Review

Microenvironmental Regulation of Epithelial–Mesenchymal Transitions in Cancer

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Abstract

The evolution of the cancer cell into a metastatic entity is the major cause of death in patients with cancer. Activation of the epithelial-to-mesenchymal transition (EMT) endows invasive and metastatic properties upon cancer cells that favor successful colonization of distal target organs. The observation that in many cancers distant metastases resemble the epithelial phenotype of primary tumors has led to speculation that the disseminated tumor cells recruited to the target organs undergo mesenchymal-to-epithelial transition (MET). However, the MET cascade has not been recapitulated in vivo, and the cellular and molecular regulators that promote MET remain unknown. In a recent report, using a model of spontaneous breast cancer, we have shown that bone marrow–derived myeloid progenitor cells in the premetastatic lung secrete the proteoglycan versican, which induces MET of metastatic tumor cells and accelerates metastases. This review summarizes recent progress in MET research, outlines a unique paracrine cross-talk between the microenvironment and the cancer cells, which promotes tumor outgrowth in the metastatic organ, and discusses opportunities for novel antimetastatic approaches for cancer therapy. Cancer Res; 72(19); 1–7. ©2012 AACR.

Introduction

Transdifferentiation of polarized epithelial cells to mesenchymal cells (EMT), a key developmental program, is evoked during tumor invasion and metastasis, and several molecular pathways that mediate EMT in cancer cells have been identified (1–4). In addition to promoting tumor cell invasion and metastasis, EMT leads to the generation of cancer cells with stem cell–like characteristics, including increased self-renewal and tumor-initiating capabilities and increased resistance to apoptosis and chemotherapy (3).

However, whereas EMT has been shown in cancer cell lines in culture, whether EMT occurs in vivo remains incompletely resolved (5, 6). Demonstration of EMT in vivo is beleaguered with both technical and biologic challenges. First, the heterogeneity of the tumor makes it difficult to distinguish differentiated tumor cells that have undergone EMT from stromal cells that display a mesenchymal phenotype using morphologic criteria and standard EMT markers. Second, the phenotypic complexity within tumor cells, such as the existence of dedifferentiated stem cell–like pools, makes it difficult to conclude if these are parental tumor cells or consequences of EMT.

Third, EMT in tumor cells is transient; once a metastatic cell has invaded a new tissue, its mesenchymal features disappear. Thus, the universality of EMT as a cardinal hallmark of metastasis has not been accepted by the clinical community (7, 8). To monitor EMT in vivo, it has become necessary to trace the lineage of individual cancer cells from the time they break off from a primary tumor to the point at which they colonize a new organ. Better markers are required to identify true tumor epithelial cells that have undergone EMT. Nonetheless, recent studies have begun to provide evidence of EMT in tumor progression in vivo. In a recent study, using cell-fate mapping strategies with stromal- and epithelial-specific cre-transgenic mice, oncogene Nyc-initiated breast tumors exhibited features of EMT (9). Using an intravital imaging approach, Giampieri and colleagues showed that single breast tumor motile cells that have an active TGF-β–Smad2/3 EMT promoting signaling were capable of hematogenous metastasis to distant organs, whereas those lacking this signaling pathway were prone to passive lymph metastasis (10). In a pancreatic cancer cell model, genetically labeled fluorescent tumor cells that invaded and entered the bloodstream were associated with EMT. Circulating pancreatic cells maintained a mesenchymal phenotype, exhibited stem cell properties, and seeded the liver (11). The ability to mark cell lineages and track their fate in transgenic mice suggests that EMT may occur in vivo; however, such a demonstration remains a challenge in human tumors.

