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Order and Disorder: The Role of Extracellular Matrix in Epithelial Cancer

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INTRODUCTION

The central problem in cancer biology is to understand why tumor cells continue to survive and proliferate in situations where normal cells would arrest growth or apoptose. Although previous approaches have characterized cancer cells as autonomous entities and focused on the genetic mutations that contribute to tumor function, it is becoming increasingly clear that such models ignore the many ways in which cells interact with, and are regulated by, their surroundings. A different approach is to view cancer as a breakdown of the structural principles by which cells are organized within a tissue. In this review, we will provide some theoretical background for this approach, and describe some of our investigations in which we have found that either alterations in the microenvironment or altered perception of the microenvironment can cause normal cells to adopt tumorigenic behaviors.

We will present an overview of the critical components of the cellular microenvironment, focusing on the large macromolecules that comprise the extracellular matrix (ECM). Then, we will summarize the large variety of cell surface adhesion molecules that sense and respond to the ECM and to neighboring cells. Finally, we will describe some of our recent investigations, in which we have used transgenic mice and a three dimensional (3D) cell culture assay to model the cell–ECM and cell–cell interactions that function to create mammary epithelial tissue. These experiments have helped define some of the molecular mechanisms by which mammary cells sense and respond to their microenvironment, how perturbations of those mechanisms can lead to breast tumors, and how reversal of those perturbations may be an approach to reverting early stage cancers.

TISSUE ORGANIZATION: COMMUNICATING WITH THE MICROENVIRONMENT

The structure and function of normal tissues is determined by reciprocal dialogue that is mediated, in part, through interactions with the ECM (1). Extracellular matrix is a complex network of macromolecules that provides both architectural support to cells and contextual information to determine the correct response to a given set of stimuli (2). Cells respond to the milieu of soluble growth factors and cytokines in the context of their particular ECM, determining to proliferate, differentiate, arrest growth, or apoptose (3,4). In addition, ECM can act as a reservoir of other factors that are released from the network after proper activation. The composition of ECM varies considerably both within and between tissues (5,6), and changes temporally, as tissues adapt to changing conditions (7,8). Normal adherent cells must contact the ECM to avoid inappropriate growth or apoptosis, a phenomenon known as

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anchorage dependence (9). Malignant cells are thought to be anchorage independent, and although they continue to respond and contribute to the ECM, they develop into unstructured tumors by subverting the normal processes of tissue organization (10).

As more than 80% of human cancers are derived from epithelial cells, this cell type has been particular focus of cancer investigations. The basement membrane (BM) is the specialized ECM that separates epithelial cells from the surrounding stroma. Normal BM is an organized network composed of laminin, collagen type IV, nidogen/entactins, and proteoglycans such as perlecan (11) (Fig. 1). Other BMs may contain these components and/or other types of collagens, fibronectin, or tenascins. Much of the information that controls development and differentiation of epithelial cells is mediated by changes in the BM (12). In turn, selective degradation of the BM is both a component of tissue remodeling and a characteristic of tumor development. Below, we briefly discuss some of the key components of ECM and the cell surface receptors that interact with it.

COMPONENTS OF THE EXTRACELLULAR MATRIX: STRUCTURE AND FUNCTION

Laminins

Laminins, a family of at least 11 glycoproteins, form an integral part of the structural scaffolding of BMs (13). In this role, laminins are essential: transgenic mice that cannot express functional laminins have an embryonic lethal phenotype, do not assemble BMs, and have disorganized extracellular deposits of collagen IV and perlecan (14,15). Laminins have a cruciform structure composed of a heterotrimer assembled from α , β , and γ chain subunits (Fig. 2) and are simultaneously secreted and incorporated into cell-associated matrices (16). The localized distribution of various laminin isoforms conveys information to direct tissue organization (17), and cell polarization (18) through subdomains of the laminin protein complex. For example, the E3 globular domain of laminin-1 is an essential component for functional differentiation of mouse mammary epithelial cells (19,20).

