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Patricia Rousselle, Konrad Beck. Laminins and matrix metalloproteinases connection: a subtle relationship that can go wrong in a tumor context, particularly if CD44 gets involved. The Extracellular Matrix and the Tumor Microenvironment. Biology of Extracellular Matrix, vol 11. Springer, Cham., 2022, 978-3-030-99708-3. hal-03834467

HAL Id: hal-03834467 https://hal.science/hal-03834467v1

Submitted on 29 Oct 2022

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Patricia Rousselle¹ and Konrad Beck²

¹ Laboratoire de Biologie Tissulaire et Ingénierie Thérapeutique, Institut de Biologie et Chimie des Protéines; UMR 5305; CNRS; Univ. Lyon 1; SFR BioSciences Gerland-Lyon Sud; 7 passage du Vercors, 69367, Lyon, France

² Cardiff University School of Dentistry, Heath Park, Cardiff CF14 4XY, U.K.

Corresponding author: Patricia Rousselle, LBTI, 7 passage du Vercors – 69367 Lyon Cedex 07, France. Tel: (33) 4 72 72 26 39; Fax: (33) 4 72 72 26 02; E-mail: <u>patricia.rousselle@ibcp.fr</u>

Keywords: laminin, basement membrane, CD44, matrix metalloproteinase, cancer, protein domain modeling

Abbreviations

ECM, extracellular matrix; EMT, epithelial-mesenchymal transition; FAK, focal adhesion kinase; GAG, glycosaminoglycan; HA, hyaluronic acid (hyaluronan); HBS, heparin binding site; HS, heparan sulfate; LG, laminin globular domain; LM, laminin; MAPK, mitogen-activated protein kinase; MMP, matrix metalloproteinase; PI3K, phosphatidylinositol-3-kinase.

ABSTRACT

Laminins (LM) are large extracellular glycoproteins involved in several biological processes, including cellular interactions, self-polymerization, and binding with other extracellular matrix proteins. LMs influence cell function by inducing various signaling pathways via cell membrane receptors and have multiple, often cell type-specific, functions in, for example, adhesion, differentiation, migration, and phenotype maintenance, and they also provide resistance to apoptosis. They are also important components of basement membranes. The basement membrane is partly degraded in the course of tumor growth, facilitating the invasion of budding cells and their migration to lymphatic or blood vessels. In this context, LMs undergo proteolytic cleavage, which disrupts their involvement in maintaining the structural and biological properties of the basement membrane. LMs are also involved via their participation in cancer cell adhesion and migration processes. These events are either supported by their major cell binding domains or triggered by cryptic interaction sites revealed by matrix metalloproteinase (MMP) induced proteolytic cleavage. While being ideal targets for MMPs, LM can enhance their expression and activity. They appear to be key matrix elements in the regulation of MMP activity via the recruitment of the CD44 receptor, a multiple MMP-interacting and activating platform playing an important role in cancer progression.

1. The laminin protein family

Laminins (LMs) are a family of glycoproteins found in basement membranes with biological and structural properties that attract a growing interest. As essential structural constituents of the extracellular matrix (ECM), LMs also maintain close relationships with cells and transmit important morphogenetic information (Miner and Yurchenco 2004) (Domogatskaya et al. 2012). All LMs are composed of three different gene products, termed α , β , and γ chains, which are assembled into a crossshaped heterotrimer $\alpha\beta\gamma$. The three chains assemble within the endoplasmic reticulum via their C-terminal regions to form a triple stranded α -helical coiled coil rod and are covalently linked by disulfide bonds at both extremities of the coiled coil (Beck et al. 1993) (Matsui et al. 1995). The primary structures of five α chains (α 1, $\alpha 2$, $\alpha 3$, $\alpha 4$, $\alpha 5$), four β chains ($\beta 1$, $\beta 2$, $\beta 3$, $\beta 4$), and three γ chains ($\gamma 1$, $\gamma 2$, $\gamma 3$) were identified by cDNA sequencing, leading to at least 18 heterotrimeric isoforms (Table 1, Figure 1). Some genes encoding LMs may produce more than one subunit isoform due to alternative splicing; short-chain and long-chain splice variants are annotated with A and B, respectively (Aumailley et al. 2005). All basement membranes contain at least one LM isoform, and some may have two or three different isoforms. The expression and assembly of the various subunits vary in a spatio-temporal manner, which suggests biological and structural roles specific to each isoform (Yap et al. 2019). Some isoforms appear very early in embryogenesis and are markers for a given ECM, whereas others appear later and in a tissuespecific manner. In general, expression of the α 5 subunit is the most widespread, whereas that of the α 1 subunit is the most restricted (Miner et al. 1997). The α 2 subunit is particularly abundant in tissues of mesodermal origin (cardiac and skeletal muscle), and the α 4 subunit is abundant in endothelial and mesenchymal cells. The

 α 3 subunit, similar to β 3 and γ 2, is concentrated in epithelial basement membranes. The β 1 and β 2 subunits often have mutually exclusive expression, whereas the γ 1 chain is present in all basement membranes (Durbeej 2009). LMs are essential at various stages of development. Thus, most LM mutants are fatal to the embryo and have made it difficult to study their functions at later stages (Yao 2017).

