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ISSN: 1040-9238 print / 1549-7798 online DOI: 10.1080/10409230701340019



The Biochemical, Biological, and Pathological Kaleidoscope of Cell Surface Substrates Processed by Matrix Metalloproteinases

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ABSTRACT Matrix metalloproteinases (MMPs) constitute a family of more than 20 endopeptidases. Identification of specific matrix and non-matrix components as MMP substrates showed that, aside from their initial role as extracellular matrix modifiers, MMPs play significant roles in highly complex processes such as the regulation of cell behavior, cell-cell communication, and tumor progression. Thanks to the comprehensive examination of the expanded MMP action radius, the initial view of proteases acting in the soluble phase has evolved into a kaleidoscope of proteolytic reactions connected to the cell surface. Important classes of cell surface molecules include adhesion molecules, mediators of apoptosis, receptors, chemokines, cytokines, growth factors, proteases, intercellular junction proteins, and structural molecules. Proteolysis of cell surface proteins by MMPs may have extremely diverse biological implications, ranging from maturation and activation, to inactivation or degradation of substrates. In this way, modification of membrane-associated proteins by MMPs is crucial for communication between cells and the extracellular milieu, and determines cell fate and the integrity of tissues. Hence, insights into the processing of cell surface proteins by MMPs and the concomitant effects on physiological processes as well as on disease onset and evolution, leads the way to innovative therapeutic approaches for cancer, as well as degenerative and inflammatory diseases.

ectodomain shedding, receptor, membrane, cancer, immunity, autoimmunity

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INTRODUCTION

Matrix metalloproteinases (MMPs) constitute a family of over 20 different endopeptidases characterized by a conserved Zn²⁺-binding motif **H**EXX**H**XXGXX**H** in the catalytic domain and a number of conserved protein domains. The three histidines in this motif are responsible for binding the catalytic Zn²⁺ ion (Figure 1) (Nagase and Woessner, 1999; Brinckerhoff and Matrisian, 2002). Expression of most MMPs is under transcriptional regulation, e.g., by growth factors, hormones, cytokines and oncogenic transformation. MMPs are neutral endopeptidases produced as secreted or membranebound pro-enzymes or zymogens, which become activated by removal of the NH₂-terminal propeptide. The interaction of a conserved cysteine in the propeptide with the catalytic Zn²⁺ ion seals the catalytic site and results in the latency of the pro-enzyme (Figure 1) (Visse and Nagase, 2003). Removal of the propeptide, for example by proteolysis, alters this coordination with Zn²⁺. Due to the subsequent conformational change, the Zn²⁺ ion becomes available for the binding of a hydrolytic water molecule and of the substrate. Therefore, the MMP activation mechanism was named the 'cysteine switch mechanism' (Van Wart and Birkedal-Hansen, 1990). This activation can be mediated by proteases and other MMPs, or chemically by means of organomercurials, urea, some detergents and also by reactive oxygen species. In addition, some MMPs are activated intracellularly by furins (Nagase and Woessner, 1999).

Examples of 'archetypical' MMPs are the collagenases, which are active against fibrillar collagens, and the stromelysins, which cleave non-collagen components of the extracellular matrix (ECM) (Folgueras et al., 2004). They contain a COOH-terminal hemopexin domain

(Figure 1), which contributes to substrate specificity, and to interactions with endogenous inhibitors and cargo receptors (Piccard et al., 2007). This hemopexin domain is absent in the smallest MMPs, the matrilysins. In addition, the gelatinases, active on denaturated collagens, incorporate three fibronectin type II repeats for the binding of gelatin, and MMP-9 is the only MMP to possess a Ser/Thr/Pro-rich O-glycosylated domain, which forms an attachment site for multiple O-linked sugars (Van den Steen et al., 2006). In addition to the secreted MMPs, six human membrane-bound MMPs (MT-MMPs) exist. These are linked to the cell surface through a COOH-terminal transmembrane domain (MT1-, MT2-, MT3- and MT5-MMP) or a glycosyl phosphatidylinositol (GPI) anchor (MT4- and MT6-MMP) (Visse and Nagase, 2003).

Once switched on, MMP proteolytic activity is under tight control by specific inhibitors, primarily the tissue inhibitors of metalloproteinases (TIMPs) (Brew et al., 2000). In plasma, the general protease inhibitor, α_2 -macroglobulin, is the predominant MMP inhibitor (Baker et al., 2002), whereas the TIMPs are considered to be the key inhibitors in tissue. In humans, four different TIMPs (TIMP-1 to -4) have been characterized that form non-covalent 1:1 complexes with MMPs. TIMP-1, TIMP-2, and TIMP-4 are present in the extracellular environment in a soluble form, whereas TIMP-3 is insoluble, sequestered by the ECM (Gomez et al., 1997). Although TIMPs bind tightly to most MMPs, some important differences exist in the inhibition profile (Table 1). For instance, TIMP-1 is known to inhibit most soluble MMPs, but it is a poor inhibitor for MT1-MMP, MT2-MMP, MT3-MMP, MT5-MMP, and MMP-19. Binding affinity to MMP-9 is high for TIMP-1, but low for TIMP-2 and TIMP-3, whereas TIMP-2, TIMP-3, and TIMP-4 bind with high affinity to



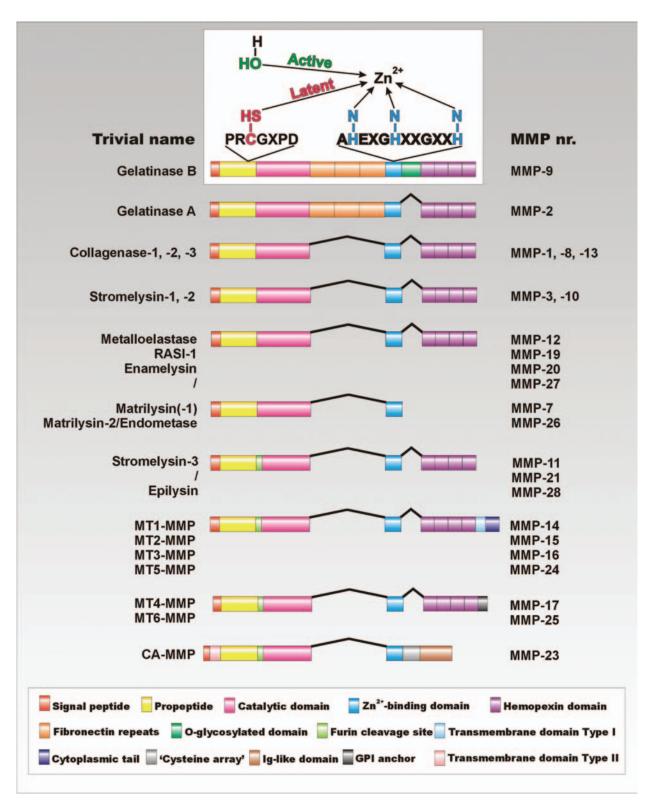


FIGURE 1 Domain structure of the human MMPs. An archetypal MMP contains a signal peptide for secretion, a propeptide, a catalytic domain with a conserved Zn²⁺-binding motif and a COOH-terminal domain. The hemopexin domain is absent in the smallest MMPs, the matrilysins, whereas the gelatinases incorporate three fibronectin type II repeats for the binding of gelatin, and MMP-9 is the only MMP to possess a Ser/Thr/Pro-rich O-glycosylated domain. Some MMPs are attached to the cell surface through a COOH-terminal transmembrane domain or a GPI anchor. The interaction of a conserved cysteine in the propeptide with the catalytic Zn²⁺ ion seals the catalytic site and results in the latency of the pro-enzyme. MMPs are activated according to the 'cysteine switch mechanism' in which removal of the propeptide frees the catalytic Zn²⁺ ion, allowing it to bind a hydrolytic water ion and the substrate. CA-MMP, cysteine array-MMP; GPI, glycosyl phosphatidylinositol; lg, Immunoglobulin; RASI-1, rheumatoid arthritis synovial inflammation-1. Based on (Van den Steen et al., 2002), (Folgueras et al., 2004) and (Nagase et al., 2006).



TABLE 1 TIMP characteristics and inhibition profiles

Localization	TIMP-1 Soluble	TIMP-2 Soluble/cell surface	TIMP-3 ECM	TIMP-4 Soluble/cell surface
MW (kDa) MMPs inhibited	28 Most MMPs, best inhibited:MMP-9	21 Many MMPs, best inhibited: MMP-2	24/27 Many MMPs, best inhibited: MMP-2	22 Many MMPs, best inhibited: MMP-2
MMPs poorly inhibited	MT1-MMP MT2-MMP MT3-MMP MT5-MMP MMP-19	None	None	None
ADAMs inhibited	ADAM-10	None	ADAM-10 ADAM-12 ADAM-17 ADAM-19 ADAMTS-4 ADAMTS-5	none

MMP-2 (Gomez et al., 1997; Nagase et al., 2006). In addition, TIMP-3 inhibits members of the 'a disentegrin and metalloproteinase (ADAM)-family', including ADAM-10/Kuzbanian, ADAM-12, ADAM-17/tumor necrosis factor- α (TNF- α)-converting enzyme (TACE) and ADAM-19, as well as the aggrecan-degrading enzymes 'a disentegrin and metalloproteinase with thrombospondin-like motif' (ADAMTS)-4 ADAMTS-5, and TIMP-1 inhibits ADAM-10 (Baker et al., 2002). As a consequence, the TIMP inhibition profile of a particular cleavage can already shed some light on the identity of the protease in charge.

Thanks to their structural diversity and broad substrate range, MMPs play a part in multiple physiological and pathological processes (Sternlicht and Werb, 2001). As it is more challenging to study membranebound molecules, the initial identification of MMP substrates included mainly soluble proteins. However, due to the fast development and fine-tuning of powerful biochemical techniques, insights into MMP cleavage of membrane-bound substrates grew in parallel with the appreciation of its relative importance in physiology as well as pathology. This review contains a survey of known membrane-bound substrates of every MMP, or more specifically of all proteins with a transmembrane domain that have been shown to be the subject of modification by one or several MMPs. In addition, we will discuss the cleavage of some important cell surface proteins that do not contain a transmembrane domain but are always attached to the cell surface by other means of anchoring. The consequences of proteolysis of cell surface proteins by MMPs will be stressed to generate, from

scattered information, a clear view on the importance of this process. Consequently, the substrates are grouped in functional classes in the context of the physiological or pathological roles they play with or without proteolysis. To facilitate comprehensive reading, all substrate molecules are grouped in a master table which includes the modifying MMPs, the context of cleavage, known cleavage sites, the biological effect of proteolysis and the physiopathological implications (Table 2). In many instances, various names, abbreviations and acronyms have been given to these substrates. For clarity, these are provided once at the beginning of each section (see also the list of abbreviations).

1. PROTEOLYTIC MODIFICATION OF CELL SURFACE PROTEINS IN CANCER **DEVELOPMENT AND EVOLUTION**

Tumorigenesis and cancer progression originate from at least seven fundamental alterations in cellular physiology: 1) production of autocrine growth signals; 2) unsensitivity to growth-inhibitory signals; 3) escape from apoptosis; 4) loss of senescence; 5) sustained angiogenesis; 6) tissue invasion; and 7) metastasis (Hanahan and Weinberg, 2000). MMPs have an impact on the microenvironment of tumors. Moreover, the expression and activity of specific MMPs is elevated in almost every kind of cancer. Some MMPs are synthesized principally by tumor cells (e.g., MMP-7), whereas other MMPs (e.g., MMP-2 and -9) are rather produced by stromal cells in the tumors, like fibroblasts, inflammatory cells, and endothelial cells (Egeblad and Werb,



Substrate ¹	CD ²	MA ³	MMP	Cleavage sites	Substrate modulation ⁴	Effects on physiology/pathology	Reference
pro- $lpha_{ m v}$ - integrin	CD51	TMD	MT1-MMP	Asp891-Leu 892 after Cys852 In vitro	ADHESION Maturation	ADHESION MOLECULES ration Activation of $\alpha_{\rm v}/\beta_{\rm 3}$, leading to increased tumor cell adhesion and migration on vitronectin; Cross-talk between $\alpha_{\rm v}/\beta_{\rm 3}$ and $\alpha_{\rm 2}/\beta_{\rm 1}$ integrins, leading to increased tumor cell adhesion to type I colladen	(Ratnikov <i>et al.</i> , 2002; Deryugina <i>et al.</i> , 2002; Baciu <i>et al.</i> , 2003)
$pro-\alpha_3$ -	CD49c TMD	TMD	MT1-MMP	In vitro	Maturation	ON DESCRIPTION OF THE PROPERTY	(Baciu <i>et al.</i> , 2003)
pro- α_5 -integrin	CD49e TMD	TMD	MT1-MMP	In vitro	Maturation	No influence on $lpha_5eta_1$ integrin function	(Baciu <i>et al.</i> , 2003)
$pro-eta_3$ -integrin	CD61	TMD	MT1-MMP	In vitro	Maturation	Activation of $\alpha_{\rm v}\beta_{\rm 3}$, leading to increased tumor cell adhesion to vitronectin	(Deryugina e <i>t al.</i> , 2000)
$\frac{1}{2}$ pro- β_4 integrin	CD104 TMD	TMD	MMP-7	In vitro	Inactivation	Reduced binding of $lpha_6eta_4$ to laminin, reducing tumor cell adhesion and migration	(von Bredow <i>et al.</i> , 1997; Abdel-Ghany <i>et al.</i> , 2001)
tTG	_	CSL	MT1-MMP MMP-2	Pro375-Val376 Arg458-Ala459 His461-Leu462 <i>In vitro</i>	Degradation	Suppression of tumor cell adhesion and migration on fibronectin; Stimulation of tumor cell migration on collagen matrices	(Belkin <i>et al.</i> , 2001; Belkin <i>et al.</i> , 2004)
			MT2,3-MMP	In vitro	Degradation	ND	(Belkin <i>et al.</i> , 2001; Belkin et al., 2004)
CD44	CD44	DMT	MT1-MMP	Gly192-Tyr193 Gly233-Ser234 (Ser249-Gln250) In vitro + in vivo	Inactivation	Stimulation of tumor cell migration and invasion	(Kajita <i>et al.</i> , 2001; Nakamura et <i>al.</i> , 2004)
			MT2,3,5-MMP	Gly233-Ser234 In vitro	Inactivation	ND (Possible stimulation of tumor cell migration and invasion)	(Suenaga e <i>t al.</i> , 2005)
ICAM-1	CD54	TMD	MMP-9	Between Arg441 and the TMD	Inactivation	Protection of tumor cells against their elimination by cytotoxic T cells and NK cells	(Fiore et al., 2002; Sultan et al., 2004)
L-selectin	CD62L TMD	TMD	MMP-1	In vitro	Q	ND (Possible effect on leukocyte rolling, transendothelial migration, activation and T-cell reentry into the peripheral lymph nodes after activation)	(Preece <i>et al.</i> , 1996)
			MMP-3		SISCHACAN	ACTAINTY SIGNATURE AND SIGNATU	
FasL	CD178 TMD	QM D	MMP-7	Glu110-Leu111 Glu113-Leu114 Ser126-Leu127 Glu142-Leu143 <i>In vitro</i> + <i>in vivo</i>	SEffector* with lower activity**	AFOR 10313 MEDIALORS SEffector* with Apoptosis induction in epithelial cells* but reduced lower apoptosis induction in tumor cells** activity**	(Tanaka <i>et al.</i> , 1998; Powell <i>et al.</i> , 1999; Mitsiades <i>et al.</i> , 2001; Vargo-Gogola <i>et al.</i> , 2002a)



(Ethell <i>et al.</i> , 2002)	(Matsuno <i>et al.</i> , 2001)	(Strand <i>et al.</i> , 2004)	(Overall e <i>t al.</i> , 2004)	(Levi <i>et al.</i> , 1996)	(Codony-Servat <i>et al.</i> , 1999)	(Koolwijk e <i>t al.</i> , 2001;	Andolfo et al., 2002;	D'Alessio e <i>t al.</i> , 2004; Serrati e <i>t al.</i> , 2006)		(Andolfo <i>et al.</i> , 2002)		
a	Reduced intra-articular apoptosis** leading to synovial (proliferation in rheumatoid arthritis	Reduced oligomerization of Fas receptors leading to reduced sensitivity of tumor cells to Fas-mediated apoptosis			Enhanced oncogenic potential including promotion of excessive and autonomous tumor cell growth, increased tumor cell survival, neovascularisation and invasiveness	- Destruction of the binding site for u-PA and vitronectin, (decreasing cell-surface associated u-PA activity (=	inactivation) and reducing tumor-induced angiogenesis + generation of uPAR molecules with chemotactic	activities (= activation) - Destruction of u-PA-dependent invasion, proliferation and morphogenesis of endothelial cells, leading to		<pre>inactivation) and reducing tumor-induced angiogenesis + generation of cell-surface activated uPAR molecules with chemotactic activities (= activation)</pre>	
		Down- regulation	Q	sInhibitor	Potentiation	Inactivation +	Activation			Inactivation + Activation		
In vitro	Glu110-Leu111 Glu113-Leu114 Ser126-Leu127 <i>In vitro</i>	Glu19-Leu20 Asn32-Leu33 <i>In vitro</i>	In vitro	Val368-Met369 In vitro	In vitro	Thr86-Tyr87	In vitro $+ ex vivo$			Thr86-Tyr87 <i>In vitro</i>		Thr86-Tyr87 Tyr87-Ser88 Ser88-Arg89 Arg89-Ser90 In vitro
	MMP-3	MMP-7	MT1-MMP	MMP-2	ND MMP	MMP-12				MMP-3		MT6-MMP
		TMD	TMD	TMD	TMD	GPI						
		CD95	_	CD331 TMD	CD340 TMD	CD87						
		Fas	Death receptor- 6	FGFR-1	HER2	uPAR						



(Continued on next page)

	•						
Substrate ¹	CD ²	MA ³	MMP	Cleavage sites	Substrate modulation ⁴	Effects on physiology/pathology	Reference
			MMP-19	Thr86-Tyr87 Tyr87-Ser88 Arg89-Ser90 In vitro			
			MMP-2,-9 MMP-8,-13 MT1-MMP	In vitro	Q	ND	(Andolfo e <i>t al.</i> , 2002)
Semaphorin 4D	CD100 TMD	TMD	MT1-MMP	In vitro + in vivo	sEffector	Promotion of tumor-induced angiogenesis	(Basile <i>et al.</i> , 2007)
LR	_	DMT QMT	XMMP-11	Ala115-Phe116 Pro133-lle134 <i>In vitro</i>	ND (sEffector)	ND (Possible enhancement of tumor cell invasion and angiogenesis)	(Amano e <i>t al.</i> , 2005b)
XLR	_	DMI	XMMP-11	Ala115-Phe116 Pro133-lle134 <i>In vitro</i> + <i>in vivo</i>	ND (sEffector)	ND (Possible promotion of larval epithelial cell apoptosis needed for intestinal metamorphosis in Xenopus laevis)	(Amano e <i>t al.</i> , 2005a, 2005b)
			MMP-2,-3–9 MT1-MMP	In vitro	ND	ND	(Amano et al., 2005b)
EMMPRIN	CD147 TMD	TMD	MT1-MMP MT2-MMP	Asn98-IIe99 Pro93-Met94	Inactivation + sEffector	Downregulation of cellular EMPRINN functions, possible diffusion and amplification of EMPRINN activities on adjacent or more dictal cells promoting tumor growth	(Egawa e <i>t al.,</i> 2006)
			MMP-1 MMP-2	In vitro	Inactivation + sEffector	augacent of more used cens, promoting turnor growth, metastasis, angiogenesis and multidrug resistance Amplification cascade of MMP activity, leading to enhanced ECM degradation in atherosclerotic plaques, promoting plaque growth and plaque destabilization	(Haug e <i>t al.,</i> 2004)
LRP	CD91	TMD	MT1,2,3,4- MMP	In vitro	Inactivation	Suppression of clearance of ECM-degrading proteases, promoting tissue remodelling by migrating tumor cells	(Rozanov <i>et al.</i> , 2004a)
PAR1	_	TMD	MMP-1	Arg41-Ser42 In vitro + in vivo	Activation	Promotion of cancer cell migration and invasion \pm induction of endothelial cell activation	(Boire <i>et al.</i> , 2005; Pei, 2005; Goerge <i>et al.</i> , 2006)
IL-2R $lpha$	CD25	TMD	MMP-9	In vitro	Inactivation	Reduced proliferation of tumor-infiltrating cytotoxic T cells, leading to tumor immune escape	(Sheu <i>et al.</i> , 2001)
CD14	CD14	GPI	MMP-12	In vitro + in vivo	Inactivation + sEffector	Reduced innate host defence activities such as impairment (Senft et $al.$, 2005) of LPS uptake and reduced LPS-induced TNF- $lpha$ production by alveolar macrophages	(Senft <i>et al.</i> , 2005)
			MMP-1	In vitro	ND CHEN	ND CHEMOKINES	(Bryniarski <i>et al.</i> , 2003)
Fractalkine	_	TMD	MMP-2	In vitro	sEffector + sInhibitor	ND	(Overall and Dean, 2006)

	(Lynch <i>et al.,</i> 2005)	(Hikita <i>et al.</i> , 2006)	(Lynch e <i>t al.</i> , 2005)	(Hikita <i>et al.</i> , 2006)	(Gearing e <i>t al.</i> , 1994;	Gearing <i>et al.</i> , 1995; Chandler e <i>t al.</i> . 1996:	d'Ortho et al., 1997;	English <i>et al.</i> , 2000; Mohan e <i>t al.</i> , 2002)							(Haro <i>et al.</i> , 2000a; Haro	e <i>t al.</i> , 2000b; Mohan e <i>t al.</i> , 2002)	(Churg <i>et al.</i> , 2003)	-	(schonbeck e <i>t al.</i> , 1998)	(Ito <i>et al.</i> , 1996)			∸	Hollenbeck <i>et al., 2</i> 004)
CYTOKINES	Promotion of prostate cancer-induced osteolysis	Downregulation of local osteoclastogenesis and bone resorption	ND	ND	Induction of inflammation in response to bacteria and	pathogen-associated molecular patterns; Excess TNF- $lpha$ in Crohn's disease. multiple sclerosis. rheumatoid	arthritis and septic shock								Induction of MMP-3, leading to spontaneous resorption	of herniated discs	ite cigarette smoke-provoked	Intlammation	Induction of inflammation; Stimulation of tumor invasion (Schonbeck et al., 1998) and angiogenesis	Downregulation of the pro-inflammatory, metastatic and (Ito et al., 1996)	angiogenic effects of active IL-1 eta		Maintenance of leukocyte homeostasis in the blood;	stimulation of proliferation of quiescent smooth muscle cells, leading to intimal hyperplasia
S	sEffector		ND	ND	sEffector													;	Activation	Degradation			sEffector	
	Met145-Met146 <i>In vitro</i> + <i>in vivo</i>		In vitro	Met145-Met146 <i>In vitro</i>	Ala74-Gln75	Ala76-Val77 In vitro			In vitro	Ala74-Gln75	In vitro	Ala76-Val77	before Leu113	In vitro	Ala76-Val77	In vitro + ex vivo	In vitro $+$ in vivo	:	In vitro	In vitro		Glu25-Leu26 <i>In vitro</i>	In vivo	
	MMP-7	MT1-MMP	MMP-3	MT2,3,5-MMP	MMP-1				MMP-2,-3	MMP-9	MT4-MMP	MT1-MMP	MT2-MMP		MMP-7		MMP-12		MIMP-2,-3,-9	MMP-1,-3,-9		MMP-2	MMP-9	
	CD254 TMD				TMD													į	5	S			TMD	
	CD25,				,														_	_			_	
	RANKL				pro-TNF- $lpha$:	pro-IL-1/β	IL-1 eta			KitL	



(Continued on next page)

TABLE 2 Proteolysis of cell surface proteins by MMPs in physiological and pathological processes (Continued)

		3			احدا داره إحدادارها		
Substrate ¹	CD ²	MA ³	MMP	Cleavage sites	Substrate modulation ⁴	Effects on physiology/pathology	Reference
pro-TGF- eta	_	CSL	MMP-2,-3,-9 MT1-MMP	In vitro	Activation GROWT	on Tumor suppression in early stages of tumorigenesis, but stimulation of angiogenesis and metastasis in later stages of cancer development GROWTH FACTORS	(Yu and Stamenkovic, 2000)
HB-EGF	~	Q D D	MMP-7	In vitro + in vivo	sEffector	- Regulation of postpartum - Pathological uterine and mammary vasoconstriction and gland involution and growth of smooth muscle maintenance of lactation cells; Induction of tumor	(Iwamoto and Mekada, 2000; Roelle <i>et al.</i> , 2003; Razandi <i>et al.</i> , 2003; Milenkovic <i>et al.</i> , 2003;
			MMP-2	In vitro + in vivo			Hao et al., 2004; Lucchesi et al., 2004; Ongusaha et al., 2004)
			MMP-9	In vitro + in vivo		 Signal transduction induced by GnRH and estradiol; Proliferation of glia cells in PVR 	
			MMP-3	Glu151-Asn152 In vitro	Caa	- Induction of tumor cell growth and angiogenesis	(Iwamoto and Mekada, 2000; Ongusaha e <i>t al.</i> , 2004)
MT1-MMP	_	TMD	MT1-MMP	Gly284-Gly285 Ala255-lle256 In vitro	Inactivation + mInhibitor	Downregulation of MT1-MMP-mediated promotion of tumor invasion and metastasis	(Toth <i>et al.</i> , 2002)
			MT3-MMP	In vitro	Inactivation	Downregulation of MT1-MMP activity in smooth muscle cells, gliomas or injured blood vessels	(Shofuda <i>et al.</i> , 2001)
ADAMTS-4	_	CSL	MT4-MMP	Lys694-Phe685 Thr581-Phe582 <i>In vitro</i>	sEffector	Degradation of aggrecan in rheumatoid arthritis	(Gao et al., 2002; Gao et al., 2004)
			MMP-9,-13	In vitro	Activation	ND	(Tortorella e <i>t al.</i> , 2005)



	(Steinhusen <i>et al.</i> , 2001; Davies <i>et al.</i> , 2001; Noe	<i>et al.</i> , 2001; McGuire <i>et al.</i> , 2003)	(Lochter <i>et al.</i> , 1997;	Steinhusen e <i>t al.</i> , 2001;	Noe <i>et al.</i> , 2001)	(2005) te te actadivo)			(Covington e <i>t al.</i> , 2006)			(Monea <i>et al.</i> , 2006)	(Ichikawa e <i>t al.</i> , 2006)	(Giebel <i>et al.</i> , 2005)	(Giebel <i>et al.</i> , 2005;	ı Pflugfelder <i>et al.</i> , 2005;	Caron et al., 2005)				(Gurney e <i>t al.</i> , 2006)	(Gorodeski, 2007)	(Gurney et al. 2006)	(Continued on next page)
INTERCELLULAR JUNCTION PROTEINS	Induction of tumor cell invasion and metastasis; rounding (Steinhusen et al., 2001; of apoptotic cells and tumor cells, promoting tumor cell Davies et al., 2001; No	exit from the epithelium; repair of injured lung epithelium	Induction of tumor cell invasion and metastasis;	promotion of epithelial-mesenchymal transition;	rounding of apoptotic cells and tumor cells, promoting	tumor cell exit from the epithelium Dieruption of cell-cell attachments during renal ischemia (Covington et al. 2006)	possibly causing intra-tubular obstructions in acute	renal failure	Disruption of cell-cell attachments during renal ischemia, (Covington et al., 2006)	possibly causing intra-tubular obstructions in acute	renal failure	ND (Possible role in mechanisms of synaptic regulation)	Acceleration of endothelial cell proliferation	BRB disruption leading to retinal edema in PDR	BRB disruption leading to retinal edema in PDR \pm	disruption of corneal epithelial barrier function, causing	ocular irritation and visual morbidity in KS	Disruption of endothelial tight junctions during renal	ischemia and possible degradation of the vascular	basement membrane, leading to acute renal failure	BBB disruption in neuroinflammation	Estrogen-mediated increase of paracellular permeability in vaginal-cervical epithelia	RBB distinction in notion	
INTERCELLULAF	sInhibitor		sInhibitor			Degradation			Degradation			ND	ND	Degradation	Degradation					-	Degradation	Degradation	Degradation	
	In vitro + in vivo		In vitro			ortiv al			In vitro			In vitro	In vitro	In vitro	In vitro $+$ in vivo						In vitro $+$ in vivo	In vitro	oviv ai + ortiv al	
	MMP-7		MMP-3			MT1_MMD			MT1-MMP			MT5-MMP	MMP-7	MMP-2	MMP-9						MMP-3	MMP-7	MMP-3	
	CD324 TMD								CD325 TMD				VE-cadherin CD144 TMD										ΣΙ	
	E-cadherin								N-cadherin				VE-cadherin	Occludin									Clandin-5	