In addition to the obstacles mentioned above, an apparent contradiction to the association between EMT and metastasis comes from clinical observations that distant metastases derived from a variety of primary carcinomas resemble an epithelial phenotype. For example, metastases in distal organs such as liver, lung, bone, and brain derived from a variety of
Bone Marrow–Derived Premetastatic Niche Mediates Mesenchymal-to–Epithelial Transition

We reasoned that to show MET in vivo, it would be imperative to identify critical mediators of MET, as this would allow us to block these mediators and evaluate the impact on MET and overall metastasis. We considered cancer cell intrinsic mediators of MET; however, genomic analysis of primary tumors and distant metastases have indicated a surprisingly high degree of similarity at the level of global gene copy number alterations, loss of heterozygosity, and single-nucleotide variation (25–28). Furthermore, gene expression profiling has shown that human primary breast tumors are strikingly similar to the distant metastases of the same patient (29). These studies suggested that MET of the disseminated tumor cell may not be driven by cell intrinsic evolving mutations but may be under the keen influence of the microenvironment prevailing in the metastatic organ of the host. Indeed, bone marrow and other cancer-associated stromal cells influence patient outcomes through paracrine and endocrine effect (30, 31). On the basis of these studies, we posited that tumor-induced premetastatic niches in distant organs, which serve as permissive hubs for future metastases, may also contribute to MET of disseminated tumor cells (32, 33). To explore these putative MET-promoting niches, we used a spontaneous breast cancer model (MMTV-PyMT), which is metastatic to the lungs. As expected, cancer cells in the mammary gland and in the metastatic lesions in the lungs showed epithelial phenotypes, as revealed by increased expression of E-cadherin compared with vimentin. Importantly, genetically tagged single disseminated breast tumor cells that had colonized the lung showed a mesenchymal phenotype as determined by elevated vimentin levels (D. Gao, et al.; unpublished data), suggesting that epithelial tumor cells had undergone EMT at the primary tumor site followed by MET in the metastatic organ. To identify mediators of MET, bone marrow–derived hematopoietic cells that make up the premetastatic niche were profiled for gene expression, and a subset of the bone marrow–derived myeloid cells composing the monocytic CD11b+Ly6Chigh fraction was found to express elevated versican, an extracellular matrix chondroitin sulfate proteoglycan. Previous studies have shown that versican expressed by intratumoral stromal cells is associated with a worse prognosis in patients with cancer (34, 35). Notably, during kidney development, the conversion of metanephric mesenchyme to epithelium involves MET that is regulated by versican (36, 37), suggesting that bone marrow–derived versican may also induce MET of tumor cells in a paracrine fashion.

Versican expressed by the myeloid progenitor cells promoted metastatic tumor outgrowth by enhancing cell proliferation, and specific knockdown of versican in the bone marrow cells did not affect primary tumors but resulted in a severe reduction in macrometastases, without affecting micrometastases (38). These data were further supported by the observation that depletion of versican–producing bone marrow myeloid progenitor cells produced vimentin-positive micrometastatic lesions. Versican suppression did not perturb the recruitment of myeloid progenitor cells in the lung microenvironment, nor did it change the immune microenvironment, suggesting that the immunosuppressive arm of the myeloid cell function was not affected.

Mesenchymal-to–Epithelial Transition Is Associated with Enhanced Proliferation and Accelerated Metastases