Although LMs are differentially recognized by cellular receptors, they all share a molecular organization based on the repetition of structural modules, giving them a common molecular organizational pattern. LM-111, which was initially extracted from the Engelbreth-Holm-Swarm tumor, was the first LM described as an asymmetric cross comprising one long arm and three short arms carrying globular domains linked by linear segments (**Figure 2A**). Other LMs do not exhibit all of the short arms, as they include "truncated" subunits at the N-terminal ends (α 3, α 4, β 3, and γ 2)

(Figures 1 and 2B). The N-terminus of each full-length LM chain consists of cysteine-poor sequences and are named LN domain. The short-arm rod-like portions consist of tandem arrays of LE modules, which sequences are related to the epidermal growth factor but contain one additional C-terminal disulfide bond. Inner globular structures within the short arms are the L4 domains resulting from a long insert between cysteines 3 and 4 of the canonical 8-cysteine pattern of an LE domain. The LF domains have a distant structural similarity to L4 but are unique with respect to their cysteine pattern (Pulido et al. 2017). The LFx domains share similar sequences at the N- and C-terminal regions of the α , β , and γ chains assemble into a three-strand α -helical coiled coil forming the long arm (Macdonald et al. 2010). The amino acids involved in this structure are organized in a heptad repeat in which the first and fourth residue are of hydrophobic, and the fifth and seventh

frequently of charged character (Paulsson et al. 1985). Within the β chains, the coiled coil region is interrupted by domain L β consisting of 30 to 40 residues including six cysteines which biological function is not yet known. All LM α chains possess a large globule at the C-terminal end that consists of five similar domains (LG1 to LG5), each containing approximately 200 residues (Timpl et al. 2000) (Hohenester 2019). LG3 and LG4 are separated by a flexible hinge providing access for proteolytical attack. All LMs are glycosylated, which regulates their biological functions in addition to stabilizing them (Morita et al. 1985) (Inamori et al. 2016).

2. Laminins as multifunctional elements within basement membranes

Early molecular and *in vivo* studies in Drosophila, *C. elegans*, and mice support the idea that LMs are the basic building block for initiating basement membrane formation (McKee et al. 2007) (Jayadev and Sherwood 2017). Most LMs can self-associate into polymeric sheet-like networks that are tightly associated with the cell surface through their LG domains (Yurchenco et al. 1992) (Li et al. 2003). This polymerization process is reversible and depends on both the concentration and presence of divalent cations. This assembly model involves and absolutely requires the N-terminal domain LN of the α , β , and γ subunits (Cheng et al. 1997) (Hohenester and Yurchenco 2013) (**Figure 2A**). LM networks are non-covalent in nature and appear more dynamic than the cross-linked collagen IV networks described as being responsible for the mechanical strength of basement membranes. Thus, collagen IV recruitment and further basement membrane assembly appear to depend on LM self-assembly and its LG-mediated cell surface anchorage. LMs containing at least one truncated subunit, and therefore lacking one LN domain (*i.e.*, the α 3A, α 4, and γ 2

chains), are non-polymerizing LMs and form other types of supramolecular arrays to integrate the basement membrane (**Figure 2B**). The epithelial LM heterotrimers $\alpha 3A\beta 3\gamma 2$, $\alpha 3A\beta 1\gamma 1$, and $\alpha 3A\beta 2\gamma 1$ establish specific molecular interactions leading to the formation of anchoring structures characteristic of epithelial basement membranes (Champliaud et al. 1996; Rousselle and Beck 2013). The matrix integration of LMs comprising a truncated α chain assembled with the $\beta 1$ and $\gamma 1$ subunits, such as LM-3A11 and LM-411, may involve known interactions between the $\beta 1$ and $\gamma 1$ chains with agrin, nidogen (entactin), and perlecan.

LMs provide interaction sites for many other constituents including cell surface receptors. Some LM isoforms are modified extracellularly by proteolytic processing at the N- or C-terminal ends prior to binding cellular receptors or other matrix molecules (Tzu and Marinkovich 2008). Cellular receptors, such as integrins, syndecans, α dystroglycan, Lutheran glycoprotein, or sulfated glycolipids, predominantly bind to the five LG domains at the C-terminal end of the α chain. The LG1-LG3 region contains the integrin binding domains, which often require the context of the LM heterotrimer and, most importantly, the C-terminal end of the y chain to be fully effective (Deutzmann et al. 1990; Rousselle et al. 1995; Ido et al. 2004; Ido et al. 2007; Ido et al. 2008; Navdaev et al. 2008). The major LM-binding integrins are α 3 β 1, α 6 β 1, α 7 β 1, and α 6 β 4 (Nishiuchi et al. 2006). The LG1-LG3 region of the LM α 5 chain also binds to the Lutheran blood group antigen/basal cell adhesion molecule, a cell surface protein consisting of five immunoglobulin-like domains (Udani et al. 1998; Vainionpää et al. 2006; Kikkawa et al. 2007). The LG45 region contains binding sites for α -dystroglycan, syndecans, and sulfated glycolipids (Gee et al. 1993; Talts et al. 1999; Smirnov et al. 2002; Wizemann et al. 2003; Yamashita et al. 2004; Utani et al. 2003; Hozumi et al. 2009; Carulli et al. 2012; Suzuki et al. 2005). The N-terminal

globular LN domains of the α 1 (Colognato-Pyke et al. 1995) and α 2 chains (Colognato et al. 1997) as well as LN (Nielsen and Yamada 2001) and L4 (Sasaki and Timpl 2001) of the α 5 chain can bind to α 1 β 1, α 2 β 1, α 3 β 1, and α V β 3 integrins.

Deregulated expression and involvement of LMs and their integrin receptors in tumor development and aggressiveness have been demonstrated in recent years. They will not be the subjects of this review as they have been exhaustively covered recently (Maltseva and Rodin 2018; Qin et al. 2017; Ramovs et al. 2017; Rousselle and Scoazec 2020). Instead, here we will focus on the link between LMs and matrix metalloproteinases (MMPs) and demonstrate how it can become toxic in cancer by amplifying the tumor process. We will also examine the current state of understanding the status of LMs as ligands for the CD44 receptor and seek for a potential link with MMP activity.