TABLE 2 Proteolysis of cell surface proteins by MMPs in physiological and pathological processes (Continued)

Substrate ¹	CD ²	MA ³	MMP	Cleavage sites	Substrate modulation ⁴	Effects on physiology/pathology	Reference
Betaglycan	_	D TWD	MT1-MMP MT3-MMP	In vitro	STRUCTUR sInhibitor	STRUCTURAL PROTEINS bitor Inhibition of TGF- eta -induced tumor angiogenesis	(Velasco-Loyden et al., 2004; Bandyopadhyay et al., 2005)
MUC1	CD227	CD227 TMD	MT1-MMP	In vitro	QN	Possible role in the defense of epithelial surfaces like uterine, lung and intestinal epithelia; Possible influence on tumor cell proliferation, metastasis and immune evasion	(Thathiah and Carson, 2004)
Syndecan-1	CD138	CD138 TMD	MT1,3-MMP	Gly245-Leu246 In vitro	Inactivation	Enhanced tumor cell migration on collagen	(Endo <i>et al.</i> , 2003)
			MMP-7	In vitro + in vivo	sEffector	Release of a syndecan-1/KC complex from the mucosal surface of injured lungs, forming a chemokine gradient that directs neutrophils to the site of injury	(Li <i>et al.</i> , 2002)
			MMP-9	In vitro	Inactivation	ND	(Brule e <i>t al.</i> , 2006)
Syndecan-3	_	TMD	ND MMP	In vitro + In vivo	Inactivation	Abrogation of Schwann cell adhesion to $\alpha 4 (V)$ collagen <i>in</i> (Asundi <i>et al.</i> , 2003) <i>vitro</i> and in the peripheral nerve tissue of newborn rats during the myelin-forming process in Schwann cells	(Asundi <i>et al.</i> , 2003)
Syndecan-4	/	TMD	MMP-9	In vitro	Inactivation	ND	(Brule <i>et al.</i> , 2006)
BP180	_	TMD	MMP-9	In vitro	Degradation	Disruption of BP180-mediated anchoring of dermis and epidermis (in vitro), possibly leading to blister formation in BP	(Liu e <i>t al.</i> , 1998)
MBP	_	≧	MMP-9	Phe90-Lys91 Ser110-Leu111 Phe114-Ser115 Asp133-Tyr134	Degradation	Demyelination and generation of encephalitogenic peptides, causing neuroinflammation in multiple sclerosis	(Proost <i>et al.,</i> 1993; Chandler <i>et al.,</i> 1995; Asahi e <i>t al.,</i> 2001)
			MMP-1,-2,-3 MMP-7,-12	In vitro	Degradation	ND	(Chandler e <i>t al.</i> , 1995; Chandler e <i>t al.</i> , 1996)
NG2 proteo- / glycan		M D M	MMP-9	In vitro + in vivo	Degradation	Removal of NG2 proteoglycan-mediated inhibition of oligodendrocyte maturation and differentiation, thus promoting remyelination after CNS injury	(Larsen et al., 2003)



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eta dystrogly- / can	TMD	MMP-2,-9	In vitro $+$ in vivo	Degradation	BBB breakdown, CNS infiltration by leukocytes and development of multiple sclerosis disease symptoms	(Agrawal et al., 2006)
`	TMD	MMP-2	Lys687-Leu688* Glu668-Val669** <i>In vitro</i>	sEffector	Release of sAPP α^* , preventing A β formation in Alzheimer's disease; or release of sAPP β^{**} , promoting A β formation; inhibition of MMP-2 by sAPP	(Miyazaki <i>et al.</i> , 1993, 1994; LePage <i>et al.</i> , 1995)
		MMP-3	Glu668-Val669 Glu674-Phe675 <i>In vit</i> ro	ND	ND	(Rapala-Kozik <i>et al.</i> , 1998)
		MT1-MMP	Asn579-Met580# In vitro	sEffector	Release of sAPPtrc#, which displaces the MMP-2 inhibitory (Higashi and Miyazaki, activity of APP or sAPP, promoting MMP-2-catalyzed 2003b) ECM degradation and tumor cell migration; or release of sAPP $\alpha^{\#\#}$, reducing A β formation in Alzheimer's disease	(Higashi and Miyazaki, 2003b)
		MT3-MMP	Ala463-Met464 Asn579-Met580# His622-Ser623 His685-GIn686##	sEffector		(Ahmad e <i>t al.</i> , 2006)
Soluble A eta /	S	MT5-MMP MMP-3	ND <i>In vitro</i> In vitro	ND Degradation	ND Possible reduction of the accumulation of extracellular $A\beta$ (White et al., 2006) peptides in toxic amyloid plaques during Alzheimer's disease	(Ahmad <i>et al.</i> , 2006) (White <i>et al.</i> , 2006)
		MMP-2	Lys16-Leu17 Leu34-Met35 Met35-Val36		מואכמאס	(Roher <i>et al.</i> , 1994; White <i>et al.</i> , 2006; Yin <i>et al.</i> , 2006)
		MMP-9	Lys16-Leu17 Phe20-Ala21 Asp23-Val24 Ala30-Ile31 Gly33-Leu34 Leu34-Met35			(Backstrom e <i>t al.</i> , 1996; Yan e <i>t al.</i> , 2006; Yin et al., 2006)
A eta fibrils /	S	MMP-2,-9	<i>In vitro</i> + <i>in vivo</i> Phe20-Ala21 Ala30-lle31 <i>In vitro</i>	Degradation	Degradation of $A\beta$ fibrils in amyloid plaques, possibly contributing to the clearance of plaques from Alzheimer's diseased brains	(Yan et al., 2006)

Aβ, β-amyloid protein; APP, amyloid precursor protein; BBB, blood-brain barrier; BP, bullous pemphigoid; BRB, blood-retinal barrier; CNS, central nervous system; GnRH, gonadotropin-releasing hormone; KS, keratitis sicca; PDR, proliferative diabetic retinopathy; PVR, proliferative vitreoretinopathy; X, Xenopus. ¹Substrate: for the meaning of the acronyms, see the list of abbreviations.



²CD: Cluster of differentiation of human (glyco)proteins.

³MA: type of cell membrane association: TMD, transmembrane domain; CSL, cell surface localization; GPI, glycosyl phosphatidylinositol anchor; S, soluble; IM, integral membrane protein.
⁴Substrate modulation: mlnhibitor, membrane-bound inhibitor; slnhibitor, release of soluble inhibitor, release of soluble offector, ND, not defined.

2002). In earlier studies, the MMPs were claimed to be important in migration, invasion and metastasis mainly by the degradation of basement membranes and structural components in the ECM. However, more recent findings show that proteolysis of a panacea of essential secreted and membrane-bound molecules, like growth factor precursors and receptors, tyrosine kinase receptors (TKRs), cytokines and chemokines, cell adhesion molecules, and other proteases, modifies the tumor microenvironment. These modifications will affect tumor progression at all levels (Nelson et al., 2000; McCawley and Matrisian, 2001). In this first part we will discuss proteolytic modifications of cell surface proteins by MMPs and their concomitant effects on cancer evolution (see Figure 2). Insight into the paradoxical consequences of proteolysis of cell surface proteins by MMPs might be of paramount importance in the design of new cancer therapies based on MMP inhibition.

1.1 Promotion or Inhibition of Cancer **Cell Proliferation**

MMPs stimulate tumor cell proliferation by catalysing the release of growth factors from the ECM, by the activation of membrane-bound growth factor receptors or by cleavage of membrane-bound substrates, e.g., integrins, that assist in the induction of cell proliferation. Conversely, MMPs might also negatively regulate cancer-cell growth by releasing pro-apoptotic molecules like Fas ligand (FasL) and TNF- α , or by activating transforming growth factor- β (TGF- β), which has a tumor suppressing effect in early phases of oncogenesis (Egeblad and Werb, 2002).

1.1.1 Fibroblast Growth Factor Receptor-1 (FGFR-1)

The fibroblast growth factors (FGFs) constitute a family of twenty structurally related polypeptides with a common high affinity to heparin. Their biological functions are broad and range from the induction of cellular proliferation to tissue regeneration, neurite outgrowth, and angiogenesis (Powers et al., 2000). FGFs elicit their biological response by binding to four different cell surface TKRs, which are typically composed of an extracellular part with three immunoglobulin (Ig)-like domains, a single transmembrane domain and a bipartite TKR domain. Regulation of FGF biological activity may be achieved through several mechanisms, including binding to high and low affinity receptors on the cell surface, release of FGF from the ECM by heparanases or other proteases or binding to a carrier protein that can deliver FGFs to their receptors. In addition, FGF activity might be regulated by the release of the entire ectodomain of the FGF receptor-1 (FGFR-1, basic fibroblast growth factor receptor-1 (bFGF-R), fms-like tyrosine kinase 2, c-fgr, CD331) into the circulation and the ECM (Levi et al., 1996; Powers et al., 2000). MMP-2 is able to free the entire FGFR-1 ectodomain from an immobilized FGFR1 ectodomain-alkaline phosphatase (FRAP) fusion protein in vitro by hydrolyzing the Val368-Met369 bond, eight amino acids upstream of the transmembrane domain (Figure 3). By this truncation, the ligand binding site is released as a soluble ectodomain retaining its FGF binding ability (Levi et al., 1996). FGFs may stimulate tumor cell growth in at least one of the following ways: 1) by acting as mitogens for the tumor cells themselves; 2) by promoting angiogenesis for the growing tumor and 3) by inhibiting apoptosis and allowing tumor cells to keep growing beyond normal constraints (Powers et al., 2000). In this regard, release of the FGFR-1 ectodomain by MMP-2 would counter these mechanisms in two ways. On the one hand, the released FGFR-1 ectodomain might bind extracellular FGF and in this manner diminish the biological availability and growth promoting activity of FGF. On the other hand, treatment of FGFR-1 overexpressing cells with MMP-2 clearly reduces binding of the FGF mitogen (Levi et al., 1996). Thus, investigating the release of the FGFR-1 ectodomain by MMP-2 or by related MMPs in vivo may provide new insights in tumor cell growth inhibition.

1.1.2 Heparin-Binding Epidermal Growth Factor-Like Growth Factor (HB-EGF)

The heparin-binding epidermal growth factor (EGF)like growth factor (HB-EGF, also called diphtheria toxin receptor [DT-R]) is a member of the EGF family of growth factors, which encompasses the receptor family of a number of structurally homologous mitogens like EGF, transforming growth factor- α (TGF- α) and amphiregulin (AR) (Raab and Klagsbrun, 1997; Iwamoto and Mekada, 2000). HB-EGF binds to the EGF receptor (EGFR/HER1/ErbB1) as well as to HER4/ErbB4, inducing homo- or heterodimerisation of the monomeric receptors with consequent tyrosine phosphorylation in the cytoplasmic domains, resulting in the activation of several signal tranduction pathways (Zwick et al., 1999; Herbst, 2004). HB-EGF is synthesized as a transmembrane protein (mHB-EGF) with the ectodomain



to survive and proliferate. Formation of new vessels is crucial for the survival of a growing tumor. Cleavage of proteins on the endothelial cell membranes by MMPs may have a growth factor receptors may amplify the promotion of cell proliferation (HER2) or on the contrary release a soluble decoy receptor that binds soluble growth factors, thus decreasing pro-angiogenic (VE-cadherin, PAR1) as well as an anti-angiogenic effect (uPAR, Betaglycan). Furthermore, alternation of adhesion and anti-adhesion is required as the cell migrates their binding to intact growth-promoting receptors (FGFR-1). Proteolysis of FasL and Fas disturbs trimerization, which attenuates apoptosis induction, allowing the tumor cells receptors (PAR1, EMMPRIN, LRP) and structural proteins (syndecan-1, APP). Many of these cleavages are mediated by MT1-MMP, which colocalizes with CD44 at the ruffling edge of migrating tumor cells. CD44 forms a platform to cluster MMPs, which stimulate migration by cleaving substrates on the cell surface and by degrading the ECM. Finally, cleavage of FIGURE 2 Proteolytic modification of cell surface proteins by MMPs in cancer development and evolution. All cell surface-associated molecules cleaved by MMPs during cancer development are presented on the cell membrane of a migrating tumor cell. These susbstrates are grouped according to the most affected cancer mechanism. Ectodomain cleavage of during the processes of invasion and metastasis. MMPs promote metastasis by proteolysis of adhesion molecules (integrin precursors, tTG, CD44, E-cadherin), cytokines (RANKL), the transmembrane proteins, IL-2Rlpha and ICAM-1 on transformed leukocytes, allows tumor cells to escape assaults from the immune system. Arrows indicate cleavages by MMPs. For details of the substrate acronyms, see the list of abbreviations.

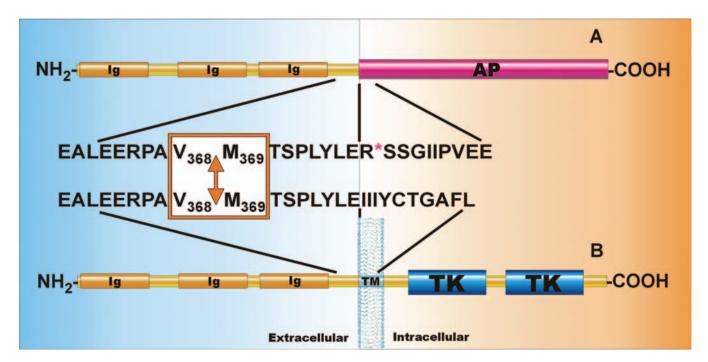


FIGURE 3 Cleavage of the human FGFR-1 ectodomain-AP fusion protein by MMP-2 and comparison with murine FGFR-1. MMP-2 cleaves the FGFR-1 ectodomain from an immobilized FGFR1 ectodomain-alkaline phosphatase (FRAP) fusion protein in vitro at the Val368-Met369 bond, eight amino acids upstream of the transmembrane domain (A). This truncation releases a soluble ectodomain that retains FGF binding ability, thus decreasing FGF binding sites on the tumor cell and competing with the remaining intact FGFR-1. Murine FGFR-1 is shown for comparison (B). Arrow, cleavage site of MMP-2; AP, alkaline phosphatase; Ig, immunoglobulin domain; TK, tyrosine kinase domain; TM, transmembrane domain; R*, start of the AP. Adapted from (Levi et al., 1996).

containing a heparin-binding and an EGF-like domain. mHB-EGF can be cleaved at the plasma membrane to vield soluble HB-EGF (sHB-EGF) (Raab and Klagsbrun, 1997; Iwamoto and Mekada, 2000). mHB-EGF is not only a precursor for sHB-EGF but is a bioactive molecule itself, which inhibits growth of neighboring cells. As a contrast, sHB-EGF is a potent mitogen for a number of cells including smooth muscle cells, epithelial cells and keratinocytes. Therefore, release of HB-EGF causes the conversion of a juxtacrine growth inhibitor into a paracrine/autocrine growth factor, with an opposite impact on cell growth (Iwamoto and Mekada, 2000; Higashiyama, 2004). mHB-EGF proteolysis is probably mediated by metalloproteinases as it is prevented by the broad spectrum metalloproteinase inhibitor batimastat (Prenzel et al., 1999). In cell cultures, MMP-3 cleaves mHB-EGF in the juxtamembrane domain at the Glu151-Asn152 site (Suzuki et al., 1997; Wu et al., 2004), whereas MMP-7, MMP-2 and MMP-9 and some proteases of the ADAM family [ADAM-9, ADAM-10, ADAM-12, and ADAM-17/TACE] mediate mHB-EGF cleavage in vivo under specific circumstances (Higashiyama, 2004; Hao et al., 2004).

HB-EGF plays an important role in a multitude of biological processes and diseases. According to the concerned process, the mHB-EGF proteolysis is induced by varying stimuli and mediated by different metalloproteinases. Release of sHB-EGF allows cross-talking between G protein-coupled receptors (GPCRs) and TKRs in accordance with the triple membrane-passing signal mechanism (TMPS) for the transactivation of TKRs (Figure 4). In the TMPS, GPCRs are activated by an extracellular ligand and subsequently induce the activation of metalloproteinases through the initiation of several signaling cascades. Finally, metalloproteinase activity releases sHB-EGF that activates its TKR, the EGFR (Higashiyama, 2004; Shah and Catt, 2004a). Several studies showed enhanced HB-EGF gene expression in tumors compared to normal tissue (Raab and Klagsbrun, 1997). sHB-EGF expression increased tumor growth rate, colony-forming ability, and activation of the cyclin D1 promotor, as well as induction of vascular endothelial growth factor (VEGF) in vitro. In addition, sHB-EGF induced the expression and activity of MMP-3 and MMP-9, leading to enhanced cell migration. In vivo sHB-EGF enhanced tumorigenesis and angiogenesis. Hence, release of sHB-EGF by MMPs may be an interesting step for therapeutical intervention (Ongusaha et al., 2004; Miyamoto et al., 2004).



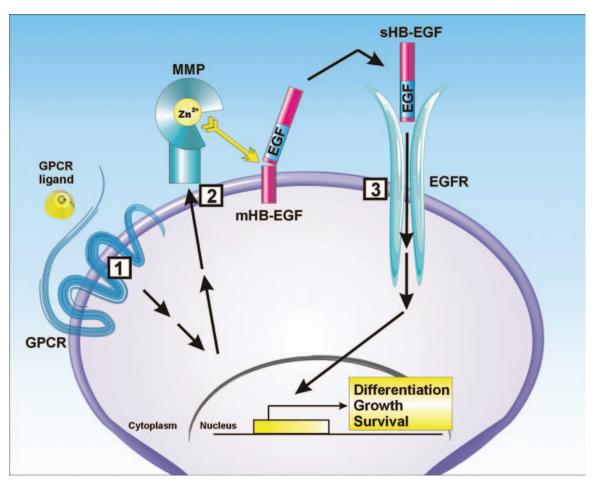


FIGURE 4 Release of sHB-EGF by MMPs allows cross-talking between G protein-coupled receptors (GPCRs) and tyrosine kinase receptors (TKRs) in accordance with the triple membrane-passing signal mechanism (TMPS). In the TMPS, GPCRs are first activated by an extracellular ligand (1) and subsequently induce the production of metalloproteinases through the initiation of several signaling cascades (2). Finally, metalloproteinase activity releases sHB-EGF that activates its TKR, the EGFR, which induces signal transduction to stimulate cell differentiation, growth and survival (3). Arrow, cleavage by an MMP. Adapted from (Shah and Catt, 2004a).

Besides stimulating tumor cell proliferation, sHB-EGF induces proliferation of Müller glial cells, which is a common feature of several diseases of the sensory retina. During proliferative vitreoretinopathy (PVR), Müller cells proliferate continuously, migrate onto retinal surfaces, and participate in the formation of periretinal cellular membranes (Rentsch, 1973; Bringmann and Reichenbach, 2001). Proliferation of Müller cells in PVR seems to be stimulated by binding of ATP to P2Y purine receptors (GPCRs) and requires the transactivation of two TKRs. Activation of P2Y receptors by ATP leads to an increase in intracellular Ca²⁺ concentration and may cause a release of platelet-derived growth factor (PDGF) from the cells. Released PDGF activates the PDGF- α receptor (1st TKR), which causes MMP-9 production. MMP-9 then releases sHB-EGF, which in turn activates the EGFR (2nd TKR). Finally, the activated EGFRs and PDGF- α receptors induce proliferative ac-

tivity in Müller cells by initiating several kinase signaling pathways. As a neutralizing antibody against MMP-9 reversed the mitogenic effect of ATP, inhibition of MMP-9 in the pathway may be a useful tool to suppress uncontrolled intraocular proliferation in PVR (Milenkovic et al., 2003; Shah and Catt, 2004a).

Besides the stimulating effects on tumor progression and PVR, proteolysis of mHB-EGF by MMPs plays a part in cardiovascular diseases (see Section 2.1.1) and reproductive endocrinology (see Section 5.2), which will be discussed in later chapters.

1.1.3 Tyrosine Kinase-Type Cell Surface Receptor HER2

The EGFR family comprises four TKRs of which tyrosine kinase-type cell surface receptor HER2 (HER2, receptor tyrosine-protein kinase erbB-2, p185erbB2, c-ErbB2, NEU proto-oncogene [neu], MLN 19, CD340)



is the most oncogenic, as it is active in the absence of a stimulating ligand. In addition, HER2 in heterodimeric receptors is highly mitogenic because it decelerates growth factor dissociation from its partner receptor, prolonging the duration of intracellular signaling. In addition, endocytosis of HER2-containing complexes is relatively slow and these complexes tend to recycle back to the cell surface, rather than being degraded in the lysosomes. HER2, a 185 kDa transmembrane glycoprotein receptor, underlies many altered functions of tumor cells, including excessive growth, invasive behavior and attraction of blood vessels (Mosesson and Yarden, 2004). It is overexpressed in 25% to 30% of breast cancers, and it has been associated with high risks of relapse and death (Slamon et al., 1987), although the prognostic value of HER2 has been the matter of some controversy (Ross et al., 2003). Blockage of HER2 with the humanized anti-HER2 monoclonal antibody trastuzumab is an example of successful immunotherapy for HER-2-positive breast cancer patients, as it has been demonstrated to reduce the risk of recurrence by roughly 50% in five randomized clinical trials (Piccart-Gebhart, 2006).

The HER2 ectodomain is released and detected in the serum of cancer patients. High serum levels of HER2 ectodomain correlate with a poor prognosis and decreased responsiveness to therapy in patients with advanced breast cancer. This may be due to the enhanced signaling activity of the remaining cell-associated part of HER2. The cleavage is inhibited by the metalloproteinase inhibitors batimastat and TNF- α protease inhibitor (TAPI), as well as by TIMP-1, which inhibits soluble MMPs (Codony-Servat et al., 1999). In addition, trastuzumab inhibits basal and induced HER2 cleavage, preceding antibody-induced receptor downmodulation (Molina et al., 2001). Further identification of the metalloproteinase in charge could lead to new options for the therapy of patiens with breast cancer and high levels of HER2 shedding, for example by combining MMP inhibition with trastuzumab therapy.

1.2 Survival of Cancer Cells or **Induction of Apoptosis**

Evasion of apoptosis permits survival of tumor cells in spite of genetic instability. Low levels of oxygen and nutrients, host defence against the tumor by the immune system, anti-cancer treatments and local in vivo changes in the ECM with effects on invasion and metastasis alter the protease load in the tumor environment (Reed, 1999). Proteolysis by MMPs can have apoptotic as well as anti-apoptotic effects.

1.2.1 Fas Ligand (FasL)

An important effector in apoptosis is the Fas/FasL system, which is involved in three types of immuneassociated killing: 1) elimination of virally infected cells and tumor cells by cytotoxic T cells (CTLs) and natural killer (NK) cells; 2) maintenance of immune privilege or survival of tumor cells; and 3) regulation of lymphocyte development and maintenance of peripheral immune homeostasis. Fas ligand (FasL, tumor necrosis factor ligand superfamily member 6, CD95 L, apoptosis antigen ligand (APTL), APO-1 L, CD178) is a ~40 kDa type II transmembrane protein of the TNF family of death factors. It is expressed on activated T lymphocytes like CTLs and tumor infiltrating lymphocytes (TILs), on macrophages and NK cells and on cells within immune privileged tissues including the eye, testis, uterus, and placenta (Linkermann et al., 2003). After trimerization FasL induces apoptosis by binding to a trimer of its receptor Fas (tumor necrosis factor receptor superfamily member 6, apoptosis-mediating surface antigen FAS, APO-1, FASLG receptor, CD95). FasL can be released form the cell surface by MMP-3 and MMP-7. However, the effects of soluble FasL (sFasL) on apoptosis and tumor progression seem to vary. Apoptosis may be induced in epithelial cells through cleavage of membrane-bound FasL to functional sFasL by MMP-7. Furthermore, this cleavage turns out to be crucial for apoptosis of prostate epithelium after castration, as prostate involution is significantly reduced in MMP-7 deficient mice (Powell et al., 1999). In contrast with apoptosis induction in epithelial cells, FasL shedding by MMP-7 has an anti-apoptotic effect in tumor cells, protecting them from chemotherapeutic drug toxicity (Mitsiades et al., 2001). This protection of tumor cells may be explained by the fact that the ability of sFasL to induce apoptosis is significantly lower than that of its cell surface precursor (Tanaka et al., 1998). A possible explanation for the paradoxical effects of FasL in both cell types might be the higher sensivity of epithelial cells to apoptotic signals, while FasL confers a kind of immune privilege to tumors by inducing apoptosis in infiltrating lymphocytes. Tumor cells indeed express lower levels of Fas and increased levels of FasL, which allows them to 'counterattack' Fas-bearing immune cells (Kim et al., 2004). Acute overexpression of MMP-7 in vitro



as well as in vivo induces apoptosis, whereas chronic or repeated exposure to MMP-7 can select for tumor cells that are less sensitive to death-inducing stimuli (Fingleton et al., 2001; Vargo-Gogola et al., 2002b). Another potential explanation for the mentioned discrepancies in sFasL activity came up after the identification of novel MMP-7 cleavage sites in murine and human FasL. Mutational analysis showed that MMP-7 cleaves human and murine FasL at an ELAELR sequence, close to the transmembrane domain (Figure 5), followed by a secondary cleavage at the COOH-terminally located SL sites. Strong indications exist that cleavage of human FasL also occurs at another ELR sequence in the trimerization domain. As trimerization of FasL has been shown to be important for its activity, cleavage within the trimerization domain may play a significant role in the regulation of sFasL function, releasing less active FasL. Human sFasL peptides generated after MMP-7 cleavage at ELAELR contain 13 or 16 additional amino acids compared to the peptides formed after proteolysis at the SL site. The entire extracellular portion of FasL was shown to be pro-apoptotic in vitro, whereas sFasL produced by cleavage at the SL site was inactive in the same assay (Hohlbaum et al., 2000). This implies that the amino acid sequence between the SL cleavage site and the transmembrane domain contributes to the pro-apoptotic activity of sFasL. Therefore, truncation at the SL site might release inactive sFasL peptides (Vargo-Gogola et al., 2002a). Differential FasL proteolysis by MMP-7 might thus lead to the release of sFasL molecules with diverse biological activities.