To better understand the mechanism by which versican promotes metastases in vivo, an experimental metastasis
system was used to enable exclusive analysis of post-EMT events in the metastatic organ. A metastatic human breast cancer cell line, MDA-MB-231, was used, as it exhibits an E-cadherin/vimentin mesenchymal (post-EMT) phenotype and is, therefore, amenable to MET analysis. Administration of these cells in immunocompromised severe combined immunodeficient mice gave rise to E-cadherin metastatic lesions in the lung, consistent with previous studies (39). In this setting, specific depletion of versican-producing bone marrow myeloid progenitor cells blocked formation of E-cadherin mesenchymal and resulted in vimentin micrometastatic lesions, implicating a role of versican in inducing MET. Versican inhibited the TGF-β-Smad2/3 signaling pathway to stimulate MET. Versican-induced MET resulted in increased cell proliferation in agreement with published studies showing that TGF-β inhibits the proliferation of breast cancer lines, including MDA-MB-231, by regulating expression of cytostatic genes (40, 41). Consistently, versican-mediated blockade of the TGF-β-Smad2/3 pathway resulted in increased cell proliferation and, notably, expression of constitutively activated TGF-β–R1–rescued versican-mediated blockade of TGF-β–Smad2/3 pathway, reversed MET and proliferation, and suppressed metastases. In a similar fashion, microRNAs (miRNA), particularly the miR-200 family, have been implicated in EMT/MET transitions in cancer (42). miR-200c inhibited EMT and induced an epithelial phenotype (43) and was sufficient to prevent TGF-β–dependent EMT induction. Furthermore, by virtue of targeting ZEB1/2 in mesenchymal cells, miR-200 induced MET (44). Importantly, in a negative feedback fashion, ZEB1/2 regulated miR-200 expression via the possession of conserved ZEB-binding sites in the miR-200 promoter (45, 46). This feedback loop explains the loss of miR-200 expression in invasive breast cancer cells that exhibit a mesenchymal phenotype (44). On the other hand, miR-200 expression is also associated with increased metastatic potential and survival in patients with breast cancer, owing to miR-200-mediated direct suppression of Sec23a, a regulator of metastasis-suppressive proteins (47). In this context, recent studies have identified a potential second loop composed of miR34-Snai1 as a driver of epithelial–mesenchymal plasticity (48, 49). Thus the ZEB/miR-200 and Snail1/miR-34 feedback loops seem to regulate the reversible phenotypic switch that allows the cancer cell to exhibit EMT/MET plasticity in response to the changing microenvironment at the primary tumor site and the distant metastatic site (50). Notably, tumor suppressor p53 has been shown to regulate expression of these miRNAs in many cancer types, and p53-miR200-ZEB1/2 and the p53-miR34-Snai1 axis have emerged as important regulators of cancer cell EMT/MET programs (48, 51).

The Host Microenvironment Regulates Epithelial–Mesenchymal Plasticity of Tumor Cells

Interactions of cancer cells with the tumor microenvironment are important determinants of cancer progression toward metastasis. Thus, tumor cells exhibit EMT/MET plasticity to adapt to the changing microenvironment that they encounter both at the primary and distant sites (Fig. 1). Diverse interactions between the host microenvironment and cancer cells determine the course of tumor progression and metastasis (52). For example, in a spontaneous murine model of melanoma, recruited bone marrow–derived inflammatory myeloid-derived suppressor cells induced EMT via the TGF-β–, EGF–, and hepatocyte growth factor (HGF)–signaling pathways (53). In a recent study, interaction between platelets and tumor cells in the circulation conferred a prometastatic potential upon tumor cells (54). Platelet-derived TGF-β activated the TGF-β/Smad and NF-kB pathways in cancer cells, resulting in EMT and enhanced metastasis in vivo. Inhibition of NF-kB signaling in cancer cells or ablation of TGF-β expression in platelets protected against lung metastasis in vivo. Significant upregulation of EMT-specific markers was also observed.