3. Laminins are involved in the regulation of MMP expression and activity

MMPs are a family of secreted and membrane-bound zinc-dependent endopeptidases that have the capacity to degrade all components of the ECM. MMPs play central roles in morphogenesis, wound healing, tissue repair and remodeling in response to injury, and in the progression of diseases, such as inflammatory and neoplastic diseases (Nagase et al. 2006). The MMP family comprises 25 related but distinct vertebrate gene products, 24 of which are found in mammals and can be divided into six groups: collagenases (MMPs 1, 8, 13, 18), gelatinases (MMPs 2, 9), stromelysins (MMPs 3, 10, 11, 17), matrilysins (MMPs 7, 26), membrane-type MMPs (MT-MMPs; MMPs 14, 15, 16, 17, 24, 25), and other MMPs (MMPs 12, 19, 20). The expression of MMP genes is transcriptionally regulated by a variety of extracellular

factors including cytokines, growth factors, and ECM proteins (Gaffney et al. 2015). A number of studies have revealed that LMs or their proteolytic fragments can be involved in the regulation of MMP expression and/or activity. These subtle regulations that occur in a physiological context can be amplified in pathological situations such as cancer, contributing to tumorigenesis and invasion (Karamanos et al. 2021).

Early studies revealed that an interaction between LM-111 and the 67-kDa LM receptor promotes MDA-MB231 breast carcinoma cell aggressiveness through the upregulation of MMP-14 and enhanced gelatinolytic activity of MMP-2 (Berno et al. 2005). Subsequent studies have shown that LM-111 can increase MMP activity in human neural stem cells (Sypecka et al. 2009). Later, activation of MMP-9 expression was associated with an $\alpha 2\beta 1$ integrin-dependent migration process when the human cervical cancer SiHa cell line was cultured on an LM-111-coated surface (Maity et al. 2011). A mechanism involving focal adhesion kinase (FAK), integrin linked kinase, phosphatidylinositol-3-kinase (PI3K), and extracellular signal regulated kinase was followed by increased DNA-binding activity of NF-kB and Ap1 and subsequent stimulation of MMP-9 gene expression (Maity et al. 2011). A similar signaling pathway was revealed when human breast cancer MCF-7 cells were plated on an LM-111-coated surface (Pal et al. 2014). In this study, the concomitant downregulation of TIMP1, a negative regulator of MMP-9 activity, led to enhanced MMP-9 proteolytic activity. Another context in which a link between LM and MMPs was established is the kidney. The LM α 2 chain was shown to contribute to pathogenesis in the Alport glomerular syndrome *via* activation of FAK on glomerular podocytes leading to the downstream activation of MMP-9, MMP-10, and MMP-12 gene expression (Delimont et al. 2014). A ß1 chain fragment released through MMP-2 processing, LN–LE1-LE4, was shown to modulate the behavior of pluripotent stem

cells and promote the epithelial-mesenchymal transition (EMT) in an α 3 β 1-integrin– dependent fashion, whatever the fragment was delivered to the cells as a soluble or immobilized factor (Horejs et al. 2014). The β 1 chain fragment triggered the downregulation of MMP-2 in human and mouse cells, as well as the up-regulation of Ecadherin and MMP-9 in mouse cells during spontaneous stem cell differentiation.

The cryptic domains of LMs (*i.e.*, hidden in full-length LMs and exposed upon proteolysis) can elicit biological responses and be involved in the regulation of MMPs. For example, peptides containing the sequence S₂₀₉₉IKVAV, which is adjacent to the N-terminus the C-terminal LG1 domain of the LM a1 chain, have been shown to induce the expression of MMP-9 by monocytes/macrophages (Corcoran et al. 1995; Khan and Falcone 1997), whereas intact LM-111 does not (Khan and Falcone 2000). A mouse α 5 LG1 domain-derived peptide was shown to induce macrophage and neutrophil chemotaxis both in vitro and in vivo and to enhance MMP-9 and MMP-14 activities (Adair-Kirk et al. 2003). Furthermore, human y2 chain fragments and LG4derived peptides from the α 3, α 4, and α 5 chains exhibit strong chemotactic activity towards leukocytes, neutrophils, and monocytes (Mydel et al. 2008; Kenne et al. 2010; Senyürek et al. 2014). Whether these activities are associated with activation of MMP expression or activity is an interesting question that remains to be answered. Another study revealed that LM-332 potentiates human monocyte differentiation to tumor-associated macrophage-like cells secreting a high level of MMP-9 (Kamoshida et al. 2014). Upregulation of MMP-1 and MMP-9 expression was also reported at both the transcriptional and protein levels in epidermal keratinocytes upon treatment with recombinant C-terminal LG4 or LG45 domains of the a3 chain, an event that relies on an IL-1ß autocrine loop through the mitogen-activated protein kinase (MAPK) pathway (Momota et al. 2005; Utani et al. 2003; Michopoulou et al. 2020).

Several peptide sequences involved in this mechanism were identified as heparin binding sites (HBSs) and characterized as ligands for the proteoglycan-type cell surface receptors, the syndecans (Utani et al. 2003; Carulli et al. 2012; Rousselle and Beck 2013). However, the role of LM was not limited to this transcriptional activation as the α 3 LG45 domain participated in establishing the gelatinolytic activity of epithelial podosomes in migrating keratinocytes during wound healing (Michopoulou et al. 2020). We showed that the α 3 LG45 domain triggers the proteolytic activity of MMP-9 and MMP-14 in epithelial podosomes *via* a mechanism involving the cellular receptor syndecan-1 (Michopoulou et al. 2020).