1.2.2 Fas

MMP-7 expression also contributes to another strategy by which tumor cells can resist Fas-induced apoptosis. As a matter of fact, Fas too is cleaved by MMP-7, between Glu19-Leu20 and Asn32-Leu33 (Figure 6) (Strand et al., 2004). These cleavages remove 19 or 32 amino acids from the extracellular NH2-terminus of the Fas molecule and delete part of a domain for self-association termed 'preligand assembly domain' (PLAD). The PLAD domain has been shown to facilitate oligomerization of Fas receptors before ligand binding. Preassembly of Fas receptors might be crucial for the regulation of Fas signaling (Siegel et al., 2000). Fas proteolysis by MMP-7 indeed results in attenuated apoptosis induction (Strand et al., 2004). MMP-7 is produced by the tumor cells themselves at early stages of tumor development. Therefore, the impact of this MMP on apoptosis resistance provides a potential target for new combination therapies in which MMP inhibition may significantly augment the efficacy of conventional chemotherapy (Poulaki et al., 2001).

1.3 Regulation of Angiogenesis

Oxygen and nutrients, provided by the vascular system, are crucial for cell function and survival, obligating virtually all cells in a tissue to reside within 100 μ m of a capillary blood vessel. Consequently, angiogenesis or the formation of new blood vessels, is a prerequisite for the survival of proliferating cells and is the result of subtle and often complex interactions between regulator and effector molecules (Hanahan and Weinberg, 2000; Pepper, 2001; Bergers and Benjamin, 2003).

1.3.1 Urokinase-Type Plasminogen Activator Receptor (uPAR)

The urokinase-type plasminogen activator receptor (uPAR, monocyte activation antigen Mo3, CD87) is a GPI-anchored receptor containing three homologous domains (D1, D2, and D3) (Blasi and Carmeliet, 2002). D1 is involved in the binding of the urokinase-type plasminogen activator (urokinase or u-PA) and enhances the interaction with the ECM by binding the ECM molecule vitronectin. D2 and D3 are also indispensable for high-affinity interactions (Hoyer-Hansen et al., 1997a; Oda et al., 1998). uPAR regulates u-PA activitythe activation of plasminogen to plasmin that degrades fibrin (Blasi and Carmeliet, 2002)-on the cell surface and is also important for the activation of signaling pathways through the interaction with several integrins (Reuning et al., 2003). Besides the membrane-anchored uPAR, a soluble receptor (suPAR) is released after proteolysis of the GPI anchor by cellular phospholipase D (Figure 7) (Wilhelm et al., 1999). Both uPAR and suPAR can be cleaved between the D1 and D2 domain, generating a D1-fragment and a D2D3-fragment (Blasi and Carmeliet, 2002). The D1 domain can be released by proteolytic activity of u-PA, directly or indirectly through activation of plasminogen (Hoyer-Hansen et al., 1997b), or by other proteases such as chymotrypsin and elastase (Ploug and Ellis, 1994). The specificty of the cleaving protease is crucial, as uPAR fragments may or may not be chemotactically active on different cell types in vitro, depending on the presence or



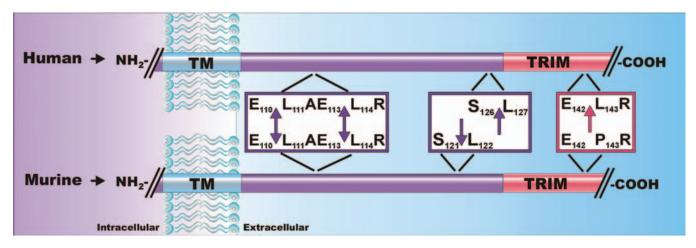


FIGURE 5 Cleavage sites of MMP-7 in the ectodomain of human and murine FasL. MMP-7 cleaves human and murine FasL at an ELAELR sequence, close to the transmembrane domain (TM), followed by a secondary cleavage at COOH-terminally located SL sites. Human sFasL peptides generated after MMP-7 cleavage at ELAELR were shown to be pro-apoptotic in vitro. However, the peptides formed after proteolysis at the S₁₂₆-L₁₂₇ site, which contain 13 or 16 amino acids less, were inactive in the same apoptosis assay. This might mean that the amino acid sequence between the SL cleavage site and the transmembrane domain contributes to the pro-apoptotic activity of sFasL. Cleavage of human FasL almost certainly occurs at an additional ELR sequence, E₁₄₂-L₁₄₃R, in the trimerization domain (TRIM). As trimerization of FasL has been shown to be important for its activity, cleavage within the trimerization domain may release less active FasL. Arrows indicate the cleavage sites of MMP-7. Adapted from (Vargo-Gogola et al., 2002a).

absence of a specific NH₂-terminal peptide, SRSRY, on the D2D3-fragment (Fazioli et al., 1997). Inhibition of MMPs in a three-dimensional fibrin matrix, used as an experimental angiogenesis model, caused enhanced formation of capillary-like tubular structures and showed that the cleavage between D1 and D2 can also be performed by MMPs. The first MMP to be identified as uPAR sheddase was MMP-12 (Koolwijk et al., 2001), but also several other MMPs were able to release the D1 domain of suPAR in vitro: MMP-2, MMP-3, MMP-8, MMP-9, MMP-13, MMP-19, MT1-MMP, and MT6MMP (Andolfo et al., 2002). However, the most efficient MMPs for uPAR cleavage were MMP-3, MMP-12, MMP-19, and MT6-MMP. In particular, MMP-3, MMP-12, and MT6-MMP show the same specificity of cleavage having the Thr86-Tyr87 peptide bond as major cleavage site, while MMP-19 cleaves suPAR predominantly at Tyr87-Ser88 (Figure 7). uPAR cleavage by MMPs results in the exposure of the chemotactic epitope SRSRY at the NH₂-terminus of the generated D2D3-fragment and may thus generate biologically active fragments. Murine uPAR is cleaved by MMP-12

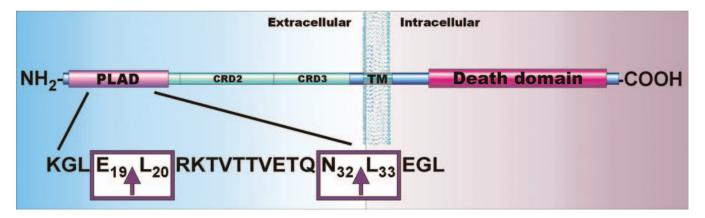


FIGURE 6 MMP-7 cleaves the 'preligand assembly domain' (PLAD) in the Fas ectodomain. Fas is cleaved by MMP-7 between Glu19-Leu20 and Asn32-Leu33. These cleavages remove 19 or 32 amino acids from the Fas NH2-terminus and delete part of a domain for self-association termed 'preligand assembly domain' (PLAD). The PLAD domain facilitates oligomerization of Fas receptors before ligand binding. Preassembly of Fas receptors may be crucial for the regulation of Fas signaling and proteolysis of the PLAD domain by MMP-7 indeed results in decreased sensitivity of tumor cells to Fas-mediated apoptosis. Arrows indicate the cleavage sites of MMP-7; CRD, cysteine-rich domain; TM, transmembrane domain. Adapted from (Strand et al., 2004).



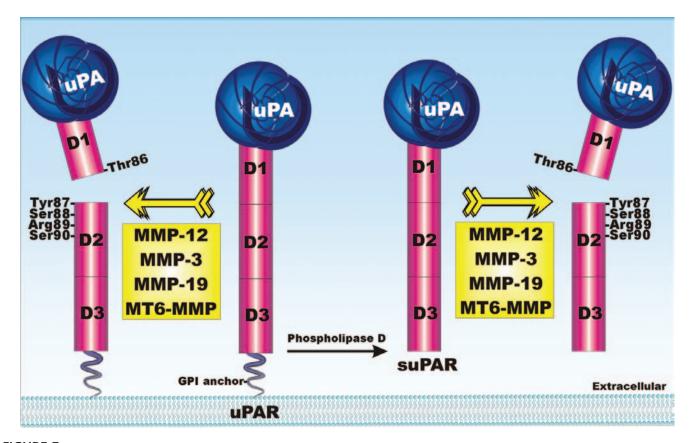


FIGURE 7 Cleavage of uPAR and suPAR by MMPs releases the u-PA-binding domain D1. uPAR is a GPI-anchored receptor for u-PA containing 3 homologous domains (D1, D2, and D3). In addition to the membrane-anchored uPAR, a soluble receptor (suPAR) is released after cleavage of the GPI anchor by cellular phospholipase D. Both uPAR and suPAR can be cleaved between the D1 and D2 domains, generating a D1-fragment and a D2D3-fragment. Release of the D1 domain can be mediated by MMPs, but also by serine proteases such as u-PA, plasmin, chymotrypsin and elastase. The first MMP to be identified as uPAR sheddase was MMP-12 but also several other MMPs release the D1 domain of suPAR in vitro. However, the MMPs most efficient at uPAR cleavage are MMP-3, MMP-12, MMP-19 and MT6-MMP. In particular, MMP-3, MMP-12 and MT6-MMP show the same specificity of cleavage with the Thr86-Tyr87 peptide bond as major cleavage site, whereas MMP-19 cleaves suPAR predominantly at Tyr87-Ser88. Loss of the D1 domain results in less cellular u-PA binding and, consequently, in diminished formation of new capillary structures in an angiogenesis model.

as well (at the Pro89-Gln90 peptide bond), despite the limited sequence homology between the linker regions (Andolfo et al., 2002).

Unexpected enhanced angiogenesis through MMP inhibition might be caused by the higher availability of functional uPAR at the cell surface, resulting in increased u-PA binding and, subsequently, enhanced formation of new capillary structures. As plasmin activates several MMPs (for reviews, see: Collen, 2001; Pepper, 2001; Van den Steen et al., 2001), release of the D1 fragment by an MMP might be a kind of feedback regulation. Since angiogenesis in and growth of some tumors are inhibited by competitors of uPAR, and taking into account that some MMPs (such as MMP-9) exert proangiogenic effects, the influence of MMP inhibition on uPAR levels and on angiogenesis certainly requires further examination.

Cleavage of uPAR by MMP-12 may also play a role in the autoimmune disease systemic sclerosis. This will be detailed in a subsequent paragraph (see Section 3.4.4).

1.3.2 Betaglycan

Betaglycan, also known as the TGF- β type III receptor, is a membrane-anchored proteoglycan whose glycosaminoglycan chains consist of heparan and chondroitin sulfate. Membrane-bound betaglycan is generally considered a positive regulator of TGF- β because it increases the binding affinity of TGF- β for its receptor II, enhancing cell responsiveness to TGF- β (Lopez-Casillas et al., 1994). TGF- β controls many physiological processes and has tumor-suppressing activity in the early phases of carcinogenesis. In subsequent stages of tumor progression, the increased secretion of TGF- β by both tumor cells and stroma cells, is involved in the



enhancement of tumor invasion and mestastasis, accompanied by immunosuppression (Kim et al., 2004). TGF- β upregulates MMP-9 activity, which may also amplify angiogenesis and tumor growth. Additionally, MMP-9 is capable of activating latent TGF- β (Yu and Stamenkovic, 2000; Bandyopadhyay et al., 2005), thanks to the anchoring of MMP-9 and TGF- β to CD44 on the cell surface (see Section 1.4.7) (Yu and Stamenkovic, 1999).

Two soluble forms of betaglycan are relased by proteolytic cleavage. In some cell types these cleavages are induced by the tyrosine phosphatase inhibitor, pervanadate, and generate a bigger fragment of 120 kDa (sBG-120), which encompasses almost the entire extracellular domain, and a smaller 90 kDa fragment (sBG-90). The cleavage that generates sBG-90 is inhibited by TIMP-2, but not by TIMP-1, which points to an MT-MMP as the involved protease. Overexpression of MT1-MMP and MT3-MMP, but not of the other MT-MMPs, indeed releases the sBG-90 fragment. Surprisingly, MT2-MMP overexpression decreases the levels of betaglycan and of MT1-MMP (Velasco-Loyden et al., 2004). In contrast with membrane-bound betaglycan, recombinant soluble betaglycan has been shown to inhibit TGF- β in vitro (Lopez-Casillas et al., 1994). Therefore, betaglycan might function as a dual modulator of TGF- β activity: as a membrane-anchored protein it enhances TGF- β activity, whereas its soluble form causes TGF- β inhibition. TGF-β-promoted tumor-host interactions leading to enhanced angiogenesis have been shown to be effectively attenuated by the systemic administration of soluble betaglycan in a xenograft model of prostate cancer. The inhibition of tumor angiogenesis and consequently of tumor growth appears at least in part due to the inhibition of TGF- β -induced MMP-9 upregulation (Bandyopadhyay et al., 2005). Further investigation will clarify if sBG-90 and sBG-120 have the same TGF- β -inhibiting activities and if proteolysis of betaglycan by MT1-MMP or MT3-MMP can reduce angiogenesis and tumor growth.

1.3.3 Vascular Endothelial Cadherin (VE-Cadherin)

Vascular endothelial-cadherin (VE-cadherin, cadherin-5, 7B4 antigen, CD144) is a member of the large cadherin family that includes Ca²⁺-dependent cell-cell adhesion molecules responsible for cell-to-cell recognition and adhesion in solid tissues. Cadherins dimerize through the extracellular domain with other cadherin

molecules on adjacent cells (trans-interaction). In this homotypic interaction, the intracellular domain interacts with various catenin proteins to form the cytoplasmic cell-adhesion complex (CCC), which is crucial for strong cell-cell adhesion and potent suppression of invasion. Cadherins are expressed in several types of tissues with some specificity: Epithelial (E)-cadherin is mostly present in epithelial cells, Neuronal (N)-cadherin in the nervous system, smooth muscle cells, fibroblasts and endothelial cells, and VE-cadherin is specific for the endothelium (Cavallaro and Christofori, 2004; Cavallaro et al., 2006).

MMP-7 treatment of human umbilical endothelial cells (HUVECs) accelerates HUVEC proliferation and degrades VE-cadherin on the cell surface, with concomitant accumulation of β -catenin in the nucleus and an increase of MMP-7 expression. These results suggest that MMP-7-mediated cleavage of VE-cadherin releases β catenin from the VE-cadherin/catenin complex, allowing it to translocate from the cytoplasm to the nucleus, where it can activate T-cell factor DNA binding protein, which accelerates cell proliferation and MMP-7 expression (Ichikawa et al., 2006). However, MMP-7 also has another important role in angiogenesis as it cleaves plasminogen and converts it to angiostatin (Patterson and Sang, 1997), which is one of the strongest inhibitors of angiogenesis. In light of this, it is crucial to further examine the sometimes paradoxical effects of MMP-7 on angiogenesis before targetting its activity in anti-cancer therapy.

1.3.4 Semaphorin 4D

Semaphorins are secreted, transmembrane or GPIlinked proteins, defined by cysteine-rich semaphorin protein domains, that have essential roles in a variety of tissues. Functionally, semaphorins were initially characterized for their importance in the development of the nervous system and in axonal guidance. More recently, they have been found to play a role in a wide range of processes, including tissue organization during development, angiogenesis, immunoregulation, and tumor progression. A common theme in the mechanisms of semaphorin function is that they alter the cytoskeleton, i.e., the organization of actin filaments and the microtubular network, through binding with their receptors. The best characterized semaphorin receptors are members of the neurophilin and plexin families (Yazdani and Terman, 2006). Plexin-1B is highly expressed in endothelial cells and promotes migration and



tubulogenesis in vitro as well as in vivo when bound by its ligand, semaphorin 4D (BB18, A8, GR3, CD100) (Basile et al., 2004). Semaphorin 4D is highly expressed in head and neck squamous cell carcinomas as well as in some of the most prevalent solid tumors, including breast, prostate, colon and lung cancer tissues (Basile et al., 2006).

In order to exert its pro-angiogenic functions, semaphorin 4D, a transmembrane protein, must be processed and released into a soluble form to act in a paracrine manner on endothelial cells. Semaphorin 4D is expressed on the cell surface as a homodimer (see Figure 2), which is a prerequisite for its proteolytic release from the cell surface (Elhabazi et al., 2001). The shedding process can be inhibited by the metalloproteinase inhibitors EDTA, EGTA and Ilomastat/GM6001, as well as by TIMP-2, but not by TIMP-1 (Elhabazi et al., 2001; Basile et al., 2007). The inhibitor profile, combined with the observation that MT1-MMP, while not expressed in non-tumorigenic epithelial cell lines, was present in several head and neck squamous carcinoma cell lines, pointed to MT1-MMP as the semaphorin 4D sheddase. Basile and coworkers (2007) demonstrated that MT1-MMP was required for processing and release of semaphorin 4D from these cells, thereby inducing endothelial cell chemotaxis in vitro and blood vessel growth in vivo. As a consequence, MT1-MMP-dependent shedding of semaphorin 4D may play a critical role in tumorinduced angiogenesis, and therefore may represent new fronts of attack in the anti-angiogenic therapy of cancer.

1.4 Stimulation or Inhibition of Migration, Invasion, and Metastasis

Much like tumorigenesis, the processes of invasion and metastasis are highly complex. In its simplest form, metastasis requires the tumor cell to detach from its primary location, invade through stromal elements or existing junctions between normal cells, enter and leave blood vessels or lymphatics, and then establish a colony at the metastatic site. These steps require molecular processes at the cell surface in which contacts between the invading tumor cell and surrounding cells and stroma are repeatedly broken (anti-adhesion) and new contacts established as the tumor cell moves forward (adhesion). This alternation of adhesion and anti-adhesion can be achieved through coordinated expression of pro-

teases and adhesion molecules (Chambers et al., 2002; Hollingsworth and Swanson, 2004).

1.4.1 Mucin-1 (MUC1)

Mucin-1 (MUC1, polymorphic epithelial mucin [PEM, PEMT], episialin, tumor-associated mucin, carcinomaassociated mucin, tumor-associated epithelial membrane antigen [EMA], H23AG, peanut-reactive urinary mucin [PUM], breast carcinoma-associated antigen DF3, CD227), a transmembrane mucin, plays a key role in the inhibition of embryo implantation, in the protection of mucosal surfaces against microbial and proteolytic degradation, and in some aspects of tumor progression. It is expressed on several epithelial surfaces like uterine, lung and intestinal epithelia as well as on tumor cells. The relatively short cytoplasmic tail associates with cytoskeletal elements, cytosolic adaptor proteins and/or participates in signal transduction. The extracellular domain can be released form the cell surface, which might serve practical functions, such as the facilitation of rapid clearance of mucosa surface-associated material, or cell mobility. The mechanism controling this ectodomain release has not yet been elucidated, even though it has been postulated that alterations in pH, ionic concentration or hydration might trigger proteolytic release by specific proteases (Hollingsworth and Swanson, 2004). The major protease in this cleavage process is TACE (Thathiah et al., 2003). However, according to the TIMP-inhibition profile (see Table 1), an additional MUC1 shedding activity belonging to the MT-MMP family was identified in TACE deficient cells. MT1-MMP is expressed on these cells and, in addition, MT1-MMP overexpression or deficiency causes increased or inhibited MUC1 shedding, respectively. Furthermore, MT1-MMP indeed cleaves MUC1 in vitro and is colocalized with MUC1 in vivo in human uterine epithelia (Thathiah and Carson, 2004). Cancer cells, especially from adenocarcinomas, express aberrant forms and levels of mucins, which have an impact on the biological properties of tumors in several ways (Hollingsworth and Swanson, 2004). Evidences are emerging that cell surface mucins contribute to the regulation of differentiation and proliferation of tumor cells, through ligand-receptor interactions and morphogenetic signal transduction. In addition, MUC1 expression on tumor cells causes anti-adhesion through steric hindrance by forming multiple exposed glycosylated rod-like structures and by the binding of receptors on the same cell (cis-interactions), preventing



interaction of these receptors with other cells. This antiadhesion permits tumor cells to detach form the tumor mass and to invade the surrounding stroma. Invasion is subsequently enhanced, as MUC1 also has an adhesive action by binding adhesion molecules on stroma cells and endothelial cells (trans-interactions). Finally, MUC1 also contributes to immune evasion by forming a leukocyte-impermeable barrier around the tumor and through immunosuppressive effects on T-cell proliferative responses. Since MT1-MMP is often expressed by cancer cells, the cleavage of MUC1 may affect all these processes.

1.4.2 Epithelial Cadherin (E-Cadherin)

Epithelial cadherin (E-cadherin, uvomorulin, cadherin-1, CAM 120/80, CD324) is another member of the cadherin family and is expressed mostly in epithelial cells (see Section 1.3.3). Loss of E-cadherin-mediated cell-cell adhesion has been shown to be a prerequisite for tumor cell invasion and metastasis (Birchmeier and Behrens, 1994). Proteolytic degradation of E-cadherin by MMPs is one of the regulation mechanisms by which epithelial cell-cell adhesion can be ablated. MMP-3 and MMP-7 both cleave the 120 kDa transmembrane E-cadherin, releasing a 80 kDa soluble form (sE-cadherin) (Lochter et al., 1997; Noe et al., 2001). Treatment of prostate cancer cells with hepatocyte growth factor/scatter factor (HGF/SF) causes shedding of E-cadherin through the induction of MMP-7, resulting in cell scattering and a switch to a more invasive phenotype (Davies et al., 2001). Released sE-cadherin induces invasion in vitro and inhibits cell aggregation indicating that it disturbs cell-bound E-cadherin functions in a paracrine way (Noe et al., 2001). However, it is not clear whether sE-cadherin induces invasion by perturbation of cellcell interaction and/or by engaging a signalling pathway in which free β -catenin can act as a transcriptional coactivator (Hecht and Kemler, 2000). An induction of MMP-2, MMP-9, and MT1-MMP expression was observed both at the mRNA and protein levels in the presence of sE-cadherin. ECM degradation by these MMPs might be an extra mechanism by which E-cadherin ectodomain shedding contributes to tumor invasion and metastasis formation (Nawrocki-Raby et al., 2003). Besides the influence on invasion and metastasis, proteolysis of E-cadherin also plays a role in epithelialmesenchymal transition, a conversion to an altered cellular phenotype which is associated with aggressive malignant behaviour (Cavallaro and Christofori, 2004).

Induction of MMP-3 expression in mammary epithelial cells results in E-cadherin cleavage and triggers a progressive phenotypic conversion cumulating in cells that are unable to undergo lactogenic differentiation and that become invasive (Lochter et al., 1997; Sternlicht et al., 1999). Finally, during apoptosis, the cytoplasmic tail of E-cadherin is truncated by caspase-3, whilst a 84 kDa ectodomain fragment is released by a metalloproteinase. This simultanous cleavage of intracellular and extracellular domains might be a highly efficient mechanism to disrupt E-cadherin-dependent cell-cell contacts in apoptotic cells or tumor cells, which is a prerequisite for cell rounding and exit from the epithelium (Steinhusen et al., 2001).

In acute renal failure, E-cadherin degradation by MT1-MMP leads to disruption of epithelial integrity and epithelial cell shedding (see Section 2.2.3), whereas in normal physiology, MMP-7-mediated shedding of Ecadherin is required for the repair of injured lung epithelium (McGuire et al., 2003).

1.4.3 Integrin Subunit Precursors

Integrins are a diverse family of transmembrane glycoproteins that form heterodimeric receptors for ECM molecules and membrane-associated molecules of the Ig family. Every integrin is composed of a noncovalently coupled α - and β -subunit. The 18 known α -subunits and 8 β -subunits form at least 25 distinct heterodimers in human, with each pair being specific for a unique set of ligands. Integrins are crucial for cell adhesion, migration and invasion, not only through the direct physical adhesion to the ECM and to other cells, but also because they send and receive molecular signals that are essential for these processes (inside-out and outside-in signaling, respectively) (Hood and Cheresh, 2002).

The binding of integrins to ECM molecules is altered by changes in integrin expression and affinity when cancer cells become metastatic, or when endothelial cells enter the angiogenic state (Varner and Cheresh, 1996; Demetriou and Cress, 2004). Maturation of some integrin subunits requires a posttranslational cleavage of the precursor chain. The exact role of this endoproteolytical modification in integrin function is unclear, but its absence has important consequences for signal transduction pathways and leads to alterations in integrin functions such as cell adhesion to vitronectin (Berthet et al., 2000). Proteolysis of pro-integrin chains is performed by proprotein convertases (PC) of the subtilisin/



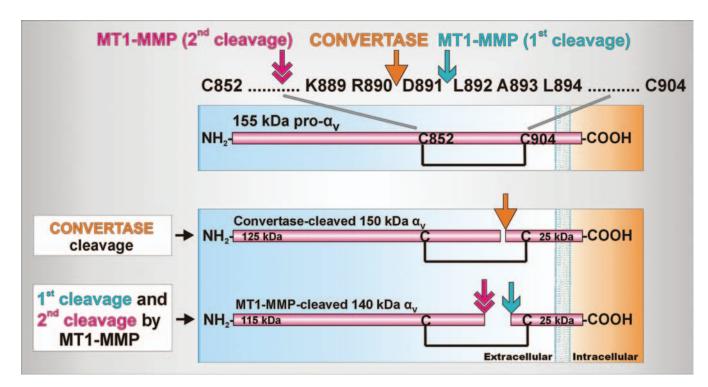


FIGURE 8 Endoproteolytic cleavage of pro- α_v -integrin by MT1-MMP and by a proprotein convertase. Proteolysis of pro-integrin chains is performed by proprotein convertases, but also by MT1-MMP. MT1-MMP cleaves the pro- $\alpha_{
m v}$ chain at two different positions between the disulfide-connected Cys852 and Cys904. The first cleavage, between Asp891 and Leu892, generates a 125 kDa heavy α -chain, disulfidebound to a 25 kDa light chain that is one residu shorter at the N-terminus in comparison with the convertase-processed chain. The second MT1-MMP cleavage removes an additional 10 kDa from the heavy α -chain and is situated downstream from the Cys852. These proteolytic modifications do not affect ligand binding of the resulting $\alpha_{\rm V}\beta_{\rm 3}$ integrin but enhance outside-in signal transduction, which results in more efficient adhesion and migration on vitronectin. Adapted from (Ratnikov et al., 2002).

kexin-like family, but also by MT1-MMP. MT1-MMP cleaves the pro- α_v chain (integrin α -V precursor, vitronectin receptor subunit α , CD51) at two different positions between the disulfide-connected Cys852 and Cys904. The first cleavage, between Asp891 and Leu892, generates the 125 kDa heavy chain, disulfidebound to a 25 kDa light chain that is one residu shorter at the N-terminus in comparison with the PC-processed chain (Figure 8). The putative second MT1-MMP cleavage site is situated downstream from the Cys852 and produces a 115 kDa heavy α -chain (Ratnikov et al., 2002). These proteolytic modifications do not affect ligand binding of the resulting $\alpha_v \beta_3$ integrin but enhance outside-in signal transduction. As a result, cells co-expressing MT1-MMP and $\alpha_v \beta_3$ integrin show more efficient adhesion and migration on vitronectin, the ECM ligand of $\alpha_v \beta_3$ (Deryugina *et al.*, 2002).