![Figure 1. Schematic depicting the contribution of bone marrow-derived cells to the formation of lung metastases from a primary breast tumor. Bone marrow contributes F4/80+ macrophages that express EMT-promoting factors in the primary tumor microenvironment and Ly6C<sup>high</sup> myeloid progenitor cells in the metastatic lungs that express versican to stimulate MET of disseminated tumor cells. FGF, fibroblast growth factor.](https://www.aacrjournals.org/content/72/19/5865/fig1?k=10.1158/0008-5472.CAN-12-1223)
following coculture of cancer cells with bone marrow–derived mesenchymal cells (MSC), with a reciprocal downregulation of E-cadherin protein expression, suggesting that MSCs may promote breast cancer metastasis by promoting EMT (55). Tumor-associated macrophages (TAM) represent a major component of the tumor microenvironment, which confers key protumorigenic functions including angiogenesis and immune suppression (56, 57). In addition, TAMs also promote EMT of tumor cells by producing TGF-β, and analysis of 491 patients with non–small cell lung cancer revealed a positive correlation between intratumoral macrophage densities, EMT markers, intraepithelial TGF-β levels, and tumor grade (58). Consistent with these observations, we have observed that differential recruitment of bone marrow cell subsets in the primary tumors and in the metastatic organ may regulate EMT and MET, respectively. In the primary breast tumors of MMTV-PyMT mice, enhanced recruitment of TAMs generated the EMT-promoting microenvironment by increasing expression of TGF, platelet-derived growth factor, and EGF. In contrast, the metastatic organ showed relatively fewer TAMs and lower levels of EMT-promoting factors, and elevated recruitment of myeloid progenitor cells via expression of versican was able to promote MET. Other components of the tumor microenvironment, such as carcinoma-associated fibroblasts (CAF), have been implicated in EMT. For example, CAFs obtained from lung cancer tissue produced HGF, thereby activating the EMT-related c-Met pathway in cancer cells. Of note, through the EMT induction by CAFs, tumor cells acquired resistance to conventional tyrosine kinase inhibitors against the EGF receptor (59). Recently, Giannoni and colleagues have reported that CAFs isolated from prostate carcinoma specimens activated the EMT programming of prostate cancer cells by producing matrix metalloproteinases (60).

Mathematical Modeling of the Epithelial-to-Mesenchymal Transition

Mathematical modeling is becoming a powerful tool for understanding and predicting the complex biologic progression of tumors (61, 62). Despite many studies on intracellular signaling pathways, reports are limited on mathematical modeling and systematic simulation of the EMT and MET progression in cancer metastasis. Neagu and colleagues reported a mathematical model of EMT in the formation of cardiac cushions (63), which can potentially be adapted to simulate the EMT and MET processes in cancer metastasis. The proposed mathematical model is a discrete model, which describes the cells, for example, epithelial and mesenchymal cells and extracellular matrix (ECM), by using a set of lattices in a 2-dimensional plane. The dynamic behavior of cells, including the migration, proliferation, and transformation from epithelial to mesenchymal cells, are guided by an energy function describing the cell–cell and cell–ECM adhesion abilities, defined as follows:

\[
e = \sum_{i=1}^{N} \sum_{j=1}^{N} \alpha_{ij} A_{ij} - \frac{1}{2} n \sum_{i=1}^{N} \beta_{ii} A_{ii},
\]

in which \(i\) and \(j\) denote the types of 2 adjacent objects, that is, cells or ECM, and \(N\) is the number of types of objects. Four objects (\(n = 4\)) are defined in (63), and \(i = 1, 2, 3, 4\) represent medium, ECM, endothelial, and mesenchymal cells. Function \(A_{ij}\) means the number of adjacent objects with different (adhesion \(\beta_{ij} A_{ij}\)) or same types (cohesion \(\beta_{ii}\)), and \(\alpha_{ij} = \beta_{ij} A_{ij} - \beta_{ii}\). The \(n\) denotes the number of interactions between the nearest, next nearest, and second nearest neighbors. Finding the stable cell organization by minimizing the aforementioned equation, the first term prefers the mixture of different objects, whereas the second term tries to keep the anisotropy (i.e., reduce the mixture of different objects). Such a model can be extended to the study of EMT and MET processes in cancer metastasis under different conditions. For example, we can integrate the signaling pathways into the model, as both EMT and MET are regulated by the ligands or molecules outside cells to activate related signaling inside the cells. The secretion and diffusion of the ligands can be described by partial differential equations (61), and the dynamics of signaling cascades could be formulated by ordinary differential equations (64). Moreover, the cell growth can be described by increasing the size of cells over time, which is also regulated by the availability of nutrients around them. Consequently, the cell–cell adhesion ability can be updated through consideration of the boundaries of cells (larger cells should have stronger adhesion ability). These adoptions will improve the predictive accuracy of the mathematical modeling of EMT in cancer metastasis and will offer insight into the in vivo EMT and MET processes, which remain unclear.