4. Laminins are cell adhesion ligands for CD44

The cell surface glycoprotein CD44, a hyaluronic acid (HA) receptor, plays a role in the regulation of cell-cell interactions, cell adhesion, cell growth, migration, and invasion (Knudson et al. 1996; Ponta et al. 2003). CD44 is an 85-200 kDa transmembrane glycoprotein ubiquitously expressed throughout the body and is detected in both normal and tumor cells. CD44 is encoded by a single gene with 20 exons but has many different isoforms (**Figure 3A**). It is composed of a distal extracellular N-terminal domain, a stem region, a transmembrane domain, and an intracellular cytoplasmic C-terminal domain (**Figure 3B**). The standard form CD44s is the shortest and most commonly expressed isoform. It results from expression of the constant exons 1 to 10, which are found in all isoforms. A number of splicing variants (CD44v) result from the insertion of variable exons in the extracellular region near the membrane, called the stem region. There are 10 variant exons expressed in mice (designated v1–v10), whereas humans express only variant exons v2–v10 due to the

presence of an in-frame stop codon in exon v1 (Screaton et al. 1993). The N-terminal portion of the ectodomain is of a compact, ordered structure, stabilized by three disulfide bridges, that contains a HA binding region and glycosaminoglycan (GAG) chains (**Figure 4A**). The stem region varies according to the expression of the splicing domains in the CD44v isoforms, and the transmembrane and intracellular domains both play important roles in CD44 functionality and connection to the actin cytoskeleton through ezrin/radixin/moesin (ERM) proteins (Tsukita et al. 1994; Gal et al. 2003; Medrano-González et al. 2021). Importantly, upregulation of CD44 is often closely associated with abnormal tumor cell behavior (e.g., proliferation, survival, migration/invasion, and chemoresistance) (Bourguignon 2019; Medrano-González et al. 2021).

Understanding the various interactions of CD44 on a molecular structural level that would allow for reliable predictions of binding sites is difficult. The complex posttranslational modifications by N- and O-linked glycosylation greatly depends on cell types, developmental and environmental conditions. Large chondroitin and dermatan sulfate GAG chains attached to the stem region in CD44s, and heparan sulfate chains found within the variable regions are highly flexible making high-resolution structural analysis challenging. Except for the most N-terminal *ca.* 160 amino acids, even the unmodified ectodomain evades exploration by showing a high degree of intrinsic disorder with nearly 30% of residues being serine and threonine (**Figure 4B**). In contrast to the classical view of structure-function relation as a lock-and-key system, the resulting flexibility on the structural level allows the protein to adapt various conformations for optimal ligand binding (Habchi et al. 2014). Even the various structures solved at high resolution by x-ray crystallography may not be regarded as static. Molecular dynamics simulations suggest that Y42 can act as a

molecular switch that upon binding to HA changes the overall HA binding domain structure from a closed to open conformation that further increases affinity for HA (Guvench 2015).

CD44 is upregulated in a variety of cancers and can be expressed as CD44s or as a number of alternatively spliced CD44v isoforms. CD44 mediates its effects on the cancer cell by activating signaling pathways, such as protein kinases and transcription factors. The functional role of CD44 is pleiotropic, including induction of EMT and anti-apoptosis, alterations in the cellular cytoskeleton, and promotion of drug resistance. CD44 is a compelling marker of cancer stem cells from many solid malignancies (Takaishi et al. 2009; Du et al. 2008; Zöller 2011). In addition, interactions between HA and CD44 promote epidermal growth factor receptor-mediated pathways, consequently leading to tumor cell growth, tumor cell migration, and chemotherapy resistance in solid cancers (Thapa and Wilson 2016; Yaghobi et al. 2021).

In addition to its direct signaling function, CD44 forms a platform at the cell membrane for the assembly of various MMPs with their substrates, ultimately to modulate cell migration (Cauwe et al. 2007) (**Figure 3B**). CD44 is an important partner of MMP-9, playing a role in its anchorage to the cell membrane and preservation of its proteolytic activity (Yu and Stamenkovic 1999, 2000). Evidence suggests that the association of MMP-9 and CD44 in mouse and human tumor cells promotes invasion (Yu and Stamenkovic 1999; Gupta et al. 2013). Clustering of CD44 mediates MMP-9 relocation in breast tumor cells promoting its proteolytic activity on the membrane (Peng et al. 2007). The interaction of CD44 and the proteolytic form of MMP-9 is involved in the invasion activity of prostate cancer PC3 cells (Desai et al. 2007).

CD44 is also a molecular partner of MMP-14, playing a role in its translocation to the front of migrating cells (Mori et al. 2002). MMP-14 has been clearly characterized as a CD44 shedding enzyme with migration-promoting activity (Kajita et al. 2001). MMP-14 and CD44 are co-expressed at the lamellopodia of cells undergoing EMT (Cho et al. 2012). In normal mouse breast and uterine epithelium, the heparan sulfate (HS) chains of CD44v containing the exon v3 derived sequence bind active MMP-7 (Yu et al. 2002; Seiki 2002). CD44 also binds MMPs 2, 15, 16, 24, and 25 through their hemopexin domains in lamellipodia edges (Mori et al. 2002; Suenaga et al. 2005; Samanna et al. 2006) and can act indirectly by activating MMP-2 through MMP-14 cleavage (Zöller 2015) (**Figure 3B**).