Laminins are capable of self-polymerization (21), and the assembly of laminin networks is coordinated with the structural organization of the other components of the BM and the underlying cytoskeleton (22). Adherence to laminin matrices by epithelial cells is essential for maintaining normal tissue organization: disruption of selected laminin isoforms produces severe neuromuscular (23), developmental (24), and blistering (25) disorders, and tumors derived from epithelial cells have aberrant production of laminin-binding integrins (26).

Collagens

Collagens are the most abundant structural components of the ECM (11). The collagen structural motif is a trimer of α chains, folded into a coiled-coil triple helix (Fig. 2). To date, collagens have been classified into 20 different types, based on the structural motifs present in the α chain subunit, although considerable diversity exists even within collagen types. Type IV collagen, which is the principal component of basement membranes, can be composed of the six known α chains, giving 56 possible combinations that vary between tissues (27). Defects in one chain can prevent incorporation of others in a tissue specific manner (28), as in Alport syndrome, a hereditary disease characterized by lethal nephritis, deafness, and ocular dysfunction (29).

Nidogen/Entactin

Nidogens are another essential component of BMs, and two nidogen isoforms with overlapping functions have been identified (30). Nidogen acts to stabilize the connection between the

collagen IV network and the laminin network. In this capacity, it is essential both for embryonic development (31) and for functional differentiation of mature tissues (32).

Proteoglycans

Proteoglycans are a distinct and highly diverse subset of glycoproteins containing glycosaminoglycan side chains (11) that play a critical role in strengthening and maintaining BMs and in wound repair (33). In epithelial BM, perlecan is the most abundant proteoglycan. Perlecan deficient mice initially assemble basement membranes normally, although regions susceptible to mechanical stress show progressive and dramatic deterioration leading to embryonic lethality (34).

Other proteoglycans have been shown to regulate growth factor responsiveness (33,35), and misregulation of GPI-linked proteoglycans has been observed in several cancers. Glypicans are GPI-linked heparan sulfate proteoglycans that contribute to enhanced growth factor action in pancreatic cancer (36). EXT1 and EXT2 are heparan sulfate transferases required for synthesis of glypicans which when defective, predispose individuals to bone tumors and other skeletal dysplasias (37,38).

Fibronectins and Tenascins

Fibronectin, normally a component of stromal ECM, contacts epithelial cells when the BM is broken down during remodeling, involution, or malignancy (39,40). Tenascins are antiadhesive components of the ECM expressed during embryogenesis, wound healing, and involution (7), as well as in pathological states including tumorigenesis and metastasis. Fibronectin and tenascin cause cell spreading, a necessary component of cell cycle progression (41), so increased expression of these molecules by tumors and tumor stroma may be a mechanism for increased proliferation.

EXTRACELLULAR MATRIX RECEPTORS

Integrins

General Properties—Integrins are cell surface adhesion molecules named for their ability to integrate the information present in the composition of the ECM and to mediate tissue-specific gene expression (42). Integrins convey signals across the plasma membrane in both directions: association of integrins with ECM ligands can transmit a conformational change on the cytoplasmic face (known as outside–in signaling), while interactions within the cytoplasmic domains can modulate the substrate binding affinity of the extracellular domains (inside–out signaling).

To date, integrins have been found as heterodimeric combinations of 17 α subunits and eight β subunits that interact noncovalently in a restricted manner to create more than 20 heterodimeric family members expressed in a cell- and tissue-specific manner (43). The specific α/β pairing determines the ligand-binding specificity of the integrin. Both α and β subunits consist of large extracellular ligand-binding domains, transmembrane sequences, and relatively shorter cytoplasmic tails. Extensive structural information is available for integrin subdomains, although inherent flexibility has so far prevented a complete structural analysis (44).

Some integrins display specificity for short sequences; the most studied of these is the tripeptide arginine–glycine–aspartate (RGD), which is present in a variety of ECM proteins (45). Other integrins recognize conformational structures composed of different amino acids (45). A particular cell may express multiple types of integrins with overlapping specificity, i.e., a particular integrin may bind to multiple ligands, as when $\alpha_v\beta_3$ binds to laminin, collagen,

fibronectin, and tenascin C (46) or, a component of the ECM may associate with multiple integrins, as when laminin associates with $\alpha_1\beta_1$, $\alpha_2\beta_1$, $\alpha_3\beta_1$, $\alpha_6\beta_1$, $\alpha_7\beta_1$ and $\alpha_6\beta_4$ (43,47). The significance of this functional redundancy is unknown, although one can presume that this has evolved to allow rapid responsiveness to changes in the microenvironment.