Conclusions

In patients with advanced cancer, widespread manifestation of distant metastases is a major cause of cancer-related deaths. Despite this important clinical problem, little is known about the mediators that promote tumor outgrowth in the metastatic organ. As early as 1889, Steven Paget proposed his “seed and soil” hypothesis, establishing the concept that a fertile “soil” (the microenvironment) is critical for the disseminated tumor cell (the “seed”) to grow (65, 66). Experimental support for this hypothesis has begun to emerge from recent studies, which show that primary tumors are able to systematically generate fertile “soil” or a premetastatic niche in the distant metastatic organs, and that these niches pave the way for future metastases (32, 33). By dissecting the components of the premetastatic niche further, our study highlights the role of the cancer cell extrinsic microenvironment prevailing in the metastatic organ as a major promoter of outgrowth of disseminated tumor cells by induction of MET.

From a therapeutic perspective, these findings support the idea that, in addition to targeting the cancer cell, targeting the stromal cell or the stroma–tumor cross-talk as a potential antimetastatic approach should be considered. Indeed, recent studies, including our own, have begun to show that the stroma mediates important hallmarks of cancer such as angiogenesis.
inflammation, immunity, and EMT, establishing a concept of stromal therapeutics (67–69). From a mechanistic perspective, bone marrow–derived versican, in a paracrine fashion, stimulated MET and increased tumor proliferation by blocking the canonical TGF-β–Smad2/3 signaling pathway in cancer cells, suggesting that, in addition to targeting versican, strategies to induce the TGF-β pathway may have antimetastatic consequences. However, targeting the TGF-β pathway is problematic, as TGF-β is considered a double-edged sword in cancer (70). TGF-β inhibits primary tumor growth in early stages, but promotes metastasis by enhancing EMT. Thus, in distant organs, if the same pathway is inhibitory again for tumor outgrowth and versican-mediated blockade promotes metastasis progression, targeting versican may not affect primary tumor dissemination and micrometastasis formation but will impair the critical progression of micrometastases to lethal macrometastases.

Several critical questions need to be addressed before we can translate the findings that both EMT and MET play equivocal roles in tumor metastasis into efficient therapeutic approaches. First, lineage-tracing strategies coupled with intravital imaging are necessary to follow epithelial–mesenchymal transitions in vivo, so that the mechanisms by which lethal macrometastatic lesions develop are understood. Second, it is not clear how universal the EMT/MET cascade is in tumor metastasis, and analysis of EMT/MET in many individual tumors and tumor types is necessary. For example, Trimboli and colleagues observed that EMT only occurred in Myc-initiated but not in T-antigen or Neu-initiated spontaneous breast cancers in mice (9). Furthermore, in some cases, EMT was not required for metastasis, because many mice bearing neu- and PyMT-initiated tumors that lacked any evidence of EMT had significant amounts of lung metastases. Therefore, if the EMT/MET cascade is only required for metastasis by certain types of tumors, specific markers to identify these tumors will be critical for the development of therapeutic strategies. Third, because both EMT and MET promote metastasis, therapeutic approaches to inhibit 1 of them may result in the activation of the other. This dual role may explain the potential controversies associated with EMT- or MET-targeting strategies. For example, the bone morphogenetic protein 7 (BMP7), by antagonizing TGF-β-induced EMT in vivo, has been shown to inhibit metastasis in some tumor models (71), whereas it promotes metastasis by increasing the anchorage-independent cell growth in others (72, 73), and higher BMP7 expression has been associated with worse prognosis of patients with cancer (73).

Thus, identification of specific mediators of EMT- and MET-signaling cascades is likely to lead to a rational approach to targeting these critical protumorigenic pathways. Our new finding that EMT and MET are regulated by selected components in the tumor microenvironment (38) provides unique opportunities to target EMT and MET individually or simultaneously, which will benefit patients with cancer who are diagnosed with either early cancer lesions or already-established metastases. However, significant developments will be required in this field before this vision can become a clinical reality.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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