CD44 has been identified as a component of podosomes, which are protrusive adhesion structures involved in ECM degradation and mechanosensing (Murphy and Courtneidge 2011; Linder and Wiesner 2016). It was shown to co-localize with the F-actin core of podosomes in osteoclasts (Chabadel et al. 2007), human primary epidermal keratinocytes (Michopoulou et al. 2020), and in 3D-cultured macrophages (Van Goethem et al. 2011). By demonstrating a direct interaction between the LM α3 LG45 domain pair and the CD44 receptor expressed by human primary keratinocytes, we have revealed a determining role for this LM isoform in regulation of the proteolytic activity of MMP-14 and -9 in epithelial podosomes (Michopoulou et al. 2020). The 200-kDa CD44 isoform identified in our study is the long form v3–10 expressed by keratinocytes (Bourguignon and Bikle 2015). It is conceivable that the LM-332 LG45 domain concentrates active MMP-9 and -14 within epithelial podosomes through recruitment of CD44. In addition, the combination of LG45 and CD44 could facilitate binding of adaptor molecules to the cytoplasmic region in CD44 and activate multiple pathways involved in cell adhesion, migration, and proliferation

including Ras, MAPK, and PI3K (Xu et al. 2020). Although this mechanism has been demonstrated in the physiological context of skin repair, it could undoubtedly be implemented in cancer cells in which the expression of LM-332 is frequently upregulated (Rousselle and Scoazec 2020). In cancer cells, the α3LG45 domain could regulate the expression and concentrate active MMP-9 and MMP-14 in invadopodia, the adhesive actin-rich membrane protrusions with high proteolytic activity found in cancer cells (Augoff et al. 2020). An argument in favor of this hypothesis is based on our study showing that Ras/IkBa-transformed keratinocytes lacking the LG45 domain exhibit a deficiency in MMP-9 and MMP-1 expression and a decreased invasive capacity (Tran et al. 2008). This deficiency was reversed by replacing LG45 through retroviral transduction. Whether the CD44 isoforms expressed in cancer cells can bind to α 3LG45 is an important question (Chen et al. 2018). We already know that, in addition to the CD44v3-10 isoform, the 100-kDa standard CD44s expressed on melanoma A375 cells also binds the α3LG45 domain (Michopoulou et al. 2020; Takahashi et al. 1999), and we may wonder whether the various CD44 isoforms will bind to a3LG45 with different affinities. For example, the presence of variable exon 3, which encodes an HS chain carrying region, may impact the interaction (Bennett et al. 1995).

A link between LM-332 and the MMP-14/CD44 tandem was already revealed a few years earlier in a study showing that interactions between mature human thymocytes and LM-332 induces strong up-regulation of active MMP-14 leading to CD44 cleavage and thymocyte migration (Vivinus-Nebot et al. 2004). As the LG45 domain was cleaved off and removed from the LM-332 used in this study, we can evaluate the possible participation of the N-terminal end of the γ 2 chain, which also comprises an HBS, in this mechanism (Sasaki et al. 2001). One study revealed that the LN

domain of the LM y2 chain induces breast cancer MDA-MB-231 cell migration as a result of its binding to CD44 and phosphorylation of its cytoplasmic tail (Sato et al. 2015). Surprisingly, interaction studies uncovered a binding site for CD44 within the LEa2-LEa3 region, away from the HBS of the v2 chain identified within the L4 and LEa domains (Sasaki et al. 2001; Ogawa et al. 2007), suggesting the involvement of a LM binding domain distinct from the GAGs in the CD44 ectodomain (Sato et al. 2015). However, the study did not mention any MMP-9 or MMP-14 recruitment, though it clearly reported a v2 chain-dependent pro-migratory activation of CD44 reinforcing the hypothesis that LM-332 is a multi-site ligand for CD44. Based on these data we performed rigid body molecular docking simulations using a model of the LM y2 LEa2-LEa3 pair and the coordinates of the HBS domain of CD44. The best result with a good global minimal energy conformation shows a good steric fit of CD44 within the groove of the LE2-LE3 connection and suggests four pairs of residues that come into hydrogen bonding distance (Figure 4C). Though this model is in agreement with the experimental data, as any glycosylation and the stem portion of CD44s were not considered, it should be viewed with caution.

LMs were identified as ligands for CD44 already nearly 30 years ago. The binding of CD44 to a commercial LM preparation was detected in an ELISA-based assay using CD44 purified from lymphocytes (Jalkanen and Jalkanen 1992). The epithelial isoform CD44v8-10 (Brown et al. 1991), which is expressed in carcinoma cells such as human colorectal carcinoma KM-12, CCL 188, and MIP-101 cells, was identified as an LM-111 receptor (Ishii et al. 1993). These studies already reported that the interaction is mediated by the proteoglycan-rich region of the extracellular domain of CD44, an interaction site distinct from that of HA, which is located in the disulfide-rich N-terminus of the molecule (Ponta et al. 2003). In a study screening the adhesive

properties of overlapping short peptides covering the entire LG1 to LG5 domains of the α 5 chain toward B16-F10 mouse melanoma cells, peptide A5G27 R_{2892} LVSYNGIIFFLK corresponding to one β strands of the LG2 module with the terminal basic residues in the surface exposed loop regions was identified as a ligand for CD44 via its GAG moieties (Hibino et al. 2004). In the human sequence, this peptide relates to R₂₉₇₁LVSYSGVLFFLK. When visualized within the solved terminal structure of LM 511 (Takizawa et al. 2017), it is evident that the basic side chains are surface exposed at opposite ends of the LG2 domain (Figure 4D). Further positively charged surface areas are generated by K3009, K3010, and K3025. These five residues form a track that could further the alignment of a GAG chain. A similar track of basic residues crucial for heparin binding has been previously reported for the LM LG4 domain (Yamashita et al. 2004). The LM α 5 chain interaction with CD44 stimulates melanoma cell growth, angiogenesis, migration, and metastasis (Hibino et al. 2005). CD44 overexpression in neural precursor cells significantly improved their spreading over LMs and increased the formation and length of filopodia, suggesting a role in migration (Deboux et al. 2013). Using a protein database approach, a role for CD44 interactions with LM-111 was predicted to play an important role in the axon growth of retinal ganglion cells during nerve regeneration (Ries et al. 2007). As CD44 is overexpressed on a wide variety of neuronal, epithelial, and hematopoietic malignancies, CD44 may be involved in either the malignant transformation of cells or the migration of malignant cells from the primary site to sites of metastasis. The mode of interaction of CD44 with LMs is very complex and can take place in a number of ways. Further work is now required to better understand these interactions and apprehend their biological consequences.