In addition, the MT1-MMP-mediated cleavage seems to regulate cross-talk between $\alpha_v \beta_3$ and $\alpha_2 \beta_1$ integrins. In MT1-MMP deficient cells, the functional activity of the collagen-binding $\alpha_2\beta_1$ -integrin, which is not cleaved by MT1-MMP, is suppressed by the presence of $\alpha_v \beta_3$

integrin, resulting in diminished cell adhesion to collagen type I. Co-expression of MT1-MMP and $\alpha_v \beta_3$ restores the $\alpha_2\beta_1$ -mediated collagen binding. Expression of both $\alpha_v \beta_3$ integrin and MT1-MMP is elevated in malignant tumor cells and is correlated with increased migration. Cross-talk between $\alpha_v \beta_3$ and $\alpha_2 \beta_1$ integrins through MT1-MMP-mediated pro- α_v -proteolysis might thus contribute to efficient adhesion of aggressive tumor cells to type I collagen, an important substratum of the ECM (Baciu et al., 2003). In addition, MT1-MMP modifies the β_3 -subunit (integrin β -3 precursor, platelet membrane glycoprotein IIIa (GPIIIa), CD61) of $\alpha_v \beta_3$ integrin from a 95 kDa to a 90 kDa chain, which is also correlated with functional $\alpha_v \beta_3$ integrin activation and increased adhesion on vitronectin (Deryugina et al., 2000). Moreover, after functional activation by MT1-MMP, $\alpha_v \beta_3$ integrin shows a higher affinity for the MMP-2 hemopexin domain, and binding to $\alpha_v \beta_3$ integrin concentrates MMP-2 at specific spots on the cell surface, which may again contribute to cell migration through the ECM. Hence, functional regulation of integrins by MT1-MMP plays an essential role in



efficient adhesion and directional migration of tumor cells. As a consequence, this pathway could be another interesting target in therapeutic approaches aiming at suppressing tumor cell spreading.

MT1-MMP also mediates maturation of the pro- α_3 (integrin α -3 precursor, galactoprotein B3 (GAPB3), VLA-3 α chain, FRP-2, CD49c) and pro- α_5 (integrin α -5 precursor, fibronectin receptor subunit α , integrin α -F, VLA-5, CD49e) chains to the respective mature disulfide-bound heavy and light α -chains (Baciu et al., 2003). However, pro- α_5 cleavage does not affect $\alpha_5\beta_1$ integrin function. The consequences of pro- α_3 cleavage have not been investigated.

MMP-7 is another tumor-derived MMP capable of integrin subunit proteolysis. MMP-7 releases a 90 kDa fragment of the 200 kDa β_4 -subunit precursor (integrin β -4 precursor, GP150, CD104), possibly through cleavage of the Tyr106-Ile107 and Gly416-Leu417 peptide bounds. The first putative cleavage site is very close to the ligand-binding domain, and cleavage might thus interfere with the binding of the $\alpha_6 \beta_4$ integrin to its ligand laminin (von Bredow et al., 1997). $\alpha_6 \beta_4$ integrin has been most implicated in epithelial carcinogenesis (Watt, 2002). In epithelium-derived carcinoma, increased levels of β_4 integrin and loss of its polarized distribution to the basolateral membrane site of the cell have been correlated with tumor aggressiveness (Rigot et al., 1999). Adhesion of breast cancer cells to endothelial cells through binding of $\alpha_6\beta_4$ integrin to a specific lungendothelial cell adhesion molecule is critical for lung metastasis, but is totally abolished after cleavage of the β_4 integrin ectodomain by MMP-7 (Abdel-Ghany *et al.*, 2001). Hence, in this case, MMP-mediated modification of an integrin subunit reduces tumor cell adhesion and migration.

Furthermore, integrins are important players in tumor cell proliferation, apoptosis and angiogenesis, in leukocyte migration and in a whole array of pathologies (Wehrle-Haller and Imhof, 2003). As a consequence, insight in the functional regulation of these bidirectional signaling molecules by MMPs may generate new possibilities for therapeutic intervention.

1.4.4 Tissue Transglutaminase (tTG)

Another adhesion and signaling receptor being cleaved by MT-MMPs is the ubiquitously expressed cell surface-associated tissue transglutaminase (tTG, protein-glutamine γ-glutamyltransferase 2, TGase C (TGC), transglutaminase-2, TGase-H). tTG catalyzes covalent cross-linking between reactive lysine and glutamine residues of proteins and protein polymers. In addition, tTG functions as a coreceptor for β_1 and β_3 integrins and promotes integrin-dependent adhesion and cell spreading on fibronectin. Good functioning of cell surface tTG is essential for regulation and maintenance of cell-matrix interactions, as well as for the mobility of tumor and host cells. On the contrary, deregulation of tTG activity is associated with multiple human diseases (Griffin et al., 2002). Overexpression of MT1-MMP by glioma and fibrosarcoma cells causes proteolytic degradation of tTG at the leading edge of motile cancer cells, leading to specific suppression of cell migration and adhesion on fibronectin (Belkin et al., 2001). 80 kDa tTG degradation is mediated in vitro by MT1-MMP, MT2-MMP, and MT3-MMP, but not MT4-MMP, and produces fragments of \sim 53 kDa, \sim 41 kDa and \sim 32 kDa. MT1-MMP cleavage at Arg458-Ala459 and His461-Leu462 generates the 53 and 32 kDa fragments, while cleavage at Pro375-Val376 splits the protein in half, providing the 41 kDa fragments. Cleavage at any of these three sites abolishes receptor and enzymatic activity by separating the NH₂terminal fibronectin-binding domain and the COOHterminal integrin-binding domain, as well as by inactivation of the catalytic domain. tTG proteolysis suppresses cell adhesion and migration on fibronectin. Reciprocally, fibronectin protects its surface receptor, tTG, from MT1-MMP-mediated proteolysis, thereby supporting cell adhesion and mobility. In contrast, cell migration on collagen matrices is stimulated by tTG degradation. This suggests that the composition of the surrounding ECM might control the proteolysis of adhesion molecules colocalized with MT-MMPs on distinct areas of the cell surface of migrating tumor cells (Belkin et al., 2001).

Additional examination shows that MMP-2 supports its activator MT1-MMP in tTG proteolysis. MMP-2 hydrolyzes cell-associated tTG very efficiently and associates predominantly with the catalytic core domain II of tTG. Furthermore, in silico simulations show that during the tTG-MMP-2 interaction, the catalytic site of MMP-2 is probably in very close proximity of the MMP cleavage sites. tTG, in turn, preferentially associates with the activation intermediate of MMP-2, which reduces MMP-2 activation and protects tTG against MMP-2 proteolysis (Belkin et al., 2004). Hence, MMP-2 is as important as MT1-MMP in the degradation of cell surfacetTG, and the cooperation of both MMPs explains the



extensive tTG proteolysis at the normal tissue/tumor boundary. Loss of adhesive and enzymatic activities of tTG at the interface between normal and tumor tissue will reduce cell-matrix interactions and inhibit matrix cross-linking, which might cause multiple pathological alterations in host cell adhesion and mobility (Belkin et al., 2004).

1.4.5 34/67 kDa Laminin Receptor (LR)

As mentioned before, the regulation of sequential tumor cell adhesion and anti-adhesion to ECM components is crucial in the complex process of tumor invasion and metastasis. Besides the modulation of integrin binding to vitronectin and type I collagen, and of tTG binding to fibronectin, MMPs also intervene in cell adhesion to laminin by modification of a major laminin binding molecule, the 34/67 kDa laminin receptor (LR, 40S ribosomal protein SA, p40, colon carcinoma laminin-binding protein, NEM/1CHD4, multidrug resistance-associated protein, MGr1-Ag). Overexpression of LR is strongly correlated with metastatic and aggressive tumor cell phenotypes (Berno et al., 2005). Using thyroid hormone-dependent Xenopus Laevis metamorphosis as a model, the 37 kDa LR precursor was identified as a potential physiological substrate of Xenopus stromelysin-3 or XMMP-11 (Amano et al., 2005b). The highly conserved 37 kDa protein is the precursor of the receptor but the exact manner by which it configures its mature 67 kDa form is not clear. It was suggested that acylation followed by homo- or heterodimerization of the 37 kDa precursor forms the mature 67 kDa laminin receptor. The heterodimer is likely to be stabilized by strong intramolecular hydrophobic interactions between fatty acids bound to the 37 kDa precursor and to an unknown galectin-3 cross-reacting molecule (Buto et al., 1998). The COOH-terminal twothirds of the LR is located extracellularly and contains a six-amino-acid laminin-binding sequence, whereas the NH₂-terminal third faces the cytoplasm preceded by a short transmembrane domain (see Figure 2). In vitro incubation of Xpro-LR with other (human) MMPs showed that all tested MMPs cleaved LR, with MMP-2 being most efficient, MT1-MMP least efficient, and MMP-3 and MMP-9 cleaving with intermediate efficiencies. However, the cleavage products generated by these MMPs were distinct from those produced by MMP-11. Whereas the cleavage sites of MMP-11, Ala115-Phe116, and Pro133-Ile134, were located between the transmembrane domain and the lamininbinding sequence, cleavage by all other MMPs occurred COOH-terminally of the laminin-binding sequence. As a consequence, only MMP-11 releases LR-fragments that contain the laminin-binding site and may alter cell-laminin interactions. In addition, human LR was cleaved by MMP-11 at the two same sites as in Xenopus LR, which means that LR is a conserved substrate for MMP-11 in vertebrates (Amano et al., 2005b). Further investigation using transgenic tadpoles overexpressing MMP-11 showed that LR is cleaved in vivo by MMP-11 during intestinal metamorphosis (Amano et al., 2005a). Besides its physiological role in Xenopus Laevis development, MMP-11-mediated cleavage of LR is likely to be involved in tumor developement and cancer progression.

MMP-11, similar to LR, is an active partner of invading cancer cells (Rio, 2005). Thus, the coexistence of MMP-11, which is expressed by the fibroblasts within the tumors but not actually by the tumor cells themselves, and LR in tumors may be expected to lead to the cleavage of tumor cell surface LR. This may alter tumor cell-ECM interaction to affect tumor development and cell migration. Peptide G, an LR peptide (residues 161 to 180) containing the laminin-binding sequence (residues 173 to 178) indeed changes the conformation of laminin-1 and increases and stabilizes laminin-1 binding on tumor cells (Magnifico et al., 1996). In addition, peptide G-modified laminin signals tumor cells to change their cytoskeleton to promote motility and invasion. It also induces the expression of a number of proteases characteristic of invasive cancer cells, and leads to increased gelatinolytic activity by MMP-2. Invasiveness of tumor cells conditioned by peptide G-modified laminin was shown to be MMP-2-dependent as it was significantly more inhibited by TIMP-2 than invasiveness induced by native laminin (Berno et al., 2005). Full-length LR shed from malignant cells also induced conformational changes in laminin after binding. In addition, the shed LR modified production of anti-angiogenic angiostatins from plasmin in vitro, in this way promoting tumorassociated neoangiogenesis (Moss et al., 2006). As LRfragments released by MMP-11 contain the lamininbinding site, they might also modulate laminin conformation and enhance tumor cell invasiveness and angiogenesis. Gaining insight into the malignant potential of these soluble LR-fragments may thus be of great interest to elucidate one of the mechanisms that underlies the detrimental effect of MMP-11 in cancer progression.



1.4.6 Syndecan-1, -3, and -4

Syndecans are transmembrane heparan sulfate proteoglycans expressed on all adherent cells (see Figure 2). They are important players in tissue morphogenesis by binding a variety of ECM components such as fibronectin, thrombospondin, various collagens and growth factors via their glycosaminoglycan chains (Beauvais and Rapraeger, 2004). In addition, they can interact with the cytoskeleton through their conserved cytoplasmic domains. Syndecan expression can alter cell adhesion, migration and morphology. The syndecan family is composed of four strongly related proteins (syndecan-1, -2, -3, and -4). The intact ectodomain of each syndecan is constitutively shed from cultured cells as part of normal cell surface heparan sulfate proteoglycan turnover and this process seems to play a role in various pathophysiological events such as host defense, wound healing, arthritis and Alzheimer's disease. How this shedding is regulated remains largely unknown. The ectodomain release of syndecan-1 (CD138) and syndecan-4 (amphiglycan, ryudocan core protein) from NMuMG epithelial and SVEC4-10 endothelial cells is accelerated by various physiological agents activating several intracellular signal transduction pathways. The proteolytic activity responsible for this accelerated shedding is associated with the cell surface and can be specifically inhibited by TIMP-3, pointing to ADAMs as possible mediators (Fitzgerald et al., 2000). However, as will be discussed in a later chapter, secreted MMP-7 also sheds the syndecan-1 ectodomain, releasing a syndecan-1/chemokine KC complex from the mucosal surface of injured lungs, in this way forming a chemokine gradient that directs neutrophils to the site of injury (Li et al., 2002; Shapiro, 2003). HT1080 fibrosarcoma cells also show constitutive shedding of the syndecan-1 ectodomain, but here the shedding activity is inhibited by TIMP-2 and batimastat, but not by TIMP-1. Therefore, the MMP in charge here is not MMP-7, but probably the endogenous MT1-MMP. Recombinant syndecan-1 is cleaved in vitro by MT1-MMP as well as by MT3-MMP preferentially at the Gly245-Leu246 peptide bond (Endo et al., 2003). Syndecan-1 expression is associated with inhibition of invasion and reduced migration of HT1080 fibrosarcoma cells. Treatment of these cells with MMP inhibitors increases cell surface syndecan-1 concentrations concomitant with formation of actin stress fibers, which results in further reduction of migration. In contrast, shedding of the syndecan-1 ectodomain by MT1MMP enhances cell motility on collagen (Endo et al., 2003).

In addition, the shedding of syndecan-4, and to a lesser extent that of syndecan-1, from HeLa cells and human primary macrophages was reported to be accelerated by the chemokine stromal cell-derived factor-1 (SDF-1/CXCL12) and mediated by MMP-9. SDF-1 increases MMP-9 mRNA and MMP-9 activity in HeLa cells, whereas MMP-9 silencing by RNA interference strongly decreases syndecan-1 and syndecan-4 ectodomain shedding accelerated by SDF-1. Shedding of syndecan-4 and syndecan-1 from human primary macrophages is accelerated by SDF-1 as well, and inhibited by anti-MMP-9 antibodies (Brule et al., 2006). As SDF-1 does not bind to soluble syndecan ectodomains, this shedding process by MMP-9 may be part of an autoregulatory/downregulation cycle: (1) SDF-1 binding to syndecan-4 facilitates its presentation to its receptor CXCR4; (2) SDF-1 activates MMP-9, which removes syndecan-1 and -4 from the cell surface; (3) decreased membrane expression of syndecans down-regulates SDF-1 binding to its receptor (Charnaux et al., 2006). In addition, MMP-9 cleaves off the NH2-terminal tetrapeptide of SDF-1, which also results in loss of binding to its receptor CXCR4 (McQuibban et al., 2001). As syndecan-4 promotes cell spreading in a β 1-integrin-dependent fashion (Thodeti et al., 2003), the role played by its MMP-9mediated ectodomain shedding in tumor cell migration and metastasis certainly deserves further investigation. Syndecan shedding has also been observed in physiological systems. *In vitro* release of the syndecan-3 ectodomain from rat Schwann cells, the myelin-forming cells of the peripheral nervous system, is also mediated by an MMP. These Schwann cells transiently express syndecan-3 during embryonic and early postnatal development. Inhibition of syndecan-3 cleavage by several MMP inhibitors such as batimastat/BB-94 and BB-3103 significantly enhances Schwann cell adhesion to the non-collagenous NH₂-terminal domain of $\alpha 4(V)$ collagen, which binds syndecan-3 and mediates heparan sulfate-dependent Schwann cell adhesion. MMPdependent syndecan-3 shedding was also observed in vivo in the peripheral nerve tissue of newborn rats, disappearing on day 10, the end of the myelin-forming process in Schwann cells (Asundi et al., 2003). As a consequence, syndecan ectodomain shedding is cell typespecific and this illustrates the varying physiological roles of these proteoglycans in different tissues. As syndecan ectodomain release has an impact on various



pathophysiological processes, the identification of the proteolytic activity in charge might be of great use in the development of new diagnostic and therapeutic strategies.

1.4.7 CD44

CD44 (phagocytic glycoprotein 1 [PGP-1]), HUTCH-1, ECM receptor-III [ECMR-III], GP90 lymphocyte homing/adhesion receptor, hermes antigen, hyaluronate receptor, heparan sulfate proteoglycan, epican) is a ubiquitous multistructural and multifunctional cell adhesion molecule involved in cell-cell and cellmatrix interactions. This family of glycoproteins consists of many isoforms generated by different use of alternatively spliced exons and extensive glycosylation. The most abundant form is the standard hematopoietic type, CD44H, which does not have any variant insertions (Naor et al., 1997). The ECM adhesion activity of CD44 is located in the NH2-terminal globular domain that forms an important receptor for hyaluronic acid, an abundant glycosaminoglycan that fills interstitial spaces between different tissues and takes part in embryonic development, healing processes, inflammation and tumor development (Toole, 2004). CD44 also binds other ECM components such as type I collagen, fibronectin, fibrin, laminin, and chondroitin sulfate. CD44 has been shown to take part in many important processes such as lymph node homing, T-cell activation, presentation of chemokines and growth factors to traveling cells, wound healing, angiogenesis, metastasis and apoptosis (Naor et al., 1997). The NH2-terminal ligandbinding domain is followed by a stem sequence, a transmembrane domain and a cytoplasmic tail. The cytoplasmic domain interacts with the actin cytoskeleton and is important for the localization of CD44 at the ruffling edge of migrating cells. MT1-MMP is co-expressed with CD44 on migrating cells and metastatic tumor cells (Seiki, 2002; Seiki, 2003; Itoh and Seiki, 2004). MT1-MMP binds the extracellular portion of CD44H by its hemopexin domain. Hence, CD44H has a major role in ECM degradation, as it forms the connection between MT1-MMP and the actin cytoskeleton, and anchors MT1-MMP at the migrating front (Figure 9) (Mori et al., 2002).

MT1-MMP, in turn, acts as a processing enzyme for CD44H, which is critical for the stimulation of cell motility, probably because it allows the cells to detach from the ECM (Kajita et al., 2001). Co-expression of MT1-MMP and CD44H increases shedding of the

commonly produced 65 to 70 kDa fragments of CD44 and generates two additional smaller fragments. Shedding of the 65 to 70 kDa fragments occurs constitutively and is inhibited by TIMP-3, but not by TIMP-1 or TIMP-2, suggesting the proteolytic activity is an ADAM-like protease, although this shedding is increased by MT1-MMP expression. In contrast, release of the two smaller fragments is abolished by TIMP-2 and TIMP-3, but not by TIMP-1, which is the inhibition pattern of MT1-MMP. The cleavage sites (CS) corresponding to the three major fragments are Ser249-Gln250 (CS3) for the big fragment, and Gly192-Tyr193 (CS1) and Gly233-Ser234 (CS2) for the two smaller fragments (Figure 9). These cleavage sites are also detected in vivo. In normal tissues, more clipping of the fragment at CS3 occurs than of those of the other sites, whereas in carcinomas CS1 fragments are significantly increased. Thus, CD44 shedding at CS1 and CS3 represents the normal physiological process, whereas increased shedding at CS1 is associated with malignant tumors (Nakamura et al., 2004).

Whereas MT1-MMPs displays the most potent CD44 H shedding activity, other MT-MMPs such as MT2-, MT3-, and MT5-MMP, but not MT4- and MT6-MMP, can also cleave CD44H in vitro at CS2, while cleavage at CS1 was hardly detectable (Suenaga et al., 2005). The interaction between the hemopexin domain and CD44 H is conserved in each MT-MMP, which suggests that CD44 is more than a receptor for ECM molecules and may also form a platform for the assembly of various MMPs with their substrates, to modulate cell migration (Figure 9) (Seiki, 2002; Suenaga et al., 2005). Like MT1-MMP, MMP-9 binds directly to CD44 (Yu and Stamenkovic, 1999) and activates latent TGF- β , which contributes to tumor-induced angiogenesis (Yu and Stamenkovic, 2000). In contrast, MMP-7 attaches indirectly to the heparan sulfate chains of the CD44 isoform with a variant exon 3, which also binds substrates of MMP-7, namely mHB-EGF and osteopontin (Yu et al., 2002; Seiki, 2002).

Furthermore, proteolysis of CD44 results in signal transduction to the nucleus. Ectodomain shedding of CD44 induces cleavage in the cytoplasmic portion, which releases the intracellular domain, CD44ICD, into the cytoplasm (Figure 9). CD44ICD migrates to the nucleus where it activates transcription mediated through the 12-O-tetradecanoylphorbol 13-acetate (TPA)-responsive element (TRE). One of the potential targets for transcriptional activation by CD44ICD is



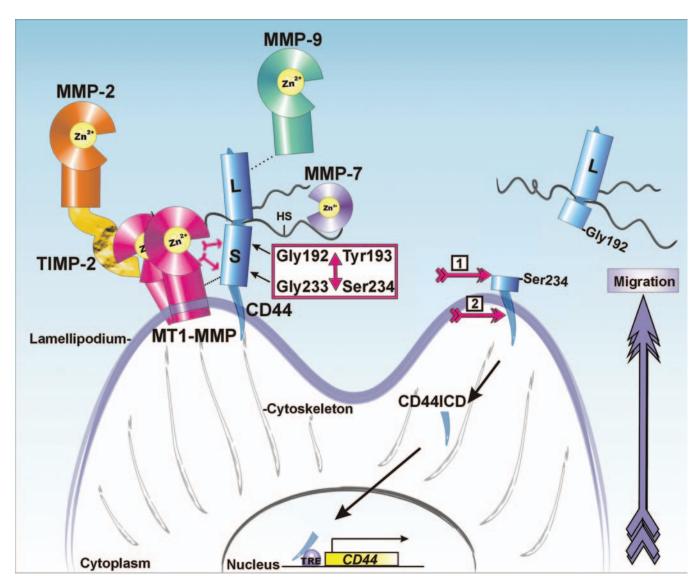


FIGURE 9 CD44 forms a platform for the assembly of various MMPs with their substrates, to modulate cell migration. The extracellular portion of CD44 binds to the MT1-MMP hemopexin domain (thin line), while the CD44 cytoplasmic domain interacts with the actin cytoskeleton, in this way anchoring MT1-MMP on the ruffling edge of migrating tumor cells. MT1-MMP, in turn, acts as a processing enzyme for CD44, which is critical for the stimulation of cell motility, probably because it allows the cells to detach from the ECM. Co-expression of MT1-MMP and CD44 generates two soluble fragments, resulting from proteolysis at Gly192-Tyr193 (CS1) (shown in the figure) and Gly233-Ser234 (CS2) (not shown). Furthermore, ectodomain shedding of CD44 by MT1-MMP (1) induces cleavage in the cytoplasmic portion (2), which releases the intracellular domain, CD44ICD, into the cytoplasm. CD44ICD migrates to the nucleus where it activates transcription mediated through the 12-O-tetradecanoylphorbol 13-acetate (TPA)-responsive element (TRE). One of the genes under control of TRE is the CD44 gene itself, suggesting that CD44 ectodomain cleavage promotes the rapid turnover of CD44 that is required for efficient cell migration. In addition, CD44 acts as a platform to assemble various MMPs with their substrates, clustering proteolytic events that regulate cell migration. MMP-9 also interacts directly with CD44 (dotted line), whereas MMP-7 attaches indirectly to the heparan sulfate chains (HS) of CD44. L, ligand-binding domain; S, stem sequence. Adapted from (Seiki, 2002).

the *CD44* gene itself, suggesting that CD44 ectodomain cleavage and the subsequent intracellular signaling promote the rapid turnover of CD44 that is required for efficient cell migration (Okamoto et al., 2001). As a consequence, disruption of the interaction between MT-MMPs and CD44 might be another strategy to inhibit metastasis of malignant tumors (Peterson et al., 2000; Ueda et al., 2003).

1.4.8 Extracellular Matrix Metalloproteinase Inducer (EMMPRIN)

A search for MMP inducing factors in tumor cells led to the identification of EMMPRIN (Extracellular matrix metalloproteinase inducer) with the numerous synonyms: basigin, leukocyte activation antigen M6 (M6), tumor cell-derived collagenase stimulatory factor (TCSF), neurothelin, OK blood group antigen, OX-47,



gp42, CE9, 5A11, 5F7, HT7, and CD147. EMMPRIN is composed of two Ig domains in the extracellular region, a single transmembrane domain and a short cytoplasmic domain containing 39 amino acids (see Figure 2). It is a highly glycosylated cell surface protein, with the different glycosylation patterns of the 28 kDa native protein accounting for a variable molecular weight, ranging between 44 and 66 kDa. Depending on the cell system, EMMPRIN can stimulate production of MMP-1, -2, -3, -9, MT1-MMP, and MT2-MMP, and only glycosylated EMMPRIN is able to induce these MMPs. The NH₂terminal Ig domain is required for the MMP induction, but also for the formation of homo-oligomers in a cisdependent manner in the plama membrane. The MMPinducing function of EMMPRIN in part involves the molecule acting as a counter-receptor for itself, also requiring the NH2-terminal Ig domain, but in this case the interaction is in a trans manner (Gabison et al., 2005; Yan et al., 2005).

EMMPRIN can be released from the cell surface in at least two different ways. A significant amount is released via vesicular shedding, whereby EMMPRIN is initially associated with microvesicles which are quickly degraded upon release from the cells to discharge full-length soluble EMMPRIN. The other pathway is MMP-dependent proteolytic shedding (Gabison et al., 2005). In addition to inducing MMPs, EMMPRIN is cleaved and shed by MMPs or other MPs, because this shedding is inhibited by Zn²⁺ chelators (EDTA and 1,10-phenanthroline) and by the broad-spectrum MMP inhibitor GM6001 (Tang et al., 2004; Haug et al., 2004). In addition, MMP-1 and MMP-2 cleave EMMPRIN at the membrane-proximal region in vitro (Haug et al., 2004). Besides release of the intact form, a new EMM-PRIN fragment of 22 kDa was identified in the culture media of two tumor cell lines (HT1080 and A431), the shedding of which was enhanced by phorbol 12myristate 13-acetate (PMA) while that of the intact form was not (Egawa et al., 2006). The EMMPRIN sheddase was hypothesized to be of the MT-MMP family, in view of its expression and inhibition profiles. In addition, HT1080 and A431 cells express MT1-MMP and EMM-PRIN was co-purified from cell lysates with MT1-MMP. Knockdown of MT1-MMP with siRNA indeed inhibited the shedding substantially, although MT2-MMP may also contribute to the shedding because knockdown of both MT1- and MT2-MMP produced slightly greater inhibition. The COOH-terminal amino acid of the 22 kDa fragment was identified as Asn98, and MT1MMP also cleaved at this site in an *in vitro* digestion. Although an additional cleavage site, between Pro93 and Met94, was observed after in vitro incubation with MT1-MMP, the corresponding fragment was not identified in cell culture media (Egawa et al., 2006). The Asn98-Ile99 cleavage site is located in the linker sequence connecting the two Ig-like domains (see Figure 2), which means that the 22 kDa fragment contains the NH₂terminal Ig domain that is crucial for MMP induction and homophilic interactions. The purified 22 kDa fragment indeed retained MMP-inducing activity. Thus, the shedding may down-regulate the cellular functions mediated by EMMPRIN, because MT1-MMP cleaves off the essential distal Ig domain. This regulation may be particularly important at the ruffling edge of migrating tumor cells, as both proteins co-localize there (Egawa et al., 2006). At the same time, the released soluble 22 kDa active fragment may act on cells either in the local tumor environment or diffuse away to act on distant cells to further stimulate MMP and EMPRINN expression and augment the migration and invasion potential of tumor cells.