Integrin Activation—Association of integrins with ECM ligands initiates the assembly of adapter proteins to form focal adhesion complexes that link to the cytoskeleton (48). In cultured adherent cells grown in the presence of serum factors, integrins first associate with talin and α -actinin, then with tensin, vinculin, and paxillin to recruit actin filaments (49) (Fig. 1). The reorganization of actin by focal adhesion complexes, in turn, causes integrin clustering and strengthens cell–ECM binding in a positive feedback mechanism. Clustered aggregates of focal adhesion complexes can be visualized by electron microscopy as focal adhesions, electron-dense structures at the cell–ECM boundary (50). This process physically links the cytoskeleton to the ECM (22), so that perturbations in the ECM are rapidly transduced to the interior of the cell and vice versa. Cytosolic enzymes that modulate cytoskeletal structure also affect the organization of the ECM. In this way, cells that contact each other are organized into a functional tissue that is able to respond to environmental changes as a unit.

The organization of the actin network has been shown to be controlled within the cell by the Rho family of small GTPases, consisting of Rho, Rac and Cdc42, each of which have been shown to control different aspects of cytoskeletal structure in fibroblasts (39). Rho controls the generation of stress fibers, thick bundles of actin filaments that connect to focal adhesions. Rac controls the formation of lamellipodia, thin actin sheets at the edges of cells that can lift up and fold backwards. Cdc42 controls the formation of filopodia, thin actin bundles at the cell surface that produce narrow protrusions (51). The complexity of the roles played by the Rho GTPases in epithelial cell shape is an active topic of investigation (52,53).

The binding activity of integrins to the ECM is also controlled by intracellular signals that modulate ligand associative properties in a process known as affinity maturation (54). Current models suggest that integrins exist on the cell surface in a low-affinity conformation, and require interaction with specific cytoplasmic components to become activated (55). Affinity maturation is generally mediated by heterotrimeric G-protein-coupled receptors of the Ras family (56) or through cytosolic modulation of cytoskeletal structure by the Rho family of GTPases (57,58).

Integrin Signaling—Ligation of integrins to ECM directly activates signal transduction pathways through kinases present in focal adhesion complexes. These include tyrosine kinases such as focal adhesion kinase (FAK), integrin-linked kinase (ILK), and members of the Src kinase family, as well as serine–threonine kinases of the Abl family. Among these, FAK has been a particular target of investigation. In normal cells, FAK is activated by cell adhesion and rapidly deactivated on cell detachment, and FAK signals through numerous pathways to mediate anchorage-dependent survival and proliferation (59). Induction of constitutively active FAK in normal cells leads to transformation and anchorage-independent growth, while overexpression of FAK in transformed cells restores anchorage dependency (60).

Focal adhesion kinase associates with Src (61) or c-Jun NH₂ terminal kinase (JNK) (62,63) to activate the mitogen-activated protein kinase (MAPK) pathway. Anchorage dependence is mediated through both MAPK signaling and cytoskeletal reorganization, processes that are functionally separable, at least in cultured cells grown on plastic substrata: artificial clustering of integrins without occupation of the integrin ligand-binding site activated MAPK signaling without cytoskeletal reorganization, and simultaneous clustering of integrins with ligand binding-site association resulted in cytoskeletal reorganization even in the presence of MAPK inhibitors (56).

We now know that integrins also modulate the activity of growth factor-dependent signaling. In normal cells, optimal activation of receptors for insulin, epidermal growth factor (EGF), platelet-derived growth factor (PDGF), and vascular – endothelial growth factor (VEGF) all require proper ECM context (64). Integrins can potentiate growth factor activation pathways by associating with receptors or components of receptor-signal transduction pathways or by directly or indirectly initiating signal transduction pathways (65,66). Through adhesion-mediated regulation of growth factor signaling, cells respond properly to the milieu of positive and negative signals from growth factors and cytokines.