5. Laminins are targets of MMPs activity

Like any other ECM protein, LMs are subject to total or partial proteolysis by MMPs, leading to the release of protein fragments, which may play a role in tumor progression. Over the years, MMPs have been found to play a remarkable number of regulatory roles at the cellular level, including pathways involved in apoptosis, immunity, cellular migration, and angiogenesis (Fingleton 2006; Itoh and Nagase 2002; Shay et al. 2015). Thus, MMPs play a major role in carcinogenesis. MMP functionality often complements classical tumor properties, leading to invasion, immune system avoidance, and metastasis (Winkler et al. 2020). The specific role of each MMP in cancer and their dysregulation in many cancer types have been accurately documented recently (Gobin et al. 2019; Piperigkou et al. 2021; Karamanos et al. 2021). An exhaustive gene expression study of 15 different types of cancers compared to normal tissue confirmed that MMP expression has a large degree of heterogeneity across cancers and revealed that the most prevalent gene expression changes were upregulation as opposed to downregulation in tumor tissue versus control tissue (Gobin et al. 2019). Facilitation of cell migration and invasion is thought to be the principal effect of the MMP-mediated breakdown of basement membranes surrounding cancer cells (Jayadev and Sherwood 2017; Hanahan and Weinberg 2011). All molecular networks, including LM networks, as well as ECM/cell adhesion complexes are targets of MMP-mediated proteolysis. Notably, even if cells can physically breach basement membrane barriers in the absence of MMPs (Kelley et al. 2019), the massive production of MMPs by cancer cells greatly enhances their invasive capacity. Another barrier to tumor cell extravasation and invasion is the basement membrane underlying the endothelium of the vessel wall, where LM-411 and LM-511 are expressed (Spessotto et al. 2001). LMs can be cleaved by MMPs 2,

3, 7, 9, 10 to 16, 19, and 20 (Okada et al. 1986; Bejarano et al. 1988; Wilson and Matrisian 1996; Chandler et al. 1996; Ohuchi et al. 1997; Pirilä et al. 2003; Sadowski et al. 2005; Itoh and Seiki 2006; Laronha and Caldeira 2020), but invasive tumor cells primarily use MMP-2, MMP-9, and MMP-14 within invadopodia to cleave or degrade ECM proteins including LMs (Jacob and Prekeris 2015). Expression of MMP-14 in cancer cells correlates with their metastatic potential (Poincloux et al. 2009) and their ability to degrade fibrillar collagen and LMs. MMP-14 has the ability to activate MMP-2, MMP-9, and MMP-9 is thought to play a detrimental role in the early stage of breast cancer as the basement membrane no longer provides the appropriate signals to restrain epithelial cell proliferation (Beliveau et al. 2010).

The effects of LM degradation on cancer cell behavior, however, are more complex in the end because proteolytic cleavage leads to the release or exposure of either ECM-sequestered cytokines or a functional ECM fragment. Some LMs can express cryptic biological functions after proteolysis thereby altering cellular behavior and phenotypes (Niland and Eble 2020). The combined elastase/MMP-9-mediated proteolytic remodeling of LM-111 has been shown to unmask an epitope that triggers proliferation of dormant breast cancer cells through an α 3 β 1 integrin signaling mechanism leading to aggressive lung metastases (Albrengues et al. 2018). This fascinating study demonstrated that the proteases present in neutrophil extracellular traps, together with DNA, are delivered to LM-111 through a DNA/LM interaction. LM-211, LM-411, and LM-511 could be degraded in the same way (Albrengues et al. 2018).

LM α 1, β 1, and γ 1 chains are subject to MMP-2 and MMP-9 cleavage, releasing proteolytic fragments endowed with integrin- or syndecan-mediated cellular functions

(Kikkawa et al. 2013). MMP-2 cleavage of the short arm of the β 1 chain is predicted to disassemble the LM network, releasing a β 1 LN–LE1-4 fragment that mediates α 3 β 1-integrin dependent embryonic stem cell adhesion (Horejs et al. 2014). Structural changes occur after LM-511 cleavage by MMP-9 (Gu et al. 2005), and fragments with activity toward inflammatory or cancer cells were identified within the LM α 5 chain (Adair-Kirk et al. 2003; Hibino et al. 2004; Kusuma et al. 2011). An 80-kDa LM α 2 C-terminal LG3-LG5 fragment possibly generated by MMP-9 is thought to play a role in reshaping the blood–testis barrier and spermatogenic function in a rat model (Gao et al. 2017). Analysis of the secretome from MDCK cells undergoing Ras-induced EMT resulted in the identification of two LM α 5 internal and C-terminal fragments generated from MMP-1 cleavage with pro-migratory and pro-angiogenic activities (Gopal et al. 2016). LM α 5 has also been reported to be cleaved by MMP-14, leading to prostate cancer cell migration (Bair et al. 2005).

