacts such as retraction or folds. TEMEM stain is a triple immunostain for predicting metastatic risk in which three antibodies are applied sequentially and developed separately with different chromogens on a Bond Max autostainer (Leica Biosystems). The pan-Mena mouse monoclonal antibody (A351F7D9) was produced in the Gertler laboratory and is not commercially available. The assessment of TEMEM scores was performed with Adobe Photoshop on 10 contiguous 400× digital images of the most representative areas of the tumor. The total TEMEM for each image was tabulated, and the scores from all 10 images were summed to give a final TEMEM density for each patient sample, expressed as the number of TEMEM per total magnification (ten 400× fields) (22). Twenty-five randomly chosen cases were each independently scored by two pathologists. Because the correlation between the scores was excellent, with a correlation coefficient r = 0.97, the remaining 75 cases were scored by one pathologist.

**Relationship of FNA sample to TEMEM**

FNA primarily collects loose tumor cells, with very few macrophages and no endothelial cells, and incurs minimal tissue damage (48). After the FNA procedure, the entire tumor was fixed in formalin and embedded in paraffin and sent for pathological examination. A representative block of FFPE tumor tissue was selected and triple immunostained for TEMEMs. Therefore, each tumor was sampled by FNA for Mena isoform expression analysis and by FFPE for TEMEM scoring (14).

**IHC and scoring of E-cadherin**

IHC for E-cadherin was done using commercially available monoclonal antibody against E-cadherin (Dako; 1:25 dilution). Antigen retrieval was performed in a steamer at 90°C for 30 min in Target Retrieval Solution (pH 6.0). The slides were incubated with the primary antibody for 30 min at room temperature and for 30 min with a secondary antibody. E-cadherin was visualized using horseradish peroxidase (HRP)–conjugated mouse-specific antibody (EnVision System, Dako) and DAB (diaminobenzidine) on an automated immunostainer (Autostainer, Dako) according to the manufacturer’s instructions. The slides were counterstained with hematoxylin using standard techniques.

Similarly to TEMEM scoring, 10 digital images were acquired at 400× total magnification for each tumor and scored by two pathologists as follows: 3, strong complete membranous staining; 2, moderate complete membranous staining; 1, weak incomplete membranous staining; 0, no staining. The cells within each scoring category were labeled with different Photoshop tools. Data were summed from all 10 images to give a final mean number (and percentage, with error) of cells per tumor with each score. Ten cases of low MenaINV—low TEMEM score (MenaINV < 1, and TEMEM < 10) and 10 cases of high MenaINV—high TEMEM score (MenaINV > 5, and TEMEM > 50) were analyzed for E-cadherin staining intensity. The cutoff levels for high and low scores were established on the basis of the scores above the top 85th and below the lowest 50th percentile.

**IHC and scoring of keratin and CD68-positive cells**

Keratin staining was done on FNA samples prepared as cytospins. The staining was performed in an automatic slide stainer (Dako Autostainer Plus). The primary mouse monoclonal antibody AE13 (catalog no. M3515, Dako; 1:200) and mouse monoclonal antibody CD68 (catalog no. M0814, Dako; 1:2000) were applied for 30 min at room temperature, followed by 30 min in HRP-conjugated anti-mouse secondary antibody (DakoCytomation EnVision+ System, catalog no. K400111). Slides were incubated with DAB Substrate kit (Dako) for 5 min, counterstained with Surgipath Hematoxylin (Fisher HealthCare), dehydrated through graded alcohols, cleared in xylene, and cover-slipped with CytoSeal 60 (Richard-Allen Scientific). The whole cytospin area (314 mm²) was scored for AE1:AE3 and CD68-positive cells; data are presented as a percentage of positive cells.
Small interfering RNA
Isoform-specific knockdown of MenaINV in MDA-MB-231 cells was achieved using siRNA. Transfections were performed by resuspending 8 × 10^7 cells in a 100 μl of Lonza kit V transfection solution with 2 μM siRNA for 96 hours. MenaINV siRNA was purchased from Ambion (Custom Select siRNA). Knockdown efficiency was measured by qPCR.

Statistical analysis
The strength of the association between MENA isoform expression and TME-M density was calculated using rank-order correlation and represented by Spearman’s correlation coefficient. Wilcoxon-Mann-Whitney rank sum test was used to assess the differences between TME density and relative MENA expression in terms of their association with tumor grade, LN status, tumor size, ER, PR, and HER2/Neu status. A regression model fit was used to rank-transformed data and assess the differences in slopes among tumor types. Given that six comparisons were done for hu-

SUPPLEMENTARY MATERIALS
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Fig S1. The experimental setup of the ITEM assay and the permeability of HMEC endothelium. Fig. S2. TME-M density score and relative MenaINV abundance in LN-positive or LN-negative cases. Fig. S3. ITEM assays engineered with HMEC-1 endothelium performed with human IDC cells obtained by FNA.

REFERENCES AND NOTES

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Invasive breast carcinoma cells from patients exhibit MenaINV- and macrophage-dependent transendothelial migration

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Retaining a Barrier to Metastasis

Metastatic disease results from the migration of cancer cells out of the primary tumor and invasion into neighboring tissue or vasculature and establishment of secondary sites. Using an in vitro transendothelial migration assay and cells obtained from fine-needle aspiration (FNA) biopsies from patients with invasive breast cancer, Pignatelli et al. examined the molecular and cellular interactions that may enable the migration of cancer cells into blood vessels (see the Perspective by Kiersse et al.). Where cancer cells colocalized with macrophages in the assay, contacts between endothelial cells were degraded. Macrophages promoted cancer cell migration by secreting the growth factors EGF and CSF-1, and cancer cells in turn secreted CSF-1, which functioned as a paracrine signal to macrophages and for some cancer cell subtypes also as an autocrine signal. Blocking the interaction of CSF-1 with its receptor prevented the transendothelial migration of cancer cells in culture, suggesting that this may be one approach to prevent metastatic progression in cancer patients.