Non-integrin Extracellular Matrix Receptors

Other cell-surface receptors have been shown to be involved in sensing the ECM. The syndecans, a family of transmembrane heparan sulfate proteoglycans, are expressed on all adherent cells (67) in a highly regulated cell-type and developmental-stage-specific manner (68). Syndecans are involved in the formation of focal adhesion and stress fibers, modulation of integrin function, and in response to mechanical stresses (69,70). A role for syndecans in mammary tumorigenesis was revealed by investigations of syndecan-1-deficient transgenic mice, which are resistant to Wnt-1-induced tumorigenesis (71).

Dystroglycan, originally isolated from skeletal muscle (72), now appears to act in all tissues as another receptor for laminin spanning the membrane and connecting to the cytoskeleton (73,74). In contrast to integrins and syndecans, so far only a single form of dystroglycan has been discovered in mammals. Dystroglycan is generated as a single polypeptide and cleaved into the extracellular α subunit and the transmembrane β subunit (75). α -Dystroglycan binds to laminin-1 (76) and to the proteoglycans, perlecan and agrin (77,78). At the cytoplasmic surface of epithelial cells, α -dystroglycan associates with actin filaments through isoforms of utrophin and dystrophin (75).

Dystroglycan acts both as a receptor of ECM signaling and in the assembly of BMs. Mice lacking dystroglycan do not survive past day 6 gestation, corresponding with defects in the Reichert's membrane, a specialized BM that separates embryonic from maternal tissue (79). Embryoid bodies lacking dystroglycan assembled nonfunctional basement membranes with disorganized and patchy laminin-1, collagen type IV, and perlecan (80). Reintroduction of dystroglycan by adenovirus infection restored the ability of the embryoid bodies to organize laminin-1.

CELL–CELL ADHESION: SENSING THE NEIGHBORS

The principal molecule responsible for the formation of direct contacts between epithelial cells is E-cadherin (81). This function is essential, as transgenic mice lacking E-cadherin display defective development at the stage of formation of the trophectoderm, the first epithelium (82,83). The extracellular domain of E-cadherin is composed of five subunits with repeating internal sequence homology and calcium binding motifs (84) (Fig. 3). Adhesion is mediated in the presence of calcium ions by E-cadherin clustering and lateral homoassociation in a zipper-like mechanism to produce adherens junctions. Removal of calcium from the extracellular environment reverses this process and releases the cell–cell adherence (85).

Like integrins, cadherins connect to the actin cytoskeleton through a complex of cytosolic adaptor proteins. In general, cadherins may interact with either β -catenin or plakoglobin, which in turn binds α -catenin. Actin filaments can associate directly with α -catenin or indirectly, through adapter proteins such as α -actinin, vinculin, or ZO-1 (81). The Rho GTPase pathway also intersects with cadherins: cell–cell attachment activates Cdc42 (86), and IQGAP1, an effector of Cdc42 and Rac1 binds to β -catenin and disassociates cell–cell contacts (87). Integrin signaling can also modulate cadherin function through the adaptor integrin-linked kinase

(ILK), as constitutive activation of ILK results in down-modulation of E-cadherin and an epithelial-to-mesenchymal transition (88).

Cadherins also interact with signal transduction pathways that impact on cell proliferation and differentiation (89). Cell–cell adhesion potentiates paracrine signaling and cadherin-mediated tight junction formation is essential for segregation of membrane receptors between apical and basolateral surfaces (90). Additionally, cadherins may indirectly participate in signaling processes by sequestering β -catenin into adherens junctions. When not sequestered, β -catenin activates gene expression through the lymphoid enhancer factor/T-cell specific factor (LEF/ TCF) pathway (91). This pathway is essential for Wnt signaling, a mechanism for regulating epithelial cell proliferation in adult and embryonic tissues that is often dysregulated in colon carcinoma (92).

Numerous studies have correlated the loss of E-cadherin with the development of cancer (93). Decreased E-cadherin function is a component of epithelial-to-mesenchymal conversion, invasive tumor growth, and metastasis, and loss of E-cadherin is a negative prognostic marker (94). Similarly, altered expression of E-cadherin cytosolic adaptor proteins in pathologic conditions can also predispose to malignancies (95).