The pathologic consequences of elevated EMMPRIN expression in tumor growth and metastasis were directly demonstrated using EMMPRIN-overexpressing cancer cells. MDA-MB-436 human breast cancer cells are normally slow-growing cells when they are implanted into nude mice. However, after EMMPRIN gene transfection, these cells adopted a more aggressive phenotype, exhibiting both accelerated growth and increased invasiveness, and increased MMP-2 and MMP-9 expression (Zucker et al., 2001). In addition to stimulating MMP production, EMMPRIN also binds MMP-1 and retains it at the cell surface, an arrangement that may promote turnover of pericellular collagen, thereby also facilitating migration and metastasis. The role of EMMPRIN in tumor cell invasion was confirmed, as EMMPRIN function-blocking antibodies inhibited invasion through a reconstituted basement membrane. Besides its role in the stimulation of invasion, migration and metastasis, EMMPRIN induces angiogenesis via stimulation of VEGF production and multidrug resistance via upregulation of HER2-signaling and cell survival pathway activities (Gabison et al., 2005; Yan et al., 2005). Targeting the release of soluble EMM-PRIN molecules by MMPs, may thus be of great interest to limit the expansion and migration of the tumor by restricting the diffusion of malignant EMMPRIN actions.



RIGHTSLINK

Besides the elevated EMMPRIN expression on tumor cells, EMMPRIN was also shown to have a broader tissue distribution, including activated T-cells, differentiated macrophages and epithelia. The presence of EMMPRIN in non-tumoral tissue suggests a role in other physiological and/or pathological situations, such as embryonic development, adult tissue homeostasis, atherosclerosis (see Section 2.1.2), arthritis and ulceration (Gabison et al., 2005).

1.4.9 Low-Density Lipoprotein Receptor-Related Protein (LRP)

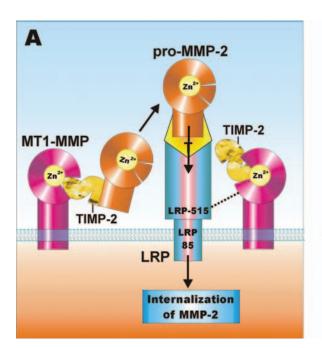
The low-density lipoprotein receptor (LDL-R) family consists of several related cargo transporters that also inform the cell of changes in its environment by mediating signaling responses. Low-density lipoprotein receptor-related protein 1 (LRP, α2-macroglobulin receptor (α_2 -MR), apolipoprotein E receptor (ApoE-R), CD91) is a membrane-bound receptor which mediates the endocytosis of a wide variety of ligands, including lipoproteins, proteases, proteinase inhibitor complexes, ECM components, bacterial toxins, viruses, intracellular proteins and growth factors. In addition to the four clusters of ligand-binding repeats, LRP consists of a 85 kDa membrane-spanning light β -chain (LRP-85) that is non-covalently associated with a 515 kDa large extracellular α -chain (LRP-515) (Figure 10). The cytoplasmic domain, containing 100 amino acids, plays a role in signal transduction by interacting with the cytoplasmic scaffold and adaptor proteins (Strickland et al., 2002; Lillis et al., 2005). In view of its multiple interactions at the cell surface, LRP is a strategic relay in the control of cell behavior. Indeed, LRP not only mediates the endocytic clearance of several major contributors of cancer development, such as ECM components (fibronectin, and thrombospondin-1 and -2) and various proteolytic enzymes (tissue-type plasminogen activator [t-PA], u-PA, MMP-2, MMP-9, and MMP-13), but it is also involved in cell signalling that regulates cell migration and possibly, survival and proliferation. Its own regulation thus appears to be a crucial process, as suggested by two opposite physiopathological examples, with, respectively, enhanced and suppressed LRP expression: the cycling human endometrium (see Section 5.1) and cancer (Emonard et al., 2005).

Invasive cancer cells derived from human prostate or breast tumors express lower levels of LRP, as compared to their non-invasive counterparts. Similarly, LRP expression decreases in late stages of melanocytic tumour progression and in invasive endometrial carcinoma (Emonard et al., 2005). In addition, MT1-MMP, which is highly expressed by the most invasive tumor cells (Seiki, 2003; Sato et al., 2005), has been shown to efficiently degrade LRP (Rozanov et al., 2004a). LRP-515 associates with the MT1-MMP catalytic domain and is highly susceptible to MT1-MMP proteolysis in vitro (Figure 10). In cells co-expressing LRP and MT1-MMP, the levels of cellular LRP are decreased and the NH₂-terminal ligand-binding portion is released in the extracellular milieu, thereby destroying the functional activity of the receptor. Similar to MT1-MMP, MT2-MMP, MT3-MMP, and MT4-MMP also degrade LRP (Rozanov et al., 2004a), suggesting that LRP is likely to be susceptible to proteolysis by several individual MT-MMPs in many cancer cell types. LRP is directly involved in the capture, internalization, and clearance of MMP-2, MMP-9, and MMP-13 from the extracellular milieu, and in the translocation into the cell compartment for subsequent lysosomal degradation (Emonard et al., 2005; Van den Steen et al., 2006). In malignant cells, MT1-MMP activates MMP-2, and protects the active enzyme from uptake and clearance by cleaving LRP (Figure 10). Thus, LRP proteolysis by MT1-MMP contributes to maintaining high levels of proteinases such as MMP-2, MMP-9, u-PA, and t-PA in the extracellular milieu, allowing for extensive degradation of the ECM by aggressive migrating cells. In this context, inhibition of MT1-MMP would have a dual beneficial effect in countering tumor invasion and metastasis; first by reducing the activation of pro-MMP-2 and second by enhancing LRP-mediated clearance of ECM-degrading proteases.

1.4.10 MT1-MMP

MT1-MMP expression levels are closely associated with invasiveness and malignancy of tumors, suggesting that MT1-MMP is one of the critical factors for tumor invasion and metastasis. Besides degrading multiple ECM molecules, MT1-MMP contributes to the process of tumor cell metastasis by cell surface proteolysis of various biologically important molecules such as MUC1, tTG, integrins, syndecan-1, CD44, and LRP, as discussed before. Furthermore, it activates pro-MMP-2 and concentrates its proteolytic activity on the cell surface, which is an important step for cancer cells to invade into basal lamina (Sato et al., 2005; Itoh and Seiki, 2006). MT1-MMP is produced as an inactive \sim 60 kDa zymogen that is activated by furin-like convertases, which cleave at





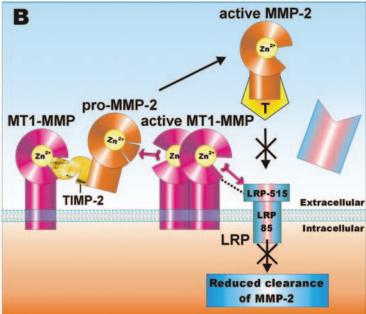


FIGURE 10 Degradation of LRP by MT1-MMP leads to reduced internalization of MMP-2. (A) When MT1-MMP activity is inhibited by TIMP-2, no MMP-2 activation occurs. MMP-2 binds thrombospondin (T) and is cleared from the extracellular milieu after binding the scavenger receptor LRP. (B) In malignant cells, which often over-express both MT1-MMP and pro-MMP-2, MT1-MMP activates MMP-2. In addition, the 515 kDa large extracellular α -chain of LRP (LRP-515), which associates with the MT1-MMP catalytic domain (dotted line), is cleaved by MT1-MMP and the NH2-terminal ligand-binding portion is released in the extracellular milieu, thereby destroying the functional activity of the receptor. Hence, active MMP-2 is protected from uptake and clearance by LRP and accumulates in the extracellular environment, where it assists MT1-MMP in degrading the ECM in front of aggressive migrating cells. LRP-85, the 85 kDa membrane-spanning light β-chain of LRP. Adapted from (Rozanov et al., 2004a).

the Arg108-Arg-Lys-Arg motif located between the propeptide and the catalytic domain. Active MT1-MMP (~57 kDa), starting at Tyr112, is then transported to the plasma membrane with the catalytic domain facing the extracellular space, where it cleaves pericellular substrates. In addition to being a sheddase, MT1-MMP is regulated by ectodomain shedding itself. Active MT1-MMP undergoes autocatalytic processing at the cell surface, leading to the formation of an inactive 44 kDa fragment and release of the entire catalytic domain (Figure 11). First, MT1-MMP cleaves itself at the Gly284-Gly285 peptide bond in the hinge region, generating the inactive 44 kDa membrane-bound fragment. The second cleavage takes place at the Ala255-Ile256 peptide bond, in the active site of MT1-MMP, near the conserved methionine turn, a structural feature of the catalytic domain of all MMPs. The released 18 kDa soluble fragment has no catalytic activity and does not bind TIMP-2 (Toth et al., 2002). Hence, the autocatalytic cleavage represents a self-regulatory mechanism that evolved to terminate MT1-MMP-dependent proteolysis both at the cell surface and in the extracellular space. The remaining 44 kDa degradation product can even negatively influence enzymatic activity. For

example, it was shown to compete with the full-length enzyme for collagen binding, reducing collagenolytic activity, and cellular invasion of a collagen matrix. Additionaly, it was speculated that the 44 kDa product may indirectly reduce pro-MMP-2 activation by reducing the clustering of MT1-MMP induced by collagen (Osenkowski et al., 2004). Inhibition of MT1-MMP activity slows down autocatalytic enzymatic turnover and consequently the mature form of the enzyme (57 kDa) accumulates on the cell surface while the level of the inactive 44 kDa fragment is reduced. In contrast, autocatalytic processing is promoted in the absence of inhibitors or under conditions of MT1-MMP overexpression. This effect of inhibition on autocatalytic processing unveiled a new paradigm in MT1-MMP regulation because it signaled a potential side effect of MT1-MMP inhibition: enhancement rather than inhibition of activity (Osenkowski et al., 2004).

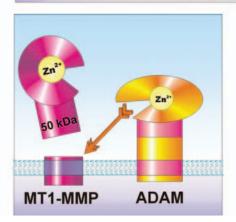
To make the picture even more complex, mature MT1-MMP is also shed from the cell surface via a non-autocatalytic process that results in the release of various soluble forms (Toth et al., 2002), and, as opposed to the autocatalytic processing, it generates active soluble forms. This shedding occurs in vivo and



Autocatalytic shedding

18 KD Ala255 Gly285-57 kDa 44 kDa MT1-MMP MT1-MMP

Non-autocatalytic shedding



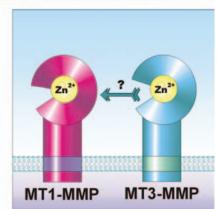


FIGURE 11 Autocatalytic and non-autocatalytic shedding regulates MT1-MMP activity at the cell surface. Active MT1-MMP undergoes autocatalytic processing on the cell surface, leading to the formation of an inactive 44 kDa fragment and release of the entire catalytic domain. First, MT1-MMP cleaves itself at the Gly284-Gly285 peptide bond in the hinge region, generating the inactive 44 kDa membranebound fragment. The second cleavage takes place at the Ala255-lle256 peptide bond, in the active site of MT1-MMP. The resulting 18 kDa soluble fragment has no catalytic activity. MT1-MMP is also shed from the cell surface via a non-autocatalytic process that results in the release of active soluble forms. This shedding is mediated by an ADAM and produces a minor form of \sim 25–32 kDa (not shown) and a major soluble form ~50-52 kDa, wich represents the entire ectodomain, including the catalytic domain. Finally, MT1-MMP may as well be degraded by MT3-MMP. However, no soluble products or cleavage sites of MT3-MMP have been characterized so far. Based on (Osenkowski et al., 2004), (Toth et al., 2006) and (Shofuda et al., 2001).

produces a minor form of ~25-32 kDa and a major soluble form \sim 50–52 kDa, wich represents the entire ectodomain, including the catalytic domain (Figure 11) (Toth et al., 2005). The inhibition pattern of this shedding process suggests that it is mediated by an ADAM (Toth et al., 2006).

A third proteolytic mechanism regulates MT1-MMP acitivity at the cell surface. While studying activities of MT1- and MT3-MMP in activated smooth muscle cells, it was shown that when MT3-MMP and MT1-MMP were coexpressed, MT1-MMP degradation was enhanced. This result supports the possibility that MT3-MMP can degrade MT1-MMP (Figure 11), providing another negative regulatory mechanism for MT1-MMP activity in cells such as smooth muscle cells and gliomas, or in tissues such as injured blood vessels and brain, where both MT-MMPs are coexpressed (Shofuda et al., 2001).

Emerging evidence points to internalization as another means of controlling MT1-MMP activity at the cell surface. Classical endocytosis depends on clathrin-coated pits and involves an intracellular pathway in which lysosomes fuse with internalized vesicles, degrading their contents (Shin and Abraham, 2001). MT1-MMP is cleared from the cell surface by dynamin-dependent endocytosis in clathrin-coated pits through its cytoplasmic domain (Jiang et al., 2001). This type of endocytosis was shown essential for MT1-MMP to stimulate cell migration and invasion into Matrigel (Uekita et al., 2001). In addition, MT1-MMP was detected in caveolae (Annabi et al., 2001; Puyraimond et al., 2001). Remacle and coworkers (2003) showed that MT1-MMP is also internalized by a clathrin-independent and caveolaedependent pathway in HT1080 cells. Caveolar traffic is required for proper MT1-MMP localization, activity and function in migrating endothelial cells (Galvez et al., 2004). Interestingly, internalized MT1-MMP can be recycled to the cell surface, which could represent a rapid mechanism for relocalizing active MT1-MMP at the leading edge during cell migration (Remacle et al., 2003).

Regarding the major role of MTl-MMP in tumor invasion and metastasis (Sato et al., 2005; Itoh and Seiki, 2006), inhibition of its activity is an obvious therapeutic approach to block spreading of the cancer. However, further insight in the proteolytic mechanisms at the cell surface that modulate MT1-MMP activity is a prerequisite in the development of new inhibitors, as unexpected effects such as the paradoxical enhancement of MT1-MMP activity by inhibition of autocatalytic processing, may fatally alter the outcome of inhibitor therapy.



1.4.11 Protease-Activated Receptor-1 (PAR1)

Thus far, the protease-activated receptor (PAR) family comprises four members defined as PAR1 to PAR4 (Coughlin, 2000). They form a unique class of GPCRs that are characterized by a distinctive mechanism of activation. Proteolytic cleavage at specific sites in the extracellular NH₂-terminus exposes a new NH₂-terminus, which serves as a tethered ligand and binds to the second extracellular loop of the same receptor, activating it intramolecularly (Figure 12). The activated PARs initiate signal transduction across the membrane to activate intracellular G proteins that regulate pathways for cell shape changes, secretion, cell proliferation, migration, and adhesion in numerous cell types. Many serine proteases, including thrombin, factor Xa, granzyme A, cathepsin G, elastase, trypsin and plasmin cleave the PAR1 scissile bond at Arg41-Ser42. PAR1 (thrombin receptor, coagulation factor II receptor) is expressed by a wide range of tumor cells and has been shown to be upregulated in breast carcinomas and pulmonary tumors. In addition, the level of expression of PAR1 on tumor cells directly correlates with metastatic potential in both primary breast carcinoma and in established cancer cell lines (Ossovskaya and Bunnett, 2004). Neither thrombin nor other serine proteases appear to be involved in PAR1-dependent breast cancer cell motility. However, MMP inhibitors (1,10-phenanthroline and MMP-200, a hydroxamate inhibitor) block both migration and invasion of breast cancer cells in vitro. Only MMP-1, not MMP-2, -3, -7, or -9, cleaves and activates PAR1 upon addition to PAR1-transfected breast cancer cells. MMP-1 inhibitors reduce both cell migration in vitro and tumor growth in nude mice (Boire et al., 2005; Pei, 2005). In addition, antagonism of either MMP-1 or PAR1 significantly attenuates tumor-induced endothelial cell activation (ECA), the transformation of the intravascular milieu to a prothrombotic, proinflammatory, and celladhesive state, as a result of tumor-endothelial crosstalk (Goerge et al., 2006). Thus, the MMP-1/PAR1 axis functions in both ways: host-derived MMP-1 activating tumor-expressed PAR1, as well as tumor-derived MMP-1 acting on endothelial PAR1 (see Figure 2). Since both MMPs and PARs have also been shown to play important roles in cardiovascular and inflammatory diseases (Ossovskaya and Bunnett, 2004), targetting the MMP-1/PAR1 pathway with therapeutics that block MMP-1 may become an attractive approach in the treatment of a variety of invasive, proliferative, and inflammatory conditions.

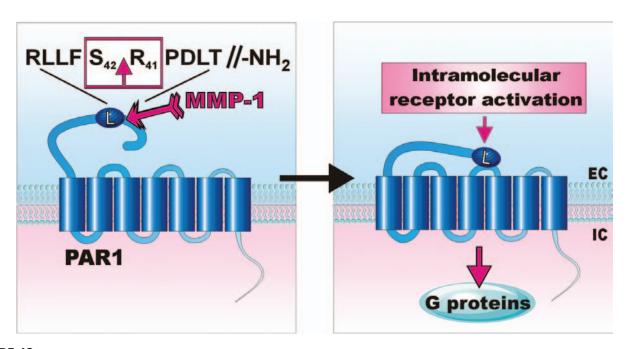


FIGURE 12 Proteolytic cleavage by MMP-1 in the NH2-terminus of PAR1 results in intramolecular receptor activation. Proteolytic cleavage by MMP-1 at Arg41-Ser42 in the NH2-terminus of PAR1 exposes a new NH2-terminus, which serves as a tethered ligand (L) and binds to the second extracellular loop of the receptor, activating it intramolecularly. Activated PAR1 initiates signal transduction across the membrane to activate intracellular G proteins that regulate pathways for cell morphology, secretion, cell proliferation, migration and adhesion in numerous cell types. EC, extracellular; IC, intracellular. Adapted from Pei (2005).



1.4.12 Receptor Activator of Nuclear Factor κB Ligand (RANKL)

Prostate cancer deaths are primarily due to metastases that are resistant to conventional therapies. The most common site for metastasis of prostate cancer is the bone, with patients often experiencing severe bone pain, pathological fractures, leukoerythroblastic anaemia, bone deformity, hypercalcaemia, nervecompression syndromes, and immobility (Mundy, 2002). Osteolytic lesions are produced by the interaction between tumor and bone stroma, commonly referred to as the 'vicious cycle,' whereby tumor cells in the bone can secrete factors such as parathyroid hormone related peptide (PTHrP) that stimulate osteoblast expression of the receptor activator of nuclear factor κ B ligand (RANKL). By binding to its receptor RANK, RANKL has been shown to be essential in mediating osteoclast activation (Figure 13). The osteoclasts degrade the bone matrix using a powerful array of proteases such as the MMPs and the cathepsins (Mundy, 2002). RANKL, also known as tumor necrosis factor ligand superfamily member 11, CD254, TNF-related activationinduced cytokine (TRANCE), osteoprotegerin ligand (OPGL) and **o**steoclast **d**ifferentiation **f**actor (ODF), is a member of the TNF family. RANKL is required in osteoclast differentiation and activation; T and B cell maturation; dendritic cell survival; and might also play a role in the cardiovascular system. The interaction with its receptor RANK and its decoy receptor osteoprotegerin (OPG) forms a molecular triad which can modulate the bone system, the immune system, and the cardiovascular system (Theoleyre et al., 2004).

To improve overall patient survival and to identify new therapeutic targets, the molecular mechanisms underlying prostate tumor-induced changes in the bone microenvironment need to be elucidated. Therefore, Lynch and coworkers (2005) developed a murine model of rat prostate cancer in the bone environment that mimics the osteoblastic and osteolytic changes associated with human metastatic prostate cancer. MMP-7 was identified as a proteolytic enzyme whose expression correlates with tumor-induced osteolysis. Interestingly, MMP-7 was expressed by the osteoclasts at the tumor-bone interface, and its secretion resulted in the solubilization of RANKL being presented by the osteoblasts, stromal cells or tumor cells in the bone microenvironment (Figure 13). Cleavage of RANKL by MMP-7 occurs at the residues Met145-Met146 in the stalk region of the protein, releasing an active soluble form of RANKL from the cell surface. MMP-3, but not MMP-2, MMP-9, or MMP-13, was also found to cleave RANKL, although the amount of sRANKL produced was significantly less. sRANKL released by MMP-7 was as active and efficient in osteoclast activation as fulllength RANKL. The shedding of RANKL is not without significance, because it eliminates the need for close contact between RANKL-expressing cells such as osteoblasts and tumor cells, and RANK-expressing osteoclast precursor cells (Blavier and Declerck, 2005). MMP-7-mediated release of RANKL was also shown in vivo, as sRANKL was clearly detected in the tumor-bone interface lysates from wild-type mice, while little or no sRANKL was detected in MMP-7 deficient animals. In addition, tumor-induced osteolysis was significantly reduced in MMP-7 deficient mice (Lynch et al., 2005). Hence, these results make MMP-7 an attractive therapeutic target for the control of cancer-induced bone metastasis.

Interestingly, RANKL was also reported to be solubilized by MT1-, MT2-, MT3-, and MT5-MMP, which will be discussed in a later section (see Section 3.4.2.2).

1.5 Inflammatory Processes and **Immune Escape in Cancer**

1.5.1 Intercellular Adhesion Molecule-1 (ICAM-1)

Intercellular adhesion molecule-1 (ICAM-1, major group rhinovirus receptor, CD54) is a transmembrane glycoprotein expressed on multiple cell types including leukocytes, epithelial cells, endothelial cells and fibroblasts. It is involved in multiple transient cellular interactions that regulate infiltration, activation and effector functions of leukocytes. Interaction of ICAM-1 with its physiological ligand lymphocyte functionassociated antigen-1 (LFA-1, CD11a/CD18 or $\alpha_L\beta_2$, the prototypic β_2 -integrin) (see Section 1.4.3) is crucial for leukocyte arrest on endothelial cells, stabilization of interactions between antigen-presenting cells and T lymphocytes by the so-called immune synapse, and for adhesion of cytotoxic T cells and NK cells to their target cells. Besides LFA-1, ICAM-1 binds other ligands such as Mac-1 (Complement receptor 3, CD11b/CD18 or $\alpha_{\rm M}\beta_2$ integrin), rhinoviruses and malaria-infected red blood cells (Fiore et al., 2002; Hopkins et al., 2004). ICAM-1 expression on resting vascular endothelial cells



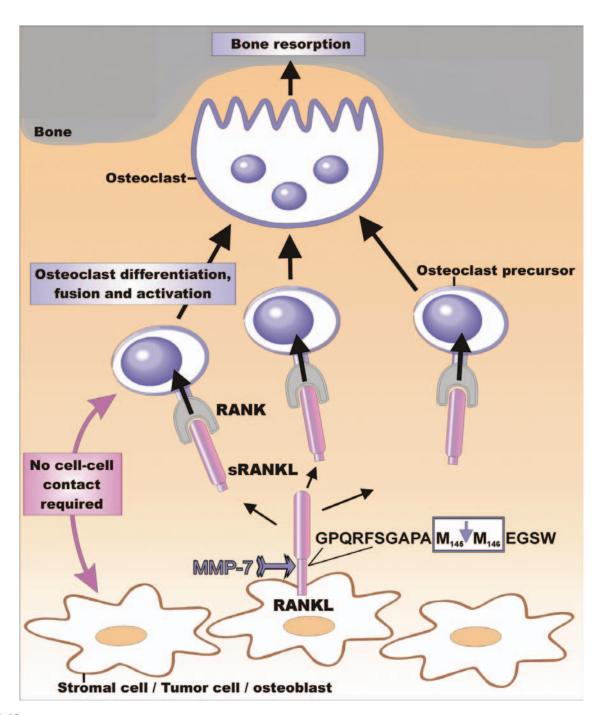


FIGURE 13 The shedding of RANKL by MMP-7 promotes cancer-induced osteolysis. Osteolytic lesions in bone metastasis are produced by the interaction between tumor and bone stroma, whereby tumor cells in the bone can secrete factors that stimulate osteoblast expression of RANKL. By binding to its receptor RANK, RANKL has been shown to be essential in mediating osteoclast activation. The osteoclasts degrade the bone matrix using a powerful array of proteases such as the MMPs and the cathepsins. MMP-7 has been shown to mediate solubilization of RANKL on osteoblasts, stromal cells or tumor cells in the bone microenvironment. Cleavage of RANKL by MMP-7 occurs at the residues Met145-Met146 in the stalk region of the protein. sRANKL released by MMP-7 was as active and efficient at osteoclast activation as full-length RANKL. The shedding of RANKL is noteworthy because it eliminates the need for cell-cell contact between RANKL-expressing cells such as osteoblasts, stromal cells and tumor cells, and RANK-expressing osteoclast precursor cells. Based on Mundy (2002) and Blavier and Declerck (2005).

and lymphocytes is low, whereas its expression on monocytes is moderate. Leukemia and carcinoma cells express ICAM-1 as well, and this would make them an easier target for CTLs (Cho et al., 2000). However,

ICAM-1 can be released from the surface of tumor cells. This cleavage inhibits cell-mediated cytotoxicity, forming a defence mechanism of primary tumor cells against CTLs and NK cells. The protease in charge of this release



is MMP-9 (Fiore et al., 2002). Sequencing of sICAM-1 peptides points to a cleavage site in the hinge region between Arg441 and the transmembrane domain (see Figure 2), with the Glu442-Val443 peptide bond being the most probable cleavage site (Sultan et al., 2004) in accordance with the substrate specificity of MMP-9 (Kridel et al., 2001). However, the exact site of proteolysis remains to be experimentally determined. In conclusion, MMP-9 might be involved in tumor cell evasion of immune surveillance.

1.5.2 Interleukin-2 Receptor-lpha Chain $(IL-2R\alpha)$

Not infrequently, cancer cell spreading occurs despite the apparent presence of TILs. These autologous CTLs seem unable to display their anti-tumor capacities in the tumor microenvironment. One of the various immune escape mechanisms of cancer cells (see Figure 2) is down-regulation of the interleukin-2 Receptor- α chain (IL2-R α , p55, TAC antigen, CD25). As IL2-R α is an essential receptor for the proliferation of T-cells, decreased expression of this receptor in vivo may result in poor clonogenicity of TILs and cause immune suppression. An in vitro cervical cancer model shows that cervical cancer cells can induce the release of soluble IL2-R α from encountered T-cells, a process inhibited by TIMPs. Immunohistochemical stainings show abundant expression of MMP-1, MMP-2 and MMP-9 in cervical cancer tissues, and MMP-9, and to a lesser extent MMP-2, are capable of IL-2R α truncation in vitro (Sheu et al., 2001). Consequently, as MMP-9 may contribute to tumor cell evasion of immune surveillance by ectodomain cleavage of ICAM-1 as well as IL-2R α , its inhibition may be an attractive perspective in countering this type of immune escape of cancer cells.

2. MODIFICATION OF MEMBRANE PROTEINS IN DISEASES AFFECTING VASCULAR AND EPITHELIAL INTEGRITY

2.1 Shedding of MMP Substrates in Cardiovascular Diseases

2.1.1 HB-EGF

sHB-EGF is a potent chemoattractant and mitogen for vascular smooth muscle cells. Atherogenesis in the arterial wall is characterized by the formation of fibrous lesions and the proliferation of neointimal smooth muscle cells. Smooth muscle cells and macrophages in atherosclerotic plaques have indeed been reported to produce large amounts of HB-EGF. Moreover, sHB-EGF-induced proliferation of smooth muscle cells is a key step in the progressive neointimal thickening seen in the development of transplant arteriosclerosis, a major obstacle to long-term graft survival after clinical organ transplantation (Higashiyama, 2004). Release of sHB-EGF is mediated bij ADAM-12 in the heart and by MMP-7 in large mesenteric arteries as a result of ligand binding to GPCRs (see Figure 4), like some adrenoreceptors and angiotensin receptors (Hao et al., 2004). The role of MMP-7 in large mesenteric arteries is taken over by MMP-2 and MMP-9 in the case of increased luminal pressure in small mesenteric resistance arteries (Lucchesi et al., 2004). As the EGFR transactivation is triggered by agonists typically overexpressed in hypertension, its blockade may have therapeutical potential for simultanously inhibiting pathological vasoconstriction and growth in hypertensive disorders like vascular inflammation, atherosclerosis, left ventricular hypertrophy, and cardiac hypertrophy (Shah and Catt, 2003; Hao et al., 2004; Shah and Catt, 2004b).