LM-332 has been the focus of increasing interest over the last few years in the cancer research field, particularly the various proteolytic cleavages of its three subunits (Rousselle and Beck 2013). Many proteases degrade LM-332 and have been exhaustively documented (Rousselle and Scoazec 2020). To fulfill its essential function of anchoring proteins in epithelial basement membranes (Rousselle et al. 1991; Rousselle et al. 1997; Champliaud et al. 1996), LM-332 undergoes several physiological post-translational modification events. This maturation process allows its supramolecular integration and promotion of cell adhesion (Rousselle and Beck 2013). In cancers, additional cleavage events occur, compromising both these adhesive and connecting functions and additionally delivering pro-migratory signals to cells (Rousselle and Scoazec 2020). Cleavage of the β 3 chain by MMP-7 or MMP-14 has been reported to enhance colon or prostate carcinoma cell migration

and invasion, respectively (Remy et al. 2006) (Udayakumar et al. 2003). MMP-2 or MMP-14 cleavage of the γ 2 chain is reported to be a pro-tumorigenic signaling event (Giannelli et al. 1997; Koshikawa et al. 2000; Gilles et al. 2001). The released N-terminal LE repeats have been shown to induce EGF signaling and downstream MAPK activity in cancer cells (Koshikawa et al. 2004). The involvement of MMPs 3, 12, 13, 19 and 20 in the cleavage of the γ 2 chain (Pirilä et al. 2003; Sadowski et al. 2005; Väänänen et al. 2001) reinforces the status of LM-332 and its γ 2 subunit as an ideal target for MMPs in tumorigenesis.

Studies of the testis have reported that MMP-2 cleavage of the LM γ 3 chain, part of the α 3 β 3 γ 3 LM heterotrimer localized at the apical ectoplasmic specialization of Sertoli cells (Yan and Cheng 2006), induces dysfunction in the Sertoli cell tight junction permeability barrier through a 50-amino-acid residue peptide sequence in domain L4 (Siu and Cheng 2004; Yan et al. 2008; Su et al. 2012; Li et al. 2020). This process is thought to provide an efficient mechanism for modulating different aspects of spermatogenesis (Li et al. 2020). During zebrafish skeletal muscle development, LM was shown to act as an MMP-11 mediator and regulator of fibronectin levels at the myotendinous junction (Jenkins et al. 2016).

Conclusion

ECM remodeling is an important contributor to tumor progression and metastasis by contributing to the dissemination of cancer cells to distant tissues as well as angiogenesis. Among the many extracellular proteases expressed by human cells, MMPs are the most prominent enzymes supporting ECM proteolytic degradation and

remodeling, as well as the modulation of cellular and ECM interactions. Whether MMPs are soluble/secreted in the tumor microenvironment or anchored to the cell membrane, their dysregulated expression in tumor cells, cancer-associated fibroblasts, and infiltrating immune cells is a hallmark of cancer. Being ideal targets of MMPs, the cleavage or degradation of LMs has structural and biological impacts favoring tumor development and metastasis. The fragments or peptides that are generated can induce the production of more MMPs in various cell types, setting up a vicious cascade. The proteolytic activity of MMPs is often localized in adhesion structures, such as invadopodia, or occurs in proximity to the cell membrane where LMs are expressed. Cellular receptors, such as CD44, play an important role in addressing and regulating MMP activity. Their connection to LMs could promote the establishment of an active MMP-rich microenvironment prone to efficient degradation and remodeling of the ECM. Thus, LMs can be targets of MMPs, bioactive factors stimulating their expression, or even interacting platforms capable of recruiting and concentrating them.

Acknowledgments

Original work leading to this review was generously supported by research grants from the French Agence Nationale de la Recherche (grant number ANR-18-CE92-0035-01, awarded to PR) and Rhône-Auvergne Pack Ambition Recherche 2020.

Table 1

Laminin isoforms

Name	Chain assembly	Previous	Original name
Laminin-111	α1β1γ1	1	EHS laminin
Laminin-211	α2β1γ1	2	merosin
Laminin-121	α1β2γ1	3	S-laminin
Laminin-221	α2β2γ1	4	S-merosin
Laminin-3A32	α3Αβ3γ2	5 or 5A	kalinin. epilegrin, nicein, ladsin
Laminin-3B32	α3Ββ3γ2	5B	
Laminin-3A11	α3Αβ1γ1	6 or 6A	K-laminin
Laminin-3A21	α3Αβ2γ1	7 or 7A	KS-laminin
Laminin-411	α4β1γ1	8	
Laminin-421	α4β2γ1	9	
Laminin-511	α5β1γ1	10	drosophila-like laminin
Laminin-521	α5β2γ1	11	
Laminin-213	α2β1γ3	12	
Laminin-423	α4β2γ3	14	
Laminin-523	α5β2γ3	15	
Laminin-522ª	α5β2γ2		
Laminin-212 ^b	α2β1γ2		
Laminin-222 ^b	α2β2γ2		
Laminin-333°	α3β3γ3		

^a Laminin-522 reported so far solely in bone marrow.

^b The existence of either LM-212 or LM-222 is proposed based on studies of

peripheral nerves in wild-type and LM $\alpha 2$ chain-deficient mice.

^c Laminin-333 is expressed at the apical specialization of adult rat testes, rather than

in the testicular basement membrane.