Until recently, these correlations were only suggestive of an underlying mechanism. Now a causal role for the loss of E-cadherin in the acquisition of invasiveness has been described in a transgenic mouse model (96): forced expression of E-cadherin during pancreatic β -cell tumorigenesis arrested tumor development, while forced expression of a dominant negative E-cadherin gene produced premature invasiveness and metastasis. Loss of E-cadherin is not always associated with increased tumor potential, however, as increased E-cadherin is associated with early stages in primary ovarian carcinomas (97). This exception proves the rule: all signaling and signaling molecules eventually need to be understood in the context of tissue and organs.

COMING TOGETHER: CELLULAR INTERACTIONS THAT DEFINE TISSUE FUNCTION IN THE MAMMARY GLAND

Integration of Signaling is Essential for Normal Function

It is clear that cells are organized in tissues by multiple signaling pathways that are integrated biochemically and physically by cell interaction with the ECM. The challenge is to understand how this comes about. To investigate the mechanisms of tissue organization and the ways in which these mechanisms break down during tumorigenesis, we have developed an assay that approximates the normal cell–ECM and cell–cell interactions in the mammary gland acini of both mice and humans (98). Our culture system uses a reconstituted basement membrane derived from the Engelbreth–Holm–Swarm (EHS) tumor (99), a mixture of laminin-1, collagen IV, and nidogen. When mouse mammary cells are cultured within this BM, nonmalignant cells organize to form physical structures that resemble the alveoli of the lactating mammary gland. As described below, this assay can be used further to distinguish between normal and malignant human breast cells, to characterize the mechanisms that define normal mammary epithelial architecture, and to characterize the defects that cause the aberrations of behavior in tumors.

Differentiation of Non-malignant Mammary Epithelial Cells

Grown on conventional tissue culture plastic substrata, mouse mammary epithelial cells grow in a flattened morphology and express little or no milk proteins, despite the presence of hormones (100). In contrast, cells grown on EHS matrix in the presence of lactogenic hormones form physical structures reminiscent of the lactating mammary gland (101) and organize into ducts and hollow structures that resemble functional alveoli. Milk proteins are apically secreted

into central lumen, and the basal surfaces are encased by a distinct basal lamina (102,103). A hierarchical model of functional mammary epithelium was established in which both cell–cell and cell–ECM interactions provide signals for cytoskeletal organization and deposition of BM (104). The latter, in turn, signals for expression of some milk proteins. The morphological changes were found to be a necessary prerequisite for the biochemical activation of other milk protein genes, including β -casein and WAP (105,106).

TUMORIGENESIS AS A BREAKDOWN OF CELL-CELL AND CELL-ECM COMMUNICATION

Nature vs. Nurture: An Origin for Malignant Cells

Many investigations have characterized cancer as the consequence of genetic mutations that inactivate tumor-suppressor genes or activate oncogenes (107,108) and view cancer progression as the accumulation of genetic defects in overlapping pathways, each providing a progressive evolutionary advantages to the malignant progeny (109,110). Such approaches have focused attention on the viewpoint of malignant cells as independent entities and on genetic instability as the principal motivating force driving tumor progression (111,112). Although it is certain that genetic instability is a principal feature of cancer (113), this viewpoint of cancer as a collection of renegade cells ignores the multiple interconnected interactions that define the role of cells within a tissue. Furthermore, many of the characterized tumorsuppressors and proto-oncogenes have been found to act as intermediates of signal transduction pathways that exist to communicate information from the extracellular microenvironment into the cell (114). As these signaling pathways are connected in a web of co-dependencies and competitive influences, defects in one pathway can lead to dysregulation of many others. In such cases, the inappropriate behavior of tumor cells can be viewed as the consequence of aberrant perception of microenvironmental stimuli. Furthermore, just as normal tissue structure and function are highly dependent on reciprocal communications between cells and their microenvironment, so imbalances in these communications can contribute to the malignant behavior of a tumor. These imbalanced communications can be caused by mutations of genes encoding critical transduction intermediates, but can also be epigenetic, caused by aberrations in the microenvironment.