2.1.2 EMMPRIN

MMPs seem to play an important role in atherosclerotic plaque growth, neointima formation, and plaque disruption by inducing smooth muscle migration and proliferation (e.g., after release of sHB-EGF, as discussed before), and by enhancing ECM degradation (Rouis, 2005). Deposition of low-density lipoproteins (LDLs) in the vessel wall and their oxidative modification seem to initiate, or at least accelerate, the atherosclerotic process by several mechanisms, including promotion of foam cell formation, chemotactic effects on monocytes, and mitogenic effects on smooth muscle cells. In addition, oxidized LDLs increase the expression of MMPs in endothelial cells, monocyte-derived macrophages, and smooth muscle cells (Haug et al., 2004). EMMPRIN (see Section 1.4.8) regulates MMP release and activity in fibroblasts, endothelial cells, and tumor cells (Gabison et al., 2005; Yan et al., 2005). In addition, EMMPRIN has been shown to be expressed in macrophage-rich atheromas from human coronary arteries (Major et al., 2002) and in cultured human coronary artery smooth muscle cells (HCA-SMCs) (Haug et al., 2004). Oxidized LDLs significantly enhanced the release of soluble EMMPRIN (~50 kDa), as well as the release of MMP-1 and MMP-2 into HCA-SMC



supernatants. Oxidized LDL-induced release of soluble EMMPRIN was parallelled by a decrease in cellassociated EMMPRIN. These effects were antagonized by antioxidants as well as by EDTA and the MMP inhibitor GM6001. In addition, MMP-1 and MMP-2 cleaved off the cytoplasmic and transmembrane domains of EMMPRIN in vitro. Purified soluble EMM-PRIN significantly enhanced MMP-1 and MMP-2 release by HCA-SMC. Thus, oxidized LDLs might induce an amplification cascade of increased MMP activity, enhanced MMP-dependent shedding of soluble EMM-PRIN, and EMMPRIN-induced upregulation of MMP production. This cascade might accelerate ECM degradation in atherosclerotic plaques and thereby promote plaque growth and plaque destabilization (Haug et al., 2004). Thus, inhibiting MMP-mediated production of soluble EMMPRIN-molecules, which may diffuse and act on multiple cells, may be an interesting therapeutic tactic to interupt or prevent the atherosclerotic cascade.

2.2 Degradation of Intercellular Junction Proteins in Inflammation, Stroke, Acute Renal Failure and **Ophtalmic Pathologies**

Adhesion between vertebrate cells is generally mediated by three types of adhesion junctions: 1) tight junctions, 2) adherens junctions, and 3) desmosomes. Together they constitute the intercellular junctional complex, which has an important role in defining the physiological function of a cell; that is, they define whether and how a cell will be integrated in functional structures, such as organ epithelia or stroma (Cavallaro and Christofori, 2004).

Occludin and claudins were identified as the major integral membrane proteins forming the tight junctions in epithelial and endothelial cell sheets. Tight junctions are sites of cell-cell contacts composed of a number of transmembrane and cytoplasmic proteins, assembled into a complex tethered to the cytoskeleton. Paracellular permeability, or the flow of ions and molecules between cells, is regulated by these tight junctions. Both, occludin and claudins have four transmembrane domains and their NH2- and COOH-terminal ends are located in the cytoplasm. This conformation generates two extracellular loops that are supposed to provide the intercellular interaction sites (Figure 14). The COOHterminal domains of occludins and claudins serve as binding sites for a complex set of signaling proteins including zonula occludens (ZO)-1, -2 and -3, kinases and phosphatases. Compared to occludin (65 kDa), however, claudins are smaller (20 to 25 kDa). Different cellular sheets have their own unique set of claudin species, and this compositional heterogeneity explains the

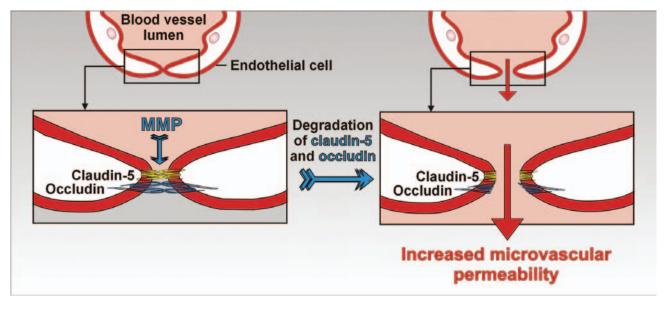


FIGURE 14 Degradation of tight junction proteins by MMPs disrupts endothelial integrity. Occludin and claudins are the major components of tight junctions in endothelial cell sheets. Both, occludin and claudins have four transmembrane domains and their NH2- and COOH-terminal ends are located in the cytoplasm. This conformation generates two extracellular loops that are supposed to provide the intercellular interaction sites. Degradation of intercellular junction proteins is mediated by various MMPs and increases microvascular permeability. The widening of interendothelial tight junctions allows for increased solute exchange and immune cell diapedesis, which is a hallmark of inflammation and brain damage after BBB opening.



diversified barrier properties of tight junctions. Claudin-5 (also named transmembrane protein deleted in velo-cardio-facial syndrome [VCFS]) was shown to be a key molecule in the blood-brain barrier (BBB) in mice (Feldman et al., 2005; Koval, 2006; Bazzoni, 2006; Furuse and Tsukita, 2006). Adherens junctions and desmosomes are cell-cell junctions that are formed by cadherins and additional associated proteins into which actin filaments are inserted.

Degradation of intercellular junction proteins by MMPs disrupts endothelial and/or epithelial integrity and has major consequences in inflammation, stroke, acute renal failure and ophthalmic pathologies, which will be illustrated in the following paragraphs.

2.2.1 Occludin and Claudin-5 Degradation in Inflammation

Increased microvascular permeability is a central hallmark of inflammation and allows for increased solute exchange and extravasation of leukocytes into the inflamed tissue. These inflammatory changes in microvascular permeability are correlated with the reorganization and widening of interendothelial tight junctions. MMPs have been reported to be responsible for the tight junction disruption by degradation of occludin and some claudins (Figure 14) (Alexander and Elrod, 2002). In human umbilical vein endothelial cells and in porcine brain capillary endothelial cells, the tyrosine phophatase inhibitor phenylarsine oxide (PAO) induced increased MMP activity, which was parallelled by severe disruption of cell-cell contacts and degradation of occludin. PAO-induced occludin proteolysis could be prevented by different MMP inhibitors (GM6001 and 1,10-phenantroline) (Wachtel et al., 1999; Lohmann et al., 2004). In addition, MMP-7 has been reported to proteolyse VE-cadherin (see Section 1.3.3). Degradation of intercellular junction proteins by MMPs thus contributes to increased endothelial permeability, a prereguisite for solute exchange and leukocyte extravasation during inflammation.

2.2.2 Occludin and Claudin-5 Degradation in the Blood-Brain Barrier

Tight junction proteins in endothelial cells such as occludin and claudins are major structural components of the BBB formed by components of the neurovascular unit (Bazzoni, 2006). Cerebral ischemia is a complex insult that involves a loss of blood flow accompanied by depletion of oxygen and essential nutrients. In vitro

models of the BBB have indicated that hypoxia and hypoxia/reoxygenation lead to increased permeability and/or disruption of BBB tight junctions (Hawkins and Davis, 2005). Focal ischemia with reperfusion in spontaneously hypertensive rats lead to opening of the BBB and degradation of occludin and claudin-5 (see Figure 14). Treatment with an MMP inhibitor (BB-1101) prevented the opening and reversed the degradation of the tight junction proteins (Yang et al., 2007). In addition, using green fluorescent protein (GFP)-tagged occludin and live cell imaging, it was shown that monocytes scroll over the brain endothelial surface toward cell-cell contacts, inducing gap formation, which is associated with local disappearance of GFP-occludin, and subsequently traverse the endothelium paracellularly. The broad spectrum MMP inhibitor BB-3103 significantly inhibited endothelial gap formation, occludin loss, and the ability of monocytes to pass the endothelium (Reijerkerk et al., 2006). In addition, after lipopolysaccharide (LPS)-induced opening of the BBB, less BBB disruption was observed in MMP-3 deficient mice than in wild-type controls, as well as diminished degradation of claudin-5 and occludin (Gurney et al., 2006). Hence, use of MMP inhibitors in stroke might reduce or prevent BBB damage by minimizing degradation of tight junction proteins and subsequent immune cell diapedesis.

2.2.3 Degradation of E-Cadherin, N-Cadherin and Occludin in Acute Renal Failure

Acute renal failure (ARF) is characterised by a rapid fall in glomerular filtration rate, clinically manifested as an abrupt and sustained raise in urea and creatinine in plasma. Life threatening consequences include volume overload, hyperkalemia, and metabolic acidosis. ARF is increasingly common and carries a high morbidity and mortality (Hilton, 2006). Although ischemia is a leading cause of ARF, the molecular mechanisms leading to renal injury and failure are not completely understood. In ischemia-induced ARF, a loss of epithelial integrity and shedding of epithelial cells occurs in the tubuli. After injury, both viable and non-viable cells are shed, leaving the basement membrane as the only barrier between filtrate and interstitium, which allows for backleak of the filtrate and tubular obstruction by intraluminal aggregation of cells, proteins, and glycoproteins, such as fibronectin (Bonventre and Weinberg, 2003).



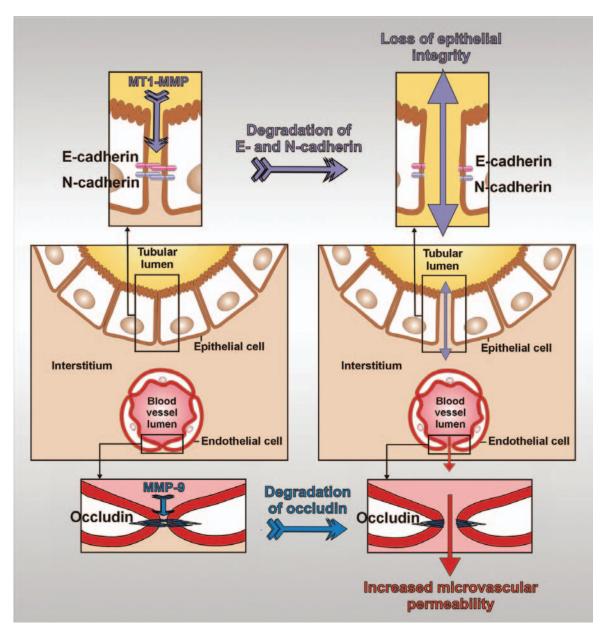


FIGURE 15 Degradation of intercellular junctions by MMPs in acute renal failure. Cadherins in the adherens junctions and occludins in the tight junctions are key molecules in the regulation of paracellular permeability by the intercellular junction. In ischemia-induced ARF, MT1-MMP-mediated degradation of E-cadherin and N-cadherin results in disruption of epithelial integrity and shedding of epithelial cells in the tubuli, leaving the basement membrane as the only barrier between filtrate and interstitium, which allows for backleak of the filtrate and tubular obstruction by intraluminal aggregation of cells and proteins. In addition, degradation of occludin by MMP-9 leads to the disruption of intercellular endothelial junctions and concomitant cell detachment and vascular injury.

Application of an *in vitro* model of ischemia-reperfusion resulted in selective fragmentation/loss of E-cadherin and loss of N-cadherin (neural-cadherin, cadherin-2, CD325) levels from normal rat kidney cells that could be blocked by the MMP inhibitors GM6001 and TAPI-0 (Figure 15). TIMP-3 completely blocked both cleavage and/or loss of E-cadherin and N-cadherin, whereas TIMP-2 protected full-length E-cadherin protein expression and TIMP-1 had no effect (Covington et al., 2005). This implies that different MMPs may play a role

in E-cadherin and N-cadherin regulation. Chemical inhibitors against a number of soluble MMPs (1, 2, 3, 8, and 9) failed to completely attenuate ischemia-induced E- and N-cadherin loss. Under ischemic conditions, there was increase in active MT1-MMP, and the role of MT1-MMP in ischemia-induced cadherin loss was confirmed by blocking MT1-MMP activity with a neutralizing antibody or by blocking MT1-MMP expression with siRNA constructs, which protected full-length Eand N-cadherin during ischemia and preserved cell-cell



contacts (Covington et al., 2006). Consequently, therapeutic inhibition of MT1-MMP may preserve epithelial integrity and inhibit epithelial cell shedding in ARF. In normal physiology, MMP-7-mediated shedding of Ecadherin is required for the repair of injured lung epithelium (McGuire et al., 2003). Similarly, N-cadherin cleavage also occurs under physiological conditions. Indeed, MT5-MMP was shown to produce a ~35 kDa Ncadherin degradation product in neurons, possibly contributing to mechanisms of synaptic regulation (Monea et al., 2006). Therefore, targetting MT1-MMP in ARF must occur by using extremely specific inhibitors, as not to disturb any vital physiological process.

As discussed above, occludin is one of the major integral membrane proteins forming the tight junctions in endothelial cell sheets. During acute in vivo reversible ischemia induced in rat kidneys by vascular clamping, pro-MMP-2, pro-MMP-9, and active MMP-9 were upregulated in the endothelial cell fractions. This increase in MMP-9 during ischemia is accompanied by a lower level of occludin in endothelial fractions. This finding suggests that the induction of MMP-9 during kidney ischemia leads to an increased degradation of occludin (Caron et al., 2005). Thus, ischemia in kidneys could lead to the disruption of intercellular endothelial junctions by MMP-9 and concomitant cell detachment and vascular injury (Figure 15). In addition, active MMP-9 in ischemic kidney may also contribute to vascular basement membrane degradation and increased permeability. Accordingly, blocking MMP-9 and MT1-MMP may be a way to reduce mortality in ARF.

2.2.4 Occludin Proteolysis in Ophtalmic **Pathologies**

Breakdown of the blood-retinal barrier (BRB) is an early feature of proliferative diabetic retinopathy (PDR) and results in vascular leakage and the developent of retinal edema (Frank, 2004). As in the BBB (see Section 2.2.2), tight junction proteins such as occludin and claudins are an integral structural component of the BRB. Both TGF- β and MMP-9 increased the permeability of retinal endothelial cells and reduced the levels of occludin (see Figure 14) (Behzadian et al., 2001). Treatment of retinal microvessel endothelial cells and retinal pigment epithelial cells with MMP-2 and MMP-9 also revealed specific degradation of occludin, but not of claudin-5 (Giebel et al., 2005). These results suggest that elevated expression of MMPs in the retina may facilitate an increase in vascular permeability by a mechanism involving proteolytic degradation of occludin, followed by disruption of the entire tight junction complex. Thus, a greater understanding of the role of MMPs in altering tight junction proteins in PDR may provide future targets for therapeutic intervention.

Corneal epithelial disease, termed keratoconjunctivitis sicca (KS), is a severe and sight-threatening complication of dry eye syndrome. A key clinical feature of KS is disruption of epithelial barrier function. This results in eye irritation, corneal surface irregularity, blurred and fluctuating vision, and increased risk for corneal ulceration (Pflugfelder, 1998; Pflugfelder et al., 2005). Concentration and activity of MMP-9 in the tear fluid was found to be significantly increased in these eyes, as well as in an experimental murine model of dry eye. Corneal epithelial permeability increased in dry eye wild-type mice, but not in MMP-9 deficient mice. Compared to MMP-9 knockout mice, wild-type mice showed greater desquamification of differentiated apical corneal epithelial cells and this was accompanied by an increase in lower sized (50 kDa) occludin in the corneal epithelia of wild-type mice. The same effects were observed in cultured human corneal epithelial cells treated with active MMP-9 (Pflugfelder et al., 2005). These observations show that increased MMP-9 activity on the ocular surface in response to dryness disrupts corneal epithelial barrier function (Figure 16). The mechanism appears to be similar to BBB and BRB disruption (see above), that is, through disruption of tight junctions by proteolysis of occludin. Accordingly, reducing barrier degradation in human KS by targeting MMP-9 may lessen the severity of clinical disease.

3. SHEDDING OF MMP SUBSTRATES IN THE MODULATION OF INFLAMMATION AND INNATE **IMMUNITY**

Innate immunity comprises several rapid defence mechanisms against invading microorganisms and other types of damage to the host. During inflammatory reactions, MMP-mediated cleavage of cell surface molecules leads to activation of pro-inflammatory cytokines. This is a fundamental step in the regulation of leukocyte recruitment and homeostasis. In addition, the previously mentioned modifications of mHB-EGF, E-cadherin, integrin subunit precursors, MUC1, ICAM-1 and IL- $2R\alpha$, also have major effects on immune responses and wound healing. Finally, proteolysis of cell surface



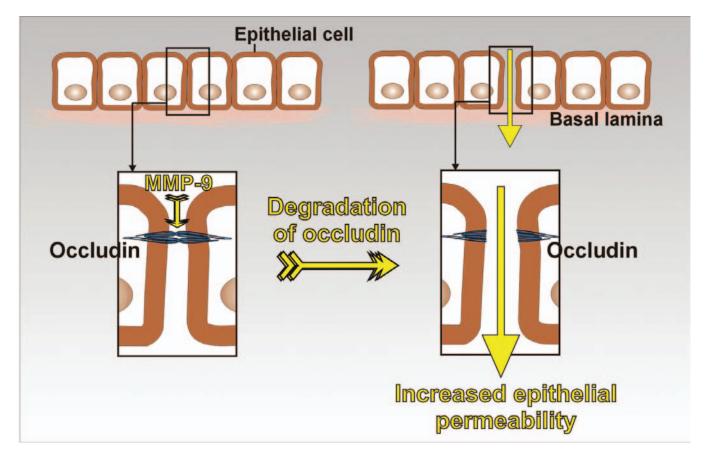


FIGURE 16 MMP-9-mediated degradation of occludin increases corneal epithelial permeability in keratoconjunctivitis sicca. Occludins in the tight junctions between epithelial cells mediate intercellular adhesion and hence, are essential in epithelial barrier function. Increased MMP-9 activity on the ocular surface in response to dryness leads to degradation of occludin and disruption of the corneal epithelial barrier. Subsequent desquamification of apical corneal epithelial cells leads to keratoconjunctivitis sicca.

proteins by MMPs plays a non-negligible role in various autoimmune diseases.

3.1 Activation of Membrane-Bound **Pro-Inflammatory Cytokines**

3.1.1 Tumor Necrosis Factor- α (TNF- α)

Tumor necrosis factor- α (TNF- α , tumor necrosis factor ligand superfamily member 2, cachectin) is a pleiotropic cytokine with potent immunomodulatory and proinflammatory properties. Excessive or prolonged production of TNF- α is a feature of septic shock and several important autoimmune diseases like rheumatoid arthritis, Crohn's disease and multiple sclerosis (Kollias et al., 1999). TNF- α is initially expressed on T cells and macrophages as an active 26 kDa membrane-bound protein (pro-TNF- α), which is cleaved by TACE to form the 17 kDa soluble cytokine (Black et al., 1997; Moss et al., 1997; Mohan et al., 2002). TNF- α proteolysis is inhibited in vitro and in vivo by broad-spectrum metalloproteinase inhibitors (McGeehan et al., 1994; Mohler

et al., 1994). MMP-1, MMP-2, MMP-3, MMP-7, and MMP-9 also cleave recombinant pro-TNF- α fusion proteins in vitro, as do MMP-12, MT1-MMP, MT2-MMP and MT4-MMP (Gearing et al., 1994; Gearing et al., 1995; Chandler et al., 1996; d'Ortho et al., 1997; English et al., 2000). Of all these MMPs, only MMP-7 processes pro-TNF- α at the natural cleavage site, between Ala76 and Val77 (Table 3). However, this reaction shows a 30-fold lower specificity constant relative to the TACEmediated proteolysis (Mohan et al., 2002). MMP-7 and MMP-12 are both capable of TNF- α shedding from isolated macrophages. MMP-7-mediated release of TNF- α from peritoneal macrophages is essential for the induction of MMP-3 in coculture with vertebral disc cells. This MMP-3 in turn generates a macrophage chemoattractant, resulting in the macrophage infiltration that is essential for the spontaneous resorption of herniated discs (Haro et al., 2000a; Haro et al., 2000b). TNF- α solubilization by MMP-12 is a crucial step in acute cigarette smoke-induced inflammation, which causes emphysema and chronic obstructive pulmonary disease



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(Churg et al., 2003). To summarize, it may be stated that, whereas TACE is the main enzyme responsible for the inducible release of TNF- α in response to bacteria and pathogen-associated molecular patterns (the ligands of Toll-like receptors), MMP-7 and MMP-12 may cause constitutive TNF- α release from macrophages during common processes as tissue resorption and resolution in response to injury (Parks et al., 2004).

3.1.2 Interleukin-1 β (IL-1 β)

Interleukin- 1β (IL- 1β , catabolin, endogenous pyrogen, granulocytic pyrogen, leukocytic pyrogen, lymphocyte activating factor, hemopoietin-1, osteoclast activating factor, mononuclear cell factor [MCF]) is a strong proinflammatory cytokine that induces fever, inflammation, induction of acute phase reactants, tissue destruction, and, in some cases, shock and death (Dinarello, 2000). IL-1 β lacks a typical transmembrane domain and most of its precursor is stored in the cytoplasm. In addition, a small fraction of the precursor can be found in the extracellular space. We discuss its cleavage in the context of the functional analogy with the above mentioned TNF- α proteolysis. IL-1 β is primarily produced by activated macrophages, monocytes and polymorphonuclear phagocytes (Delaleu and Bickel, 2004). It lacks a secretory signal peptide and, as a result, it is not secreted through the classical exocytic route, but presumably through exocytosis of secretory lysosomes, a mechanism that still requires further clarification (Andrei et al., 2004; Wewers, 2004). Whereas the COOH-terminal 17 kDa segment has full biological activity (Van Damme et al., 1985), the 33 kDa proform of IL-1 β is inactive and its maturation requires proteolytic processing into the mature protein by the IL-1 β -converting enzyme (ICE or caspase-1), an intracellular cysteine protease (Kostura et al., 1989). The possibility of extracellular precursor proteolysis and in vivo studies with ICE deficient mice suggest the existence of ICE-independent mechanisms of IL-1 β activation (Delaleu and Bickel, 2004). Indeed, various proteases cleave recombinant IL-1 β in vitro, including bacterial enzymes, trypsin, chymotrypsin, leukocyte elastase and granzyme A. However, with the exception of granzyme A, all of these cleavages result in fragments >17 kDa. On the contrary, proteolysis by MMP-2, MMP-3, and especially by MMP-9, yields biologically active forms (Schönbeck et al., 1998). In addition, prolonged incubation of mature IL-1 β with MMP-3, and to a lesser extent with MMP-1, MMP-2, and MMP-9, results in degradation of the mature cytokine (Ito et al., 1996). IL-1 β is one of the classical inducers of these MMPs in inflammation. In addition, IL-1 β is an autoregulating protein with the ability to induce its own gene expression. Thus, at sites of acute or chronic inflammation the presence of MMP-9 might result in biologically active IL-1 β , whereas MMP-3 can degrade the active IL-1 β form, mediating downregulation of its activities. As IL-1 β plays a crucial role in multiple inflammatory and autoimmune diseases, including rheumatoid arthritis, inflammatory bowel disease, and multiple sclerosis (Delaleu and Bickel, 2004), and seems to be involved in tumor invasion and angiogenesis as well (Voronov et al., 2003), it is a principal target for drug development (Braddock and Quinn, 2004). In this regard, understanding IL-1 β activity modulation by MMPs is crucial.

3.2 Regulation of Leukocyte **Recruitment, Migration and Homeostasis in Inflammation**

3.2.1 Syndecan-1

The influx of inflammatory cells to skin or mucosal sites of injury is largely directed by signals from the epithelium, but how these cells generate and modulate chemotactic gradients has not yet been completely elucidated. In murine lungs, a potential mechanism for the formation of neutrophil-attracting chemotactic gradients is based on the interaction of three components of the epithelial tissue: a secreted protease (MMP-7), a cell-bound proteoglycan (syndecan-1) and a CXC chemokine (KC) (Li et al., 2002). When damaged, lung epithelial cells secrete the chemokine KC (and probably other chemokines as well), which binds to preexisting syndecan-1 molecules. MMP-7 is also induced by tissue injury, secreted by wound-edge epithelia and anchored to the heparan sulfate chains of cell surface proteoglycans (Yu and Woessner, 2000). MMP-7 cleaves the syndecan-1 core protein to release the ectodomain-KC complex. The shed complex is then transported, either actively or passively, to the apical surface where it forms a chemotactic gradient which guides neutrophils to the alveolar space (Li et al., 2002). Syndecan-1 ectodomain shedding by MT1-MMP results in enhanced tumor cell migration (see Section 1.4.6), while cleavage by MMP-7 is required for directing neutrophil migration to injured lung tissue. Further clarification of such chemotactic processes is important to allow control of the inflammatory process, in order to improve the removal of



micro-organisms and the repair of tissues, while limiting damage (Li et al., 2002; Shapiro, 2003).

3.2.2 Leukocyte-Selectin (L-Selectin)

Leukocyte-selectin (L-selectin, lymph node homing receptor, leukocyte adhesion molecule-1 [LAM-1], leukocyte surface antigen Leu-8, TQ1, leukocyte-endothelial cell adhesion molecule-1 [LECAM-1], gp90-MEL, MEL-14 antigen, CD62L) is a member of the selectin family of adhesion molecules. L-, P-, and Eselectins each possess a C-type lectin domain, specialized to recognize specific oligosaccharides on mucins and other glycoproteins. Selectins mediate the process of reversible "rolling" in the binding of leukocytes in the bloodstream onto (activated) endothelial cells and specialized endothelial cells lining the high endothelial venules (HEVs) in lymph nodes (Gallatin et al., 1983; Ley and Kansas, 2004).

L-selectin shows the unique property of being cleaved in the membrane-proximal extracellular domain with concomitant release of a soluble fragment that contains the functional lectin and EGF domains. This provides a rapid mechanism for the regulation of L-selectin levels on leukocytes, and hence, controls their ability to migrate into tissues. An extended variety of stimuli, such as chemotactic factors, phorbol ester activation and reagents that cross-link L-selectin, induce L-selectin proteolysis (Preece et al., 1996). The hydroxamic acidbased MMP inhibitor, Ro 31-9790, completely prevents shedding of L-selectin from leukocytes in mice, rats, and humans. In vitro reduction of L-selectin-positive leukocytes is mediated by MMP-1, and to a lesser extent by MMP-3, while MMP-2 and MMP-9 have no such effect. However, lymphocytes do not express MMP-1 and MMP-3, and L-selectin levels are not affected by TIMP-1. Moreover, the L-selectin sheddase only acts in cis (on the same cell) and not in trans configuration (Preece et al., 1996). This shedding is only inhibited by TIMP-3, and not by TIMP-2 (Borland et al., 1999). TACE was identified as the L-selectin sheddase following PMA stimulation (Peschon et al., 1998). However, multiple agents induce L-selectin shedding and have structural requirements that differ from PMA-induced shedding (Smalley and Ley, 2005). In addition, with the use of TACE deficient mice, a significant sheddling of L-selectin was still detected, and a small fraction of this shedding was not inhibited by a metalloprotease inhibitor, suggesting that there may be more than one additional sheddase (Walcheck et al., 2003). Thus, separate proteolytic mechanisms of L-selectin shedding may play a role under a variety of distinctive conditions, for instance to regulate distinct antiadhesive mechanisms. As L-selectin mediates crucial leukocyte adhesion and migration processes in inflammation, the elucidation of the functional implications of L-selectin shedding was of paramount importance. Using inhibitors of Lselectin shedding it was demonstrated that L-selectin release participates in regulating neutrophil rolling. Moreover, shedding of L-selectin limits leukocyte activation and thus may limit inflammation. Interestingly, plasma of healthy humans and mice contains approximately 1.6 μ g/mL of soluble L-selectin. As sL-selectin concentrations of 0.9 μ g/mL already reduce lymphocyte migration to peripheral lymphe nodes by over 30%, shedded L-selectin was suggested to regulate normal lymphocyte trafficking and possibly the inflammatory response (Smalley and Ley, 2005). Studies with transgenic mice expressing shedding-resistant L-selectin showed that Lselectin shedding has a role in minimizing reentry of T-cells into peripheral lymph nodes following activation and limits neutrophil adhesion at sites of inflammation. Mice lacking the ability to shed L-selectin on neutrophils also showed reduced neutrophil migration to inflammatory chemokines, suggesting that L-selectin shedding is required for efficient transendothelial migration (Smalley and Ley, 2005). Specification of the other sheddases in charge might contribute to further understanding and control of leukocyte mobility in inflammatory processes.