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Figure legends

Figure 1

Schematical models of the different laminin chains

LM chains contain tandem arrays of globular and rod-like regions. Chains with identical order of domains are combined (α 1/2, β 1/2/4, γ 1/3). The N-terminal ends of all chains contain tandem arrays of a variable number of epidermal growth factor–like repeats LE with eight cysteine residues in short rod-like domains (LEa–LEc), as well as various globular domains (LN, L4, L4a, L4b, LFa, LFb, LFx), some of which can interact with integrins. Truncated LE domains containing less than 8 cysteines are depicted by half-circles. LE numbering follows the laminin nomenclature ((Ponta et al. 2003; Cauwe et al. 2007; Medrano-González et al. 2021) though frequently, including in data base entries, they are counted consecutively starting at the N-terminus. The α chains have five globular domains (LG1 to LG5) at the C-terminus. LG1–LG3 bind

mostly to integrins, with some requiring the presence of the γ chain C-terminal region. LG4 and LG5 contain binding sites for dystroglycan (α DG), syndecans, and sulfated glycolipids. The LG4–LG5 tandem is thought to be cleaved off extracellularly (arrow) in α 3, α 4, and α 5, though this is not the case for the α 1 and α 2 chains; LG domains of α 2 stay attached to the molecule after cleavage. A small six cysteine residues containing domain L β of yet unknown biological function is present in the coiled coil regions of the β chains; originally the regions N- and C-terminal of L β were denoted by roman numerals II and I, respectively, but as this is unique to the β chains, this has been abolished. The LAMB4 gene coding for the β 4 chain might be a pseudogene as no transcripts has yet been found.

Figure 2

Prototype assembly model of laminins

The α , β , and γ chains assemble to form a coiled coil in at least 18 combinations (**Table 1**). (A) LM-111 is a prototype heterotrimer able to self-assemble and form a network due to the presence of LN domains at the N-terminal ends of its three subunits. (B) LM-332 is a prototype heterotrimer unable to self-assemble as its α and β subunits are truncated. S-S at the termini of the coiled coil regions denote the presence of disulfide bridges. SH indicates the location of free cysteine residues.

Figure 3

CD44 as a platform for MMP binding

(A) Structure of the human CD44 gene, which consists of 10 constant exons
 expressed in all CD44 mRNAs and proteins (grey boxes) and 9 variant exons v
 (colored boxes) expressed in CD44 splice variants (CD44v). Other vertebrate genes

contain an additional exon v1. The examples shown are the smallest isoform (standard CD44s, expressed ubiquitously in vertebrates) and the larger variant isoforms expressed in some epithelial cells and cancers. (B) CD44 protein structural domains. The CD44 protein is composed of an extracellular link domain (green), a stem domain (red), where the variant exon products are inserted, the transmembrane region, and the intracellular cytoplasmic domain. The CD44 extracellular domain is a platform for MMP-2, MMP-7, MMP-9, and MMP-14 binding and can indirectly activate MMP-2 through MMP-14 cleavage. Figure adapted from references (Ponta et al. 2003; Cauwe et al. 2007; Medrano-González et al. 2021).

Figure 4

Molecular constraints of CD44 and laminin interactions.

(A) The protein backbone of the HA binding domain of human CD44 is shown on the left with α -helices in red and β -strands in cyan (PDB code: 4PZ4, ref. (Liu and Finzel 2014)). Terminal residues, disulfide bonds and putative acceptor sites for N-linked glycosylation are depicted as ball-and-sticks. Disulfide bonds follow a C1-C6, C2-C5, C3-C6 arrangement. Residues involved in HA binding are presented in CPK style as based on the similarity with the mouse sequence (R41, R78, Y79, Y105) (Banerji et al. 2007) Y42 (green) has been implicated in acting as a molecular switch inducing a conformational change upon interaction of R41 with HA to a higher affinity state (Guvench 2015). A solvent-accessible surface view of the same orientation is shown in the middle, and one obtained by rotation of 180° around the vertical axis on the right. The electrostatic potential is represented by red and blue for negative and positive charges, respectively. The position of various residues is indicated by dashed lines with those involved in HA binding highlighted and connected by blue

lines. (B) Prediction of the intrinsic disorder of full-length human CD44 was performed using the IUpred3 (black line) (Dosztányi 2018) (https://iupred.elte.hu/) and NetSurfP-3.0 (red line) (Klausen et al. 2019) (https://biolib.com/dtu/nsp3) algorithms. (C) Putative interactions between the CD44 HA binding domain (blue) and LM v2 LEa2-LEa3 domains are shown for the protein backbones on the left and the corresponding solvent-accessible surfaces on the right. Residues within hydrogen bonding distance between proteins are represented in CPK style, where the apostrophe denotes CD44 residues (R101-G'152, I146-Y'79, C157-S'109, R170-N'110). Simulations were performed using PatchDock (Schneidman-Duhovny et al. 2005) (https://bioinfo3d.cs.tau.ac.il/PatchDock/) and refined with FireDock (Andrusier et al. 2007) (https://bioinfo3d.cs.tau.ac.il/FireDock/). LM y2 LEa2-LEa3 was modelled with SWISS-MODEL (Waterhouse et al. 2018) (https://swissmodel.expasy.org/) using PDB structure 4AQS of the mouse LM β1 LEa1-LEa4 as a template (Carafoli et al. 2012). (D) The protein backbone (left) and the corresponding solvent-accessible surface (right) of the C-terminal region of human LM 511 is shown (PDB code 5XAU, chains A, B, C) (Takizawa et al. 2017). The LM α5 sequence R₂₉₇₁LVSYSGVLFFLK within the LG2 domain corresponding to the mouse peptide A5G27 (R₂₈₉₂LVSYNGIIFFLK) shown to be involved in CD44 binding (Hibino et al. 2004) extends over one β -strand and is depicted in CPK style with the basic terminal residues highlighted in blue. The surface view indicates that further lysine residues (K3009, K3010, K3025) are arranged along a track that could facilitate interactions with GAG chains. Sequence numbering follows UniProtKB/Swiss-Prot data base entries P16070.3 (CD44), Q13753.2 (LM γ2) and O15230.8 (LM α5).

Figure 1



Figure 2



Figure 3



В