Aberrations in the Extracellular Matrix Cause Cancer

If the ECM is instrumental in normal development and differentiation, then a remodeling of its composition can lead to alterations in the function and structure of the organs (115). Therefore, ECM remodeling is a potent mechanism of cell regulation. In the mammary gland, the massive apoptosis of milk-secreting epithelial cells during the post-lactational regression phase is triggered by degradation of BM by matrix metalloproteinases (MMPs) (116). Similarly, MMP-mediated remodeling occurs in many tissues and in diverse activities such as wound healing and angiogenesis (117). Matrix metalloproteinases also play roles in invasion, tumor angiogenesis, and metastasis (118,119).

We have investigated stromelysin-1 (SL-1), an MMP that plays an important role in both development and regression of the normal mammary gland and is found in mammary carcinomas. In mammary epithelial cells cultured on ECM, exogenous expression of SL-1 led to degradation of basement membrane, attempted re-entry into the cell cycle, and apoptosis (120,121). We also found that the stroma of mammary glands of transgenic mice that overexpressed SL-1 inappropriately (122) showed features of pre-neoplastic lesions (123) that eventually led to full malignancy (124,125). These changes were inhibited by crossing these mice with another strain that expressed an MMP inhibitor (126,127). The SL-1, expressed initially at low levels in the mammary epithelial cells, was subsequently produced at much higher levels in stromal fibroblasts (123), suggesting that disruption of ECM integrity led to a

self-sustaining tumorigenic state. Consistent with this hypothesis, cultured epithelial cells containing an inducible SL-1 transgene (128,129) formed tumors that eventually became independent of transgene expression (125). A similar mechanism has been observed for the metalloproteinases matrilysin (130) and stromelysin-3 (131,132). Matrix metalloproteinases inhibitors are currently under test in clinical trials, although early results have been disappointing; MMPs may alternatively benefit the host or the tumor, depending on tumor stage and other microenvironmental factors (133).

Increased Signaling from Growth Receptors Causes Cancer

Signals from the microenvironment control both cell morphology and gene expression, and these pathways are coupled in tissues and in cells in 3-D (134). When cultured on inappropriate ECM, normal signaling patterns become decoupled from control of morphology (135). This effect can obscure phenotypic differences between different types of cells, and even between normal and tumor cells. When grown on conventional tissue culture plastic, few differences are observed between normal human mammary epithelial cells and malignant breast cancer cells, either in morphological appearance or in biochemical characteristics (136). When cultured on appropriate ECM, however, normal cells functionally differentiate, as demonstrated by growth arrest, structural organization, and polarized secretion of BM components. Malignant cells, on the other hand, continue to proliferate, forming amorphous structures (136).

These distinct behaviors suggested to us that growth on 3-D ECM could be used to dissect the mechanisms associated with malignancy. To avoid potentially artifactual differences specific to cell lines, we used a human breast cancer progression series. Derived originally from a human reduction mammoplasty (137), HMT-3522 cells were repeatedly passaged, acquiring numerous chromosomal abnormalities (138–140). Once they also lost the ability to sense the cues from the BM, they acquired tumorigenic potential when injected into immunocompromised mice (141). The functionally normal, early passage (S1) cells and the tumorigenic, late passage (T4-2) cells were similar in appearance when cultured on plastic substrata, but very different when cultured inside or on BM. As S1 and T4-2 cells respond to their microenvironment differently, we examined the differences in ECM receptor expression between the two cell lines. Normal human mammary epithelial cells express four α/β heterodimers: $\alpha_1\beta_1$, $\alpha_2\beta_1$, $\alpha_3\beta_1$, and $\alpha_6\beta_4$; all four of which bind laminin, while $\alpha_1\beta_1$ and $\alpha_2\beta_1$ also bind collagen (135). Analysis of the S1 and T4-2 cells revealed that the tumorigenic cells expressed both an increased level of β_1 integrins and a anomalous pattern of expression (142). Integrin expression is often aberrant during tumor progression (143,144).