3.2.3 Kit-Ligand (KitL)

Kit ligand (c-KitL, stem cell factor [SCF], mast cell growth factor [MGF]) is a 31 kDa membrane-bound growth-stimulating cytokine, which is proteolyzed into an active soluble form (sKitL, 164 amino acids) (Heissig et al., 2002). KitL exists in homodimers, and binding to its cell surface receptor c-Kit (SCF receptor or CD117) thus causes dimerization of this TKR. Dimerization of c-Kit in turn results in autophosphorylation and activation of the receptor and of downstream signal transduction proteins, involved in cell proliferation, survival and chemotaxis. KitL is found on stromal cells of the bone marrow, on vascular smooth muscle cells and on endothelial cells, whereas c-Kit is expressed on a variety of cell types, including mast cells, hematopoietic progenitor cells, melanocytes, germ cells and gastrointestinal pacemaker cells (Akin and Metcalfe, 2004).



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sKitL plays a key role in the maintenance and reconsitution of the stem and progenitor cell pool. Under steady-state conditions, quiescent c-Kit⁺ hematopoietic stem cells (HSCs) and circulating endothelial progenitors (CEPs) reside in a niche in close contact with stromal cells from the bone marrow, including osteoblasts. Membrane-bound cytokines such as KitL transmit survival signals and support the adhesion of stem cells to the stroma. Bone marrow ablation (e.g., by cytotoxic agents) induces upregulation of MMP-9, which cleaves KitL. Released sKitL confers signals that enhance mobility of c-Kit⁺ HSCs and CEPs. As a result, they can translocate into a vascular-enriched proliferative zone, which stimulates differentiation and mobilization into the peripheral blood stream (Heissig et al., 2002). The net number of circulating leukocytes is dependent on the balance between production in the bone marrow, and margination and migration of leukocytes into peripheral tissues and spleen (Opdenakker et al., 1998). Consequently, sKitL release by MMP-9 is crucial for the maintenance of leukocyte homeostasis in the blood, and might be a key step in the recruitment of bone marrow stem cells during cell therapy for cancer and other diseases.

In addition, MMP-9-mediated shedding of KitL also affects smooth muscle function and development of intimal hyperplasia, as this process, characterized by transformation of medial smooth muscle cells from a quiescent contractile to a synthetic proliferative phenotype, seems to be influenced by autocrine sKitL/c-Kit signal transduction (Hollenbeck et al., 2004). The importance of KitL ectodomain proteolysis by MMP-9 is further confirmed by the extended variety of physiological processes affected by KitL/c-Kit signaling, such as maintenance of adult lymphopoiesis in bone marrow and thymus (Waskow et al., 2002), survival, differentiation, chemotaxis, and functional activation of mast cells, melanocyte development and regulation of oogenesis, folliculogenesis, and spermatogenesis (Akin and Metcalfe, 2004).

3.3 Recognition and Clearance of Pathogens in Innate Host Defense

3.3.1 CD14

Surfactant protein-D (SP-D) and CD14 are important innate immune defense molecules that mediate clearance of pathogens and apoptotic cells from the lung. CD14 (monocyte differentiation antigen CD14, myeloid cell-specific, leucine-rich glycoprotein) is a 55 kDa pattern recognition receptor that is present on the surface of monocytes, macrophages and neutrophils. As a GPI-linked receptor, it lacks a cytoplasmic signaling domain and, therefore, it requires interaction with other receptors to elicit its biological responses. CD14 binds LPS and interacts with toll-like receptor 4 (TLR4) and myeloid differentiation protein 2 (MD-2) enhancing MAPK signaling and production of cytokines and chemokines (Antal-Szalmas, 2000). Additional biological functions mediated by CD14 include the transport of lipids, phagocytosis of bacteria, and clearance of apoptotic cells. CD14 also exists as a soluble molecule (sCD14) found in normal human serum and in culture supernatans of monocytes and cell lines. Two molecular forms of sCD14 with different origins have been characterized. First, some CD14 molecules escape GPI anchor attachment. They are stored intracellularly and released spontaneously as 55 to 56 kDa full-length molecules upon a short temperature shift at 37°C. Second, various stimuli such as PMA, interferon (IFN)-γ or LPS, induce shedding of the GPIanchored CD14, resulting in sCD14 with a molecular mass of 48 to 49 kDa (Antal-Szalmas, 2000). SP-D plays a central role in the pulmonary host defence and is a member of the collectin (collagen-lectin) family, which form multimeric structures consisting of a collagenous NH₂-terminal domain and a globular COOH-terminal carbohydrate recognition domain that binds oligosaccharides at the surfaces of many microorganisms and mediates phagocytosis and killing by phagocytic cells. SP-D knockout mice (SP-D^{-/-}) develop progressive emphysema that is characterized by chronic inflammation, accumulation of surfactant phospholipids, and infiltration with lipid-laden alveolar macrophages (Hartl and Griese, 2006). CD14 is reduced on alveolar macrophages from SP-D^{-/-} mice and is associated with reduced uptake of LPS and decreased production of TNF- α after LPS stimulation. In addition, sCD14 is increased in the bronchoalveolar lavage (BAL) fluid from SP-D^{-/-} mice, while MMP-9 and MMP-12 activities are enhanced in the lungs. Since treatment of macrophages with MMP-1 reduced the level of cell surface CD14 (Bryniarski et al., 2003), MMP-9 and/or MMP-12 were also candidates for the proteolysis of cell surface CD14 to release sCD14 in SP-D^{-/-} mice. sCD14 was indeed significantly reduced in BAL fluid from MMP-9^{-/-}/SP-D^{-/-} and MMP-12^{-/-}/SP-D^{-/-} mice compared with SP-D^{-/-} mice.



In addition, MMP-12 treatment of RAW 264.7 cells increased sCD14 in the cell culture medium, supporting the concept that MMP-12 cleaves CD14 from the alveolar macrophage cell surface (Senft et al., 2005). Since it was not investigated whether MMP-9 cleaves CD14 in vitro, and MMP-12 is decreased in MMP-12^{-/-}/SP- $D^{-/-}$ mice, the exact contribution of MMP-9 remains unclear.

In conclusion, SP-D loss results in reduced innate host defence activities, such as decreased LPS uptake and TNF- α production, through shedding of CD14 by MMP-12. In addition, upon recognition of Gramnegative bacterial LPS, sCD14 has a dual regulatory role that is concentration- and environment-dependent. Low concentrations of sCD14 seem to promote beneficial pro-inflammatory responses to LPS at local sites of infection, whereas high circulating sCD14 concentrations may help control potentially harmful systemic responses to LPS (Kitchens and Thompson, 2005). In summary, MMP-12 may be an interesting target in the regulation of microbial clearance and inflammatory processes that are important for host defense and pulmonary homeostasis. However, more investigation will be required to better understand the dual activities of sCD14 in the host during infection.

3.4 Membrane-bound MMP **Substrates in Autoimmune Diseases**

3.4.1 Bullous Pemphigoid

3.4.1.1 Bullous Pemphigoid Antigen-2 (BP180)

Bullous pemphigoid (BP) is an autoimmune blistering disease of the skin affecting primarily the elderly. Blister formation by detachment of the epidermis from the underlying dermis occurs within the lamina lucida of the basement membrane and is initiated by deposition of IgG autoantibodies and complement components along the basement membrane zone. These autoantibodies are directed against two major hemidesmosomal components, the 230 kDa intracellular protein BP230 (Bullous pemphigoid antigen-1 [BPAG1], Hemidesmosomal plaque protein, Dystonia musculorum protein, Dystonin) and the 180 kDa transmembrane protein BP180 (Bullous pemphigoid antigen-2 [BPAG2]/HD4/Type XVII collagen). Autoantibody deposition causes complement activation and mast cell degranulation, essential for the recruitment and infiltration of inflammatory cells with subsequent degradation of hemidesmosomal and ECM components (Liu, 2003). Proteinases and reactive free radicals from infiltrating inflammatory cells contribute to tissue damage in BP lesions. Blister fluid and fluid at lesional and perilesional regions indeed contain proteolytic enzymes such as neutrophil elastase (NE), plasmin and plasminogen activators, cathepsin G, collagenases and gelatinases, MMP-2 and MMP-9 (Liu et al., 1998; Liu et al., 2000 a; Liu et al., 2000b). In vitro experiments show that NE as well as MMP-9 cleave the extracellular, collagenous domain of a recombinant BP180-Glutathion S-transferase (GST) fusion protein. NE deficient and MMP-9 deficient mice are resistant to blister formation after intracutaneous injection of BP180-specific antibodies, although these mice show deposition of autoantibodies at the dermis-epidermis junction. Moreover, blister formation is completely abolished by the α 1-proteinase inhibitor (α 1-PI), the major NE inhibitor (Liu et al., 2000b) and in vivo BP180 is proteolyzed by NE, but not by MMP-9 (Liu et al., 2000a). Consequently, NE is the main tissue-damaging enzyme in murine experimental BP, whereas neutrophil MMP-9 most likely contributes indirectly by inactivating α 1-PI, in this way potentiating NE action. In addition, MMP-9 might collaborate with NE in the fragmentation of other proteins, in this way generating and/or maintaining the chemoattractant gradients needed for neutrophil infiltration, an essential step in the blistering process of experimental BP (Liu et al., 1997; Liu et al., 2000b). MMP-9 activation was shown to be plasmin-dependent and independent of MMP-3 (Liu et al., 2005). NE is the BP180-cleaving enzyme in human BP as well (Verraes et al., 2001). In addition, TIMP-1 is present in five-fold molar excess to MMP-9, indicating that cleavage of α 1-PI by MMP-9 is less probable in human BP. However, in an in vitro model of BP, inhibition of MMP-9 with a specific monoclonal antibody does abolish blister formation (Shimanovich et al., 2004). As a consequence, the contribution of MMP-9 to disease progression is not as clear in humans as it is in mice. This discrepancy might be explained by the differences that exist between murine and human BP. For instance, the majority of biopsies from BP patients show large numbers of eosinophils in their lesional skin, whereas in mice neutrophils are the predominant inflammatory cells. However, some patients may have neutrophilrich or cell-poor lesions. These varying and different pathological features in human BP indicate that BP is a heterogenous disease. Subepidermal blistering can



be caused by several mechanisms and cell types, the above mentioned immunopathological cascade being one of them (Liu, 2003). Since BP180 is also an autoantibody target in several other subepidermal blistering diseases including cicatricial pemphigoid, herpes gestationis, linear IgA bullous dermatosis, and lichen planus pemphigoides (Liu, 2003), further identification of the tissue damaging-proteases in these skin autoimmune disorders might allow to develop therapies based on the use of synthetic protease inhibitors or inhibitory monoclonal antibodies.

3.4.2 Rheumatoid Arthritis

3.4.2.1 FasL

Rheumatoid arthritis is a chronic inflammatory autoimmune disease, which results in inflammation of the synovial lining and destruction of the adjacent bone and cartilage. Synovial macrophages, fibroblasts and lymphocytes are critical for the pathogenesis of this disease, in which apoptosis may play divergent roles (Liu and Pope, 2003). Insufficient intra-articular apoptosis induces proliferation of the synovial membrane (Sakai et al., 1998; Okamoto et al., 1998). In joints of patients with active rheumatoid arthritis, few apoptotic cells are detected, which might contribute to persistence of the disease (Pope, 2002). MMP-3 concentrations in the synovial fluid of rheumatoid arthritis patients are closely correlated with increased sFasL levels and with disease activity. Consequently, MMP-3 might contribute to the pathogenic mechanism by cleaving FasL, in this way reducing apoptosis (sFasL is a less potent apoptosisinducer than its membrane-bound precursor, see Section 1.2.1). However, sFasL shedding was not completely blocked by an MMP inhibitor alone, indicating that further investigation is needed for detection of the other proteases involved (Matsuno et al., 2001). Moreover, rheumatoid arthritis is characterized by a very heterogenous disease course with strong synovial proliferation in early disease, whereas in the later stages synovial proliferation is reduced and often replaced by connective tissue (Smith and Walker, 2004). As a consequence, stimulation of apoptosis, for instance by MMP inhibition, might have some therapeutic benefit, but requires further insight into the exact role of apoptosis in the subsequent stages of rheumatoid arthritis.

3.4.2.2 RANKL

Another important TNF family member in rheumatoid arthritis is RANKL. In the absence of RANKL or RANK, osteoclast differentiation from monocyte precursors does not occur (see Figure 13). RANKL is expressed on T-cells and fibroblasts within the synovial inflammatory tissue of patients with rheumatoid arthritis and its expression is regulated by pro-inflammatory cytokines. In animal models of arthritis, blockade of RANKL-RANK interactions, or a genetic absence of RANKL or RANK, protects against joint damage despite the presence of joint inflammation (Schett et al.,

As discussed before, RANKL is a transmembrane glycoprotein that can be converted to a soluble form by ectodomain shedding (see Section 1.4.12). Besides MMP-7, TACE cleaves RANKL in vitro (Lum et al., 1999), but further in vitro experiments show no difference in sRANKL shedding from fibroblasts with or without TACE (Schlondorff et al., 2001). However, two other RANKL shedding activities can be discerned in these fibroblast cultures. One is induced by the tyrosine phosphatase inhibitor pervanadate and its TIMP inhibition profile is similar to that of several MT-MMPs. The other is constitutive and is insensitive to any TIMP. MT1-MMP overexpression indeed causes increased RANKL release, the ectodomain being cleaved between Met145 and Met146 (Schlondorff et al., 2001). In accordance with these observations, Western Blot of sRANKL shows two bands with molecular weights of 25 kDa and 24 kDa, that are produced by cleavage at Arg138-Phe139 and Met145-Met146, respectively (Hikita et al., 2006). Experiments with inhibitors suggest that the upper band is produced by an ADAM and the lower band by an MMP. A large number of MMPs were shown to cleave RANKL in a RANKL shedding activity screening system, with a fusion protein. However, only MT1-MMP, MT2-MMP, MT3-MMP, and MT5-MMP cleaved full-length RANKL and generated sRANKL with the expected molecular weight. Real-time PCR showed that MT1-MMP mRNA level was much higher than that of MT2-, MT3-, and MT5-MMP in a bone marrow stromal cell line and in primary osteoblasts, suggesting that MT1-MMP is mainly involved in the production of the 24 kDa band. Reduced MT1-MMP expression in primary osteoblasts by siRNA or its deficiency in MT1-MMP knockout mouse osteoblasts reduced RANKL shedding and increased membrane-bound RANKL, which led to increased osteoclastogenic activity in the cells. Conversely, overexpression of MT1-MMP in osteoblasts suppressed osteoclastogenesis. In addition, although sRANKL produced



by MT1-MMP induced osteoclastogenesis from bone marrow macrophages, the culture medium of activated primary osteoblasts did not induce osteoclastogenesis, even when MT1-MMP was overexpressed. These results suggest that membrane-bound RANKL induces osteoclastogenesis more efficiently than sRANKL, and the ectodomain shedding of RANKL by MT1-MMP negatively regulates osteoclastogenesis, which is in accordance with a previous report (Nakashima et al., 2000). Consistent with these in vitro observations, soft X-ray images of MT1-MMP deficient mice displayed osteoporosis and a much higher osteoclast number, while the serum level of sRANKL in the MT1-MMP knockout mice was undetectable (Hikita et al., 2006). In conclusion, MT1-MMP was identified as the major endogenous RANKL sheddase in primary osteoblasts and RANKL shedding seemed to downregulate local osteoclastogenesis.

As MMP-7-released sRANKL is as efficient in osteoclast activation as its full-length precursor (see Section 1.4.12 and Figure 13), it seems paradoxical that cleavage by MT1-MMP at the same site in the ectodomain releases a less active form. However, Hikita and colleagues indeed mentioned that the concentration of the sRANKL produced by MT1-MMP in the culture media was more than tenfold lower than the concentration needed to induce osteoclastogenesis with recombinant sRANKL in vitro. It is possible that when the expression of RANKL is highly upregulated, MMP-released sRANKL does have substantial effects on general bone metabolism. Hence, further insight into RANKL shedding by MMPs and its concomitant biological consequences in vivo may be crucial in the clarification of some osteoarticular pathologies, including rheumatoid arthritis.

3.4.2.3 ADAMTS-4

Aggrecan hydrates the collagen network and thus provides cartilage with its properties of compressibility and elasticity. Degradation of aggrecan can be mediated by two proteases of the ADAMTS family: ADAMTS-4 and ADAMTS-5 (Malfait et al., 2002). ADAMTS-4 (aggrecanase-1, ADMP-1) is synthesized as a protein containing a signal peptide, prodomain, catalytic domain with a Zn²⁺-binding motif, disintegrin-like domain, thrombospondin Type I motif, a spacer region and a cysteine-rich domain (Tortorella et al., 1999). The intracellular proprotein convertases (PCs), furin, PACE4 and PC5/6 efficiently remove the prodomain

through cleavage at Arg212-Phe213, generating an active enzyme. Interestingly, the secreted proteases trypsin, MMP-9, and in a much lesser extent MMP-13, are also effective in removing the prodomain of ADAMTS-4, but the cleavage by MMP-9 occurs at a site other than the PC/trypsin cleavage site. The MMP-9-activated species cleaves the aggrecan peptide substrate, but not native aggrecan, suggesting that the alternative cleavage site changes substrate specificity of the enzyme (Tortorella et al., 2005). In addition to NH₂-terminal activation, it has been suggested that truncation of the COOH-terminus of ADAMTS-4 by a TIMP-1-sensitive GPI-anchored MMP, MT4-MMP, is required for full catalytic activity against aggrecan (Gao et al., 2002). ADAMTS-4 (p100) and MT4-MMP are first processed intracellularly by furin-mediated removal of the prodomains, followed by their association in the secretory pathway. The GPI-anchored MT4-MMP/ADAMTS-4 (p68) complex moves to the cell surface, where MT4-MMP removes the spacer domain of ADAMTS-4 (p68), generating the p53 form, which can be found in association with both chondroitin and heparan sulfate on syndecan-1. ADAMTS-4 (p40) is generated by removal of the spacer region as well as the cysteine-rich domain, and appears in the medium. Analysis with specific antibodies shows that MT4-MMP cleaves at the Lys694-Phe695 and Thr581-Phe582, to generate the p53 and the p40 form, respectively (Gao et al., 2004). Modification of synthesis, furin-mediated activation and/or GPI-anchoring of MT4-MMP may thus be ways to control ADAMTS-4 activation specifically, in this way preventing the destructive aggrecanolysis seen in human joint diseases such as arthritis. Therapeutic agents interfering with the association of ADAMTS-4, MT4-MMP and syndecan-1 on the cell surface might also be promising in this cartilageprotecting approach. In addition, if MMP-9 activates ADAMTS-4 extracellularly, it will be important to establish which ECM proteins are cleaved by MMP-9activated ADAMTS-4, and whether it has an impact on cartilage turnover in joint diseases.

3.4.3 Multiple Sclerosis

3.4.3.1 Myelin Basic Protein (MBP)

Multiple sclerosis is a chronic neurological disorder of the central nervous system (CNS), characterised by the breakdown of the BBB, perivascular infiltration of inflammatory cells and demyelination. Extracellular



proteases, such as some MMPs, plasmin and plasminogen activators form an amplification cascade in this autoimmune disease by: 1) increasing the permeability of the BBB; 2) demyelination through degradation of myelin basic protein (MBP, myelin A1 protein, myelin membrane encephalitogenic protein), a major component of the myelin sheath and one of the most abundant proteins of the CNS; 3) release of antigenic peptides which contribute to autoimmunity; and 4) facilitating infiltration and migration of immune cells through the ECM and the basal membrane (Opdenakker and Van Damme, 1994; Chandler et al., 1995; Cuzner and Opdenakker, 1999; Opdenakker and Van Damme, 2002; Opdenakker et al., 2003). Various MMPs cause MBP degradation in vitro, the most active enzymes on this substrate being MMP-2 and MMP-12, followed by MMP-3; and by MMP-1, MMP-7, and MMP-9 with comparable but lesser activity (Proost et al., 1993; Chandler et al., 1995; Chandler et al., 1996). MMP-9 activity is detected in the cerebrospinal fluid of patients with multiple sclerosis and other neurological inflammatory disorders (Gijbels et al., 1992). Furthermore, young MMP-9 deficient mice are resistant to experimental autoimmune encephalomyelitis (EAE), a murine model for multiple sclerosis (Dubois et al., 1999). MMP-9 generates encephalitogenic peptides by cleavage of human MBP at four different sites in vitro: between Phe90-Lys91, Ser110-Leu111, Phe114-Ser115, and Asp133-Tyr134 (Proost et al., 1993). Furthermore, in vivo MBP degradation is also exerted by MMP-9, as MBP proteolysis after transient focal ischemia is significantly reduced in MMP-9 knockout mice compared with wild-types (Asahi et al., 2001).

3.4.3.2 NG2 Proteoglycan

Conversely, besides these disease-promoting roles in multiple sclerosis, MMP-9 also has a beneficial role after demyelinating CNS injury. MMP-9 knockout mice are impaired in myelin reformation after lysolecithininduced demyelination. This might be explained by the role of MMP-9 in the clearance of injury-induced deposits of NG2 proteoglycan (chondroitin sulfate proteoglycan NG2, melanoma-associated chondroitin sulfate proteoglycan), an inhibitory transmembrane proteoglycan that retards the maturation and differentiation of oligodendrocytes needed for remyelination. Consequently, MMP-9 is needed for an efficient remyelination and in this way also has a reparative function in multiple sclerosis (Larsen et al., 2003).

3.4.3.3 β -Dystroglycan

Dystroglycan (dystrophin-associated glycoprotein 1) exists as an extracellular highly glycosylated α -subunit and a non-covalently associated transmembrane β -subunit, which are products derived from one gene and result from posttranslation processing of the glycoprotein. The α -subunit binds to several extracellular ligands, including laminin, agrin, perlecan and neurexin, while β -dystroglycan connects intracellularly to dystrophin, which binds to the actin cytoskeleton. Dystroglycan is expressed in many cell types and the broad range of ECM ligand partners indicates that it has an important role in the assembly and maintenance of basement membranes (Barresi and Campbell, 2006).

The 43 kDa β -subunit was shown to be processed to a 30 kDa fragment by MMPs, the inhibitor profile pointing to MMP-2, MMP-9, and MT1-MMP as possible candidates (Yamada et al., 2001). Kaczmarek and coworkers observed β -dystroglycan breakdown in the brain in response to kainate in a temporal pattern parallel to increased MMP-2 and MMP-9 activities (Kaczmarek et al., 2002). This temporal parallelism of MMP-2 increase and β -dystroglycan proteolysis was also observed in the superior cervical ganglion after postganglionic nerve lesion (Leone et al., 2005; Paggi et al., 2006). However, Agrawal and coworkers (2006) were the first to show that MMP-2 and MMP-9 cleave β -dystroglycan *in vitro* as well as in vivo, as they identified β -dystroglycan as a key substrate of MMP-2 and MMP-9 in EAE. This study demonstrates that leukocyte cuffing, as it occurs in human multiple sclerosis, is the consequence of the containment of leukocytes between the endothelial and the adjacent parenchymal basement membranes around the blood vessels in the CNS. Obviously, as long as the leukocytes are contained by the parenchymal basement membrane, synthesized by the astrocyte endfeet of the glia limitans, no disease symptoms occur. Gelatinases, both MMP-2 and MMP-9, cleave in situ β -dystroglycan in the parenchymal basement membrane and this process coincides with barrier breakdown, infiltration of the CNS parenchyma by leukocytes and development of disease symptoms. As a result, double MMP-9 and MMP-2 knockout mice are completely resistant against disease development. This cleavage is a critical event, since this MMP substrate is localized on the interface between the extracellular milieu and the astrocytes: its cleavage results in complete desintegration of the glia limitans structure and function (Agrawal et al., 2006).



Proteolysis of β -dystroglycan by MMPs may also contribute to cancer growth and spread (Jing et al., 2004), as well as to skeletal muscle degeneration in the muscular diseases sarcoglycanopathy and Duchenne muscular dystrophy (Matsumura et al., 2005).

Administration of synthetic MMP inhibitors to rodents with EAE significantly ameliorates clinical symptoms and pathological signs (Cuzner and Opdenakker, 1999). Therefore, a major challenge in multiple sclerosis therapy development is the design of selective and specific MMP inhibitors, taking into account the multiple disease-affecting functions of some MMPs, like for instance the role of MMP-9 in demyelination as well as in remyelination (Opdenakker et al., 2003).

3.4.4 Systemic Sclerosis

3.4.4.1 uPAR

Systemic sclerosis (Ssc), also called scleroderma, is a clinically heterogenous, systemic disorder which affects the connective tissue of the skin, internal organs and the walls of blood vessels. It is characterized by alterations of the microvasculature, disturbances of the immune system and massive deposition of collagen and other matrix substances in the connective tissues (Haustein, 2002; Chen et al., 2003). Defective angiogenesis, resulting in tissue ischemia, is particularly prominent in the diffuse form of Ssc. As the u-PA/uPAR system is critical in angiogenesis (see Section 1.3.1), microvascular endothelial cells (MVECs) were isolated from the dermis of healthy individuals and from the dermis of patiens with diffuse Ssc to examine u-PA and uPAR levels. Compared with MVECs from healthy skin, MVECs from Ssc patiens showed higher expression of uPAR. However, in Ssc MVECs, uPAR undergoes truncation between its D1 and D2 domains (see Figure 7), which impairs u-PA binding to uPAR. These properties of Ssc MVECs were associated with poor spontaneous and u-PA-dependent invasion, proliferation, and capillary morphogenesis. The uPAR cleavage occurring in Ssc MVECs was associated with overexpression of MMP-12 and both a general hydroxamate inhibitor of MMP activity and anti-MMP-12 antibodies restored this Ssc MVEC-induced impaired functioning (D'Alessio et al., 2004). In addition, fibroblasts from Ssc patients overexpress MMP-12, which cleaves uPAR of MVECs, thus contributing to the failure of Ssc-endothelial cells to induce an efficient angiogenic programme (Serrati et al., 2006). The overexpression of MMP-12 by both Ssc endothelial cells and Ssc fibroblasts indicates that MMP-12 overproduction may have a critical pathogenic role in Ssc-associated vascular alterations. Hence, selective inhibitors of MMP-12 are likely to be efficient at inducing reversal of Ssc-associated lack of angiogenesis, whereas MMP-12 itself seems disease limiting in cancer by blocking angiogenesis (see Section 1.3.1).