To test the hypothesis that increased signaling from β_1 integrins was contributing to the tumorigenic behavior, the relative activity of this subunit was attenuated by function blocking antibodies. This treatment resulted in conversion to an organized phenotype in the 3-D BM and a reduction in tumorigenicity when transplanted into mice. The reverted T4-2 cells arrested proliferation, organized into acini, and organized a basement membrane (142). This reversion was also accompanied by down modulation of the endogenous level of the epidermal growth factor receptor (EGFR). Subsequently, a bi-directional cross-modulation of β_1 integrin and the EGFR through the MAPK pathway was revealed by experiments in which inhibition of any of these components also led to functional reversion of the T4-2 cells (145). Thus, normalization of ECM signaling by reestablishing balance in signaling can produce an almost normal phenotype in culture and in vivo without changing the genotype (142).

Decreased Signaling from Pro-differentiation Receptors Causes Cancer

Much of the integrin literature has focused on the pro-growth properties of integrins, as normal cells require integrin signaling in order to avoid apoptosis or growth arrest (64), but it is clear

that cell differentiation is also dependent on contact with ECM. Some have speculated that tissue organization with E-cadherin may produce anti-growth effects to counter integrin signaling (64). We have found that functional differentiation of mammary epithelial cells can occur in the absence of cell–cell contact if BM is present (104). We dissected the ECM signals for differentiation of mammary epithelial cells, and discovered a requirement for contact with BM laminin through two integrins and one nonintegrin ECM receptor (146). Recently, we have discovered that this nonintegrin receptor is dystroglycan, and we are beginning to find evidence that dystroglycan may play a general role in inducing cell polarization and growth arrest (Muschler et al., submitted). Surveys of tumorigenic and non-tumorigenic cell lines have revealed that inability to organize when cultured on BM correlates with loss of cell surface dystroglycan. The hypothesis that dystroglycan signaling is complementary to integrin signaling for producing differentiation is very attractive due to the wide tissue distribution of dystroglycan (74,79). According to this hypothesis, the disorganized and tumorigenic growth of T4-2 cells could be caused by increased MAPK signaling initiated by β_1 integrins and insufficient relative signaling from dystroglycan or other growth inhibiting matrix receptors.

Thus, the pathways to organized differentiation or disorganized malignancy may be mediated by a balance between pro-growth and pro-differentiation signaling; pathways that are interconnected and self-reinforcing.

CONCLUSIONS

Cells respond to their microenvironment through ECM adhesion molecules. These interactions lead to activation of signaling cascades that impact on many other signaling pathways as well, modulating the responses to soluble growth factors and the connections to neighboring cells. In normal cells, these interacting pathways control tissue organization and development; when dysfunctional, these pathways can lead to cancer. Using transgenic and cell culture models, we have modeled aspects of both the productive and destructive interactions in breast cells. We have shown that inappropriate expression of ECM-remodeling metalloproteinases cause tissues to become disorganized, and that sustained disorganization can lead to tumorigenesis. Using cancer cell lines, we have found that misregulation of ECM-sensing adhesion molecules can be an important component of tumorigenesis, and that reasserting balance to the signaling pathways in tumor cells can revert the malignant phenotype. Thus, a balance in the network of cell-ECM interactions can determine the tumorigenic potential of a cell population, and in this way, these mediators of tissue architecture constitute a class of tumor suppressors. These networked interactions can be self-reinforcing: perturbation of normal signaling can produce tumorigenesis, while normalization of tumor signaling can lead to functional reversion. A better understanding of these pathways may lead to the next generation of cancer treatments aimed not necessarily at killing the cancer, but at restoring the natural order and consequent tissue function.

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Figure 1.

Architecture of the basement membrane and cell surface connections. Basement membrane is composed of interconnected networks of collagen IV, laminin, nidogen/entactin, and proteoglycans such as perlecan. These connect to the cell through cell surface receptors such as integrins and dystroglycan. These, in turn, connect to the actin cytoskeleton through cytoplasmic adapter protein complexes.



Figure 2.

Components of the basement membrane. Presented in diagrammatic form to relative scale (scale bar = 50 nm).



Figure 3.

Components of E-cadherin-mediated adherens junctions. E-cadherin is a cell surface molecule composed of five repeating motifs that contain calcium-binding domains. In the presence of extracellular calcium, E-cadherin molecules homodimerize and then associate with E-cadherin dimers on adjacent cells in a zipper-like mechanism. This process is coincident with association with actin filaments through cytoplasmic adapters including the catenins and α -actinin.