4. PROTEOLYSIS OF CELL SURFACE PROTEINS IN NEURODEGENERATIVE **DISORDERS: ALZHEIMER'S DISEASE**

Alzheimer's disease is a neurodegenerative disease of the CNS associated with progressive loss of recent memory, resulting in dementia. A clinical diagnosis of Alzheimer's disease is confirmed by observing neuritic (amyloid) plaques and neurofibrillary tangles in the hippocampus, amygdala, and association neocortex (Selkoe, 2004). The plaques are formed extracellularly and are composed of the 42- and 40-residue β -amyloid proteins (A β s). In healthy individuals, 90% of the A β s produced by brain cells throughout life are A β 40 peptides *versus* only 10% of A β 42. In the cortex of mentally normal elderly patients the A β deposits found are almost exclusively 'diffuse' plaques that seem to represent the relatively benign precursor lesions. These diffuse plagues are composed of A β 42, which is far more prone to aggregation than the slightly shorter and less hydrofobic A β 40. The A β hypothesis predicts that gradual elevation of A β 42 levels in brain interstitial fluid, and perhaps also inside neurons, can lead to the oligomerization of the peptide and eventually to its fibrillization, that is, amyloid formation. Such insoluble amyloid fibrils are characteristic for 'neuritic' plaques which are associated with local microglial activation, astrocytosis, and cytokine and acute phase protein release. These local inflammatory processes and other neurotoxic effects of oligomerized A β s finally lead to extensive neuronal and synaptic dysfunction and neurotransmitter deficits, which all contribute to memory impairment (Selkoe, 2004; Walsh and Selkoe, 2004).

4.1 Amyloid Precursor Protein (APP) and β -Amyloid Proteins (A β s)

 $A\beta$ is derived from a membrane-bound $A\beta$ precursor protein (APP, cerebral vascular amyloid peptide (CVAP), protease nexin-II (PN-II), Alzheimer disease amyloid protein, PreA4) after sequential cleavages by



a β -secretase and a γ -secretase (Selkoe, 2004). In normal processing of APP, the most common cut is carried out by the α -secretase and occurs between Lys 687 and Leu 688, that is 12 residues NH₂-terminal to the transmembrane region, between Lys16 and Leu17 of the A β region (Figure 17). This cleavage creates a large, soluble ectodomain fragment (sAPP α) that is released from the cell surface and leaves a COOH-terminal fragment of 83 amino acids embedded in the membrane. APP is also cleaved between Met671 and Asp672 by a β -secretase, releasing a slightly shorter fragment of APP (sAPP β) and leaving a membrane-embedded COOH-terminus of 99 amino acids. This 99 amino acid fragment can then be cleaved by a γ -secretase to create A β . In summary, proteolysis by an α -secretase releases sAPP from the cell surface, while sequential cleavages by a β - and a γ -secretase lead to A β formation (Selkoe, 2004).

The α -secretase is a membrane-associated metalloproteinase, the activity of which is readily inhibited by hydroxamate-based synthetic inhibitors (Higashi and Miyazaki, 2003b). Furthermore, release of sAPP is extremely diminished in fibroblasts from TACE deficient mice vs. control mice, making TACE a prime candidate for the α -secretase activity (Buxbaum *et al.*, 1998). MMP-2 is capable of processing APP in vitro, but it is not clear whether the cleavage occurs between Lys 687 and Leu 688, like an α -secretase (Miyazaki *et al.*, 1993; Miyazaki et al., 1994) or between Glu668-Val669,

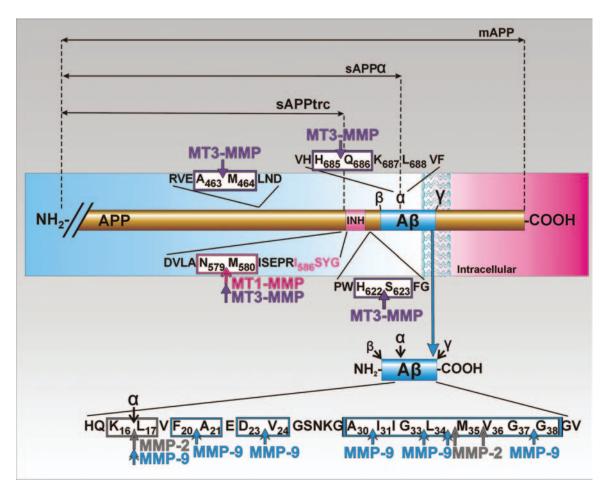


FIGURE 17 Differential cell surface proteolysis of APP and A β leads to accumulation or clearance of pathogenic A β peptides in Alzheimer's disease. A β (β -amyloid protein) is derived from the membrane-bound A β precursor protein (mAPP) after sequential cleavages by a β -secretase and a γ -secretase. However the most common processing of APP is carried out by the α -secretase and occurs between Lys 687 and Leu 688, that is between Lys16 and Leu17 of the A β region. This cleavage creates a large, soluble ectodomain fragment $(sAPP\alpha)$. A different processing of APP, between Asn579-Met580, is catalyzed by MT1-MMP and MT3-MMP, and releases a COOH-terminally truncated APP fragment (sAPPtrc) that lacks the MMP-2 inhibitor domain (INH). MT3-MMP cleaves the APP ectodomain at additional sites: at Ala463-Met464, His622-Ser623, and His685-Gln686, which is near the α -secretase cleavage site. Similar to α -secretase cleavage, proteolysis of the His685-Gln686 peptide bond destroys the A β -sequence, which diminishes pathologic A β formation and accumulation. Once released, A β may be cleared by MMP-2 and MMP-9, which cleave it at multiple sites. In addition, MMP-9 has been shown to degrade Aβ fibrils, by proteolytic cleavage at Phe20-Ala21 and Ala30-Ile31. Adapted from (Higashi and Miyazaki, 2003b).



like a β -secretase (LePage et al., 1995). Furthermore, in vivo studies with MMP-2 knockout mice suggest that MMP-2 does not play an essential role in the generation of APP fragments at physiological conditions (Itoh et al., 1997). MMP-3 was also reported to cleave a synthetic APP peptide spanning the β -secretase cleavage site at the residues Glu668-Val669 and Glu674-Phe675 in vitro, but this was not further investigated (Rapala-Kozik et al., 1998). APP binds to the ECM and contains an MMP-2-inhibitory domain, which is located in the COOHterminal glycosylated region of the sAPPs (Miyazaki et al., 1993) within the ISYGNDALMP sequence corresponding to the residues 586 to 595 of APP (Higashi and Miyazaki, 2003a). Another cell-bound MMP might thus be responsible for APP proteolysis. Cellmediated activation of MMP-2 is indeed accompanied by a different processing of APP, between Asn579 and Met580, which is catalyzed by MT1-MMP and releases a COOH-terminally truncated APP fragment (sAPPtrc) that lacks the MMP-2 inhibitor domain (Figure 17) (Higashi and Miyazaki, 2003b).

An analogy exists in cancer biology, in which APP proteolysis at the ruffling edge of migrating cancer cells (see Figure 2) may be another mechanism by which MT1-MMP promotes migration and invasion (see Section 1.4). It may indeed be suggested that the interplay of MT1-MMP, sAPPtrc, and MMP-2 takes part in the regulation of MMP-2-catalyzed ECM degradation. On the cell surface, where the MT1-MMP concentration is low, APP is liberated mainly as sAPP that inhibits MMP-2 activity. sAPP (as well as APP) binds to the ECM, which might concentrate and enhance the inhibitory effects of sAPP, in this way protecting the ECM near the cell surface from MMP-2 degradation. In contrast, a high (local) concentration of MT1-MMP converts APP to sAPPtrc, which displaces ECM-associated APP or sAPP, thereby removing the MMP-2 inhibitory activity from the ECM. In addition, MT1-MMP activates MMP-2, which can then freely exert its proteolytic activity on the ECM (Higashi and Miyazaki, 2003b). Since autodegradation is a highly critical step in the regulation of MT1-MMP activity (see Section 1.4.10), excess expression of substrates such as APP or syndecan-1 may interfere with the autodegradation and consequently augment the MT1-MMP activation of MMP-2, further promoting MMP-2 proteolytic action.

However, MT1-MMP is not the only MT-MMP expressed in the brain as MT3-MMP expression levels are highest in the brain and localized in microglial

cells in all brain tissues (Takino et al., 1995; Yoshiyama et al., 1998), whereas MT5-MMP is also present in all brain tissues, but most strongly expressed in cerebellum (Sekine-Aizawa et al., 2001). After cotransfection, MT3-MMP and MT5-MMP, but not MT2-, MT4and MT6-MMP, indeed caused cleavage and shedding of the APP ectodomain with a fragmentation pattern almost identical to that of MT1-MMP. MT3-MMP induced shedding of APP most efficiently, followed by MT1-MMP and MT5-MMP (Ahmad et al., 2006). MT3-MMP cleaves the APP ectodomain at multiple sites that are Ala463-Met464, Asn579-Met580, His622-Ser623 and His685-Gln686, which is within the A β sequence (Figure 17), indicating that MT3-MMP could be an α -secretase. Since the APP fragmentation seen after cleavage by MT1-MMP, MT3-MMP and MT5-MMP was almost identical, MT1-MMP and MT5-MMP may cleave APP at the same sites as MT3-MMP (Ahmad et al., 2006). As cleavage of APP by an α -secretase destroys the A β -sequence, shedding of APP by MT1-, MT3- and MT5-MMP might mitigate pathologic $A\beta$ formation and accumulation.

Although familial Alzheimer's disease appears to be caused by $A\beta$ overproduction, sporadic Alzheimer's disease (the most prevalent form) may be caused by impaired A β clearance. A β 40 is a potent inducer of MMP-2, MMP-3 and MMP-9 expression in vitro (Deb and Gottschall, 1996). Furthermore, MMP-2 is capable of degrading A β 40 and A β 42 in vitro at the Lys16-Leu17, Leu34-Met35 and Met35-Val36 peptide bonds, although this does not lead to a complete clearing of A β (Roher *et al.*, 1994). Treatment of cells overexpressing APP with the metal ligand clioquinol and Cu²⁺ or Zn²⁺ resulted in an \sim 85 to 90% reduction of A β 40 and A β 42. This loss of A β was not caused by altered APP processing, but was mediated through upregulation of MMP-2 and MMP-3. Inhibitors of MMP-2 and MMP-3 indeed abrogated the loss of A β 40 caused by clioquinon and Cu²⁺ (White et al., 2006). However, further investigation will be necessary to determine wether MMP-2and MMP-3-mediated cleavage is a rate-limiting step in the rapid clearance of secreted A β in vitro as well as in vivo. Interestingly, the human hippocampus of Alzheimer's disease patients shows increased levels of pro-MMP-9 near the amyloid plaques (Backstrom et al., 1996) and the same increase was reported in amyloidpositive beagle brains (Lim et al., 1997). In addition, levels of circulating MMP-9 are significantly elevated in the plasma of Alzheimer's disease patients compared



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to controls (Lorenzl et al., 2003). MMP-9 processes soluble A β 40 and A β 42 in vitro at multiple sites that are Lys16-Leu17; Phe20-Ala21; Asp23-Val24; Ala30-Ile31; Gly33-Leu34; Leu34-Met35 and Gly37-Gly38 (Figure 17) (Backstrom et al., 1996; Yan et al., 2006) However, in contrast to other proteases that also degrade sA β such as endothelin-converting enzyme, insulin-degrading enzyme, and neprylisin, MMP-9 was the only one to degrade A β fibrils in vitro. In addition, amorphous structures suggestive of decomposed fibrils were observed after incubation with MMP-9. Fibril disruption by MMP-9 produced A β fragment with molecular weights corresponding to A β 20 and A β 30, suggesting that proteolytic cleavage at Phe20-Ala21 and Ala30-Ile31 may be important for fibril degradation. MMP-9 was also shown to degrade compact amyloid plaques in brain sections from aged APP/presenilin(PS)1 mice. Fibrillar $A\beta$ in compact plaques is believed to be extremely resistant to degradation and clearance, but growing evidence suggests that endogenous mechanisms for plaque clearance exist, as amyloid plaque size in brains of AD patients does not invariably increase with disease duration and in aged APP/swedisch mutation(sw) mice (overpoducing APP β), some isolated plaques even decrease in size over time. Furthermore, MMP-9 is expressed in astrocytes surrounding plaques in the brains of aged APP/PS1 mice, and its activity is specifically detected in compact plaques (Yan et al., 2006). Thus, MMP-9 may contribute to clearance of plaques from amyloid-laden brains. In vivo, significant increases in the steady-state levels of $sA\beta$ were found in the brains of MMP-2 and MMP-9 deficient mice compared with wild-type controls. In addition, pharmacological inhibition of the MMPs with the broad-spectrum inhibitor GM6001 increased brain interstitial sA β levels and halflife in APP/sw mice. Under these disease-free steadystate conditions, gene deletion of mmp-2 appeared to have a greater effect on brain A β levels compared with mmp-9 gene deletion (Yin et al., 2006). However, it is possible that under pathological conditions, MMP-9 may play a greater role in $A\beta$ clearance, as its expression was shown to be increased in astrocytes surrounding amyloid plaques, as mentioned above. In summary, a better understanding of the role of MMPs in the clearance of extracellular $sA\beta$ and in the degradation of A β fibrils in amyloid plaques, may point to alternative therapeutical approaches that reduce plaque formation and slow down the disease cascade in early stages.

4.2 FasL

The growing evidence that $A\beta$ accumulation is a determining factor in Alzheimer's disease makes it important to elucidate the mechanism by which A β induces neuronal cell death. It was shown that A β induces neuronal cell apoptosis and that inhibition of FasL and Fas function led to a decrease in A β -induced neuronal apoptosis (Morishima et al., 2001). As discussed before, MMP-7 releases sFasL, which is a less potent apoptosisinducer than its membrane-bound precursor (see Section 1.2.1). Whereas treatment of neuronal cell cultures with $sA\beta$ alone increased the appearance of morphologically apoptotic cells and nuclei, addition of MMP-7 increased sFasL shedding in the culture media and compeletely protected neuron cultures from A β toxicity (Ethell et al., 2002). Hence, FasL shedding by MMP-7 is another important MMP-mediated proteolytic process at the cell surface. Factors that affect this shedding process may play a role in the progression of Alzheimer's disease and may provide an avenue for therapeutic intervention.

5. MEMBRANE-ASSOCIATED PROTEOLYSIS IN REPRODUCTIVE **ENDOCRINOLOGY**

5.1 LRP

Similar to the intense tissue remodelling associated with cancer progression, the human endometrium undergoes cyclic growth and tissue remodelling throughout the reproductive life of women, with the succession of proliferative, secretory, and menstrual phases. In this rapidly changing environment, successful embryo implantation requires a tight control of the integrity of the endometrial tissue at the early and mid-secretory phase. This implies a strict control of u-PA and MMPs, which are repressed by progesterone. As discussed before (see Section 1.4.9), LRP-mediated internalization of proteases is an important regulation mechanism for proteolytic activity at the cell surface. Interestingly, the expression of LRP mRNA also varies during the menstrual cycle, with a significant increase from the proliferative to the secretory phase, when progesterone concentration is the highest, possibly promoting further repression of MMP acitivity (Emonard et al., 2005). Furthermore, LRP is an important molecule during embryonic development (Herz et al., 1992). LRP is highly expressed in the placenta and increased levels of soluble



LRP (sLRP) were detected in cord blood from healthy pregnancy. While sLRP release from BeWo choriocarcinoma cells is prevented by the hydroxamic acid compound, INH-38SS-PI (Quinn et al., 1999), the cleavage is not mediated by MT-MMPs as it involves endoproteolysis of the membrane-spanning β -chain (LRP-85), whereas MT-MMPs cleave in the COOH-terminal part of the α -chain (LRP-515) (see Section 1.4.9 and Figure 10) (Rozanov et al., 2004a). In addition, the metalloproteinase responsible for the cleavage is not induced by PMA. The BeWo cell line, which is derived from a human gestational choriocarcinoma, displays morphological and functional characteristics of both invasive cytotrophoblast and syncytiotrophoblast. The release of biologically active sLRP by trophoblast cells may have implications regarding the biology of the placenta. The pattern of LRP expression in the placenta is consistent with roles for the receptor in trophoblast invasion, a tightly regulated process that involves the coordinated activation of proteases and the transport of cholesterol. In term placenta, LRP is expressed in the syncytium, which comprises the maternal-fetal interface. Increased levels of sLRP in cord blood may reflect cellular dysfunction and increased metalloproteinase activity at this important interface (Quinn et al., 1999). Hence, further investigation into the release of sLRP and its interaction with cellular LRP might be of interest to predict or monitor complications during embryonic development.

5.2 HB-EGF

Transmembrane and soluble HB-EGF have a crucial role in some events of female reproduction biology. Firstly, in blastocyst implantation, mHB-EGF, but not sHB-EGF, has been shown to promote adhesion between the blastocyst and the uterine wall, whereas sHB-EGF has been reported to induce an increase in blastocyst number and an increase in the rate of blastocyst zona pellucida hatching (Raab and Klagsbrun, 1997; Iwamoto and Mekada, 2000). Furthermore, cleavage of mHB-EGF by MMP-7 and the subsequent activation of ErbB4/HER4 by sHB-EGF appear to play a role in the regulation of postpartum uterine and lactating mammary gland involution and maintenance of lactation. CD44 plays a key role in this TMPS (by assembling MMP-7, mHB-EGF and ErbB4 in a cell surface complex (see Section 1.4.7 and Figure 9) (Yu et al., 2002). Moreover, release of sHB-EGF by MMP-2 and MMP-9 is a crucial step in neuroendocrine regulation by the

gonadotropin-releasing hormone (GnRH) which regulates the synthesis and secretion of the gonadotropins luteinizing hormone (LH) and follicle stimulating hormone (FSH) in the pituitary gland. Inhibition of MMP-2 and MMP-9 by selective inhibitors (Ro28-2653) or by specific ribozymes indeed blocks transactivation of the EGFR, induced by the binding of GnRH to its receptor (a GPCR) (Roelle et al., 2003; Shah et al., 2004). MT1-MMP comes out as an additional player in this TMPS through the activation of MMP-2 (Shah and Catt, 2004c). Similar to GnRH, the steroid hormone estradiol (E2) also binds GPCRs, an alternative type of estrogen receptors, and rapidly stimulates signal transduction through transactivation of the EGFR. In this TMPS sHB-EGF release is also mediated by MMP-2 and MMP-9 (Razandi et al., 2003). Thus, ectodomain cleavage of HB-EGF by MMPs is a crucial event in the regulation of some neuroendocrine and reproductive functions.

5.3 Occludin

In the low-resistance human vaginal-cervical epithelia, occludin is present in two main forms: the full-length 65 kDa wild-type isoform, and a truncated 50 kDa form. A shift from 65 kDa to 50 kDa can be induced by treatment with estrogen and is associated with a reversible decrease in the resistance of the tight junctions. MMPs were already described as being responsible for

TABLE 3 pro-TNF- α cleavage sites

Protease	Cleavage site(s)	Test system	References
TACE	Ala76-Val77	<i>In vitro</i> and in vivo	3
MMP-1	Ala74-Gln75 and Ala76-Val77	In vitro	1,2,3
MMP-2	Not defined	In vitro	1,2
MMP-3	Not defined	In vitro	1,2,3
MMP-7	Ala76-Val77	<i>In vitro</i> and ex vivo	1,2,3,6
MMP-9	Ala74-Gln75	In vitro	1,2,3
MMP-12	Ala74-Gln75 and Ala76-Val77	<i>In vitro</i> and in vivo	7,8
MT1-MMP	Ala76-Val77 and before Leu113	In vitro	4
MT2-MMP	Ala76-Val77 and before Leu113	In vitro	4
MT4-MMP	Ala74-Gln75	In vitro	5

^{1, (}Gearing et al., 1994); 2, (Gearing et al., 1995); 3, (Mohan et al., 2002); 4, (d'Ortho et al., 1997);



^{5, (}English et al., 2000); 6, (Haro et al., 2000b); 7, (Chandler et al., 1996); 8, (Churg et al., 2003).

TABLE 4 Potential membrane-bound MMP and MP substrates

Substrate ¹	CD	Inhibitor	Specificity ²	Reference
ACE	CD143	EDTA, O-phen Batimastat (BB-94) TAPI-2	MP Broad spectrum MMP and TACE Zn ²⁺ -dependent MP	(Parvathy <i>et al.</i> , 1997)
		TAPI(-1)	Collagenase, gelatinase, ADAM-10, TACE	(Schwager <i>et al.</i> , 1998; Schwager <i>et al.</i> , 1999)
ANF-R	/	EDTA	MP	(Abe and Misono, 1992)
AR	/	Batimastat (BB-94)	Broad spectrum MMP and TACE	(Vecchi <i>et al.</i> , 1998; Brown <i>et al.</i> , 1998)
C1qRp	CD93	O-phen Not inhibited by: TAPI-1, TAPI-2 and the broad spectrum MMP inhibitors Ro-31–9790, Ro-32–7315	MP	(Bohlson <i>et al.</i> , 2005)
CD27	CD27	GI5402	MMP-1,-3,-9,-13 and TACE	(Dekkers et al., 2000)
CD30	CD30	EDTA, O-phen	MP	(Parvathy <i>et al.</i> , 1997) (Hansen <i>et al.</i> , 1995; Hooper <i>et al.</i> , 1997)
		BB2116	MMP-3, -7, -2, -9	
CD40L	CD154	EDTA	MP	(Furman <i>et al.</i> , 2004; Otterdal <i>et al.</i> , 2004)
		llomastat (GM6001)	Broad spectrum MMP and TACE	
		KB8301	Zn ²⁺ -dependent MP	(Kato <i>et al.</i> , 1999; Jin <i>et al.</i> , 2001)
		Batimastat (BB-94)	Broad spectrum and TACE	
c-Met	/	TIMP-3	Broad spectrum MMP ADAM-10, -12, -17, -19	
		D (1 ((DD 04)	ADAMTS-4 and -5	(Nath <i>et al.</i> , 2001)
		Batimastat (BB-94) Not inhibited by TIMP-1 and TIMP-2	Broad spectrum MMP and TACE	
CXCL16	/	llomastat (GM6001) MMP inhibitor III*	Broad spectrum MMP and TACE Broad spectrum MMP	(Hara et al., 2006)
Desmocollin-3	/	FN-439 (MMP inhibitor I*) Not inhibited by TAPI(-1)	MMP-1, MMP-8 > MMP-9 > MMP-3	(Weiske <i>et al.</i> , 2001)
Desmoglein-1	/	TAPI-0 FN-439 (MMP inhibitor I*)	Collagenase, gelatinase, TACE MMP-1, MMP-8 > MMP-9 > MMP-3	(Dusek <i>et al.</i> , 2006)
Desmoglein-3	1	Ilomastat (GM6001) FN-439 (MMP inhibitor I*) Not inhibited by	Broad spectrum MMP and TACE MMP-1, MMP-8 > MMP-9 > MMP-3	(Weiske <i>et al.</i> , 2001)
EGF	/	TAPI(-1) EDTA, EGTA	MP	(Dempsey <i>et al.</i> , 1997)
231	,	Batimastat (BB-94)	Broad spectrum MMP and TACE	(Dempsey et al., 1991)
FcyRIII	CD16	GI5402 O-phen	MMP-1,-3,-9,-13 and TACE	(Dekkers et al., 2000) (Bazil and Strominger, 1994) (Galon et al., 1998)
		RU36156	MMP-8, MMP-9 and TACE	(Galon <i>et al.</i> , 1998; Mota <i>et al.</i> , 2004)



 TABLE 4
 Potential membrane-bound MMP and MP substrates (Continued)

Substrate ¹	CD	Inhibitor	Specificity ²	Reference
$Fc_{\varepsilon}RII$	CD23	O-phen	MP	(Bailey <i>et al.</i> , 1998)
		Batimastat (BB-94)	Broad spectrum MMP and TACE	
Folate-R	1	EDTA, O-phen	MP	(Elwood et al., 1991)
GHR	1	BB-3103	Broad spectrum MMP and TACE	(Amit <i>et al.</i> , 2001)
		Ro31-9790	Broad spectrum MMP and TACE	, , , , , , , , , , , , , , , , , , , ,
GM-CSF-R $lpha$	CD116	Batimastat (BB-94)	Broad spectrum MMP and TACE	(Prevost et al., 2002)
GP VI	/	TAPI(-1)	Collagenase, gelatinase, ADAM-10, TACE	
		Ilomastat (GM6001)	Broad spectrum MMP and TACE	
HER2	CD340	TIMP-1	Soluble MMPs	(Codony-Servat et al., 1999; Molina et al., 2001)
		TAPI(-1)	Collagenase, gelatinase, ADAM-10, TACE	
		Batimastat (BB-94)	Broad spectrum MMP and TACE	
HER4	/	Batimastat (BB-94)	Broad spectrum MMP and TACE	(Vecchi <i>et al.</i> , 1998)
IL-1RII	CD121b	Batimastat (BB-94)	Broad spectrum MMP and TACE	(Penton-Rol <i>et al.</i> , 1999)
IL-4R	CD124	O-phen	MP	(Jung <i>et al.</i> , 1999)
IL-6R $lpha$	CD126	TAPI(-1)	Collagenase, gelatinase, ADAM-10, TACE	_
		RU36156	MMP-8, MMP-9 and TACE	(Gallea-Robache <i>et al.</i> , 1997)
		TAPI-2	Zn ²⁺ -dependent MP	(Arribas et al., 1996)
		O-phen	MP	. ,
LDL-R	1	EDTA, EGTA	MP	(Begg <i>et al.</i> , 2004)
LDL IX	,	TAPI(-1)	Collagenase, gelatinase, ADAM-10, TACE	
Leukosialin	CD43	O-phen	MP	(Bazil and Strominger, 1994)
LIGHT	CD258	EDTA	MP	(Otterdal <i>et al.</i> , 2006)
		llomastat (GM6001)	Broad spectrum MMP and TACE	(
M-CSF	/	RU36156	MMP-8, MMP-9 and TACE	(Gallea-Robache <i>et al.,</i> 1997)
Megalin	/	MMP inhibitor III* TAPI(-1)	Broad spectrum MMP Collagenase, gelatinase, ADAM-10, TACE	(Zou <i>et al.</i> , 2004)
		TAPI-2	Zn ²⁺ -dependent MP	
MICA	1	Batimastat-derivative		(Salih <i>et al.</i> , 2002)
MICB	1	Batimastat-derivative		(Salih <i>et al.</i> , 2006)
MMR-1	CD206	BB2116	MMP-3, -7, -2, -9	(Martinez-Pomares et al., 1998)
N-CAM L1	CD171	BB-3103	Broad spectrum MMP and TACE	(Mechtersheimer et al., 2001)
		Ro-31-9790	Broad spectrum MMP and TACE	•
		TAPI(-1)	Collagenase, gelatinase, ADAM-10, TACE	(Beer <i>et al.</i> , 1999; Gutwein <i>et al.</i> , 2005)
Nectin-1 $lpha$	CD111	O-phen	MP	(Tanaka <i>et al.</i> , 2002)
		Batimastat (BB-94) KB-R7785	Broad spectrum MMP and TACE MMP-1,-2,-3,-9,-14	, , , , , ,
Netrin-1	/	llomastat (GM6001)	TACE, ADAM12 Broad spectrum MMP and TACE	(Galko and
		TADI 2	7n2+ danandan+ MD	Tessier-Lavigne, 2000)
		TAPI-2	Zn ²⁺ -dependent MP	(Continued on next page,



TABLE 4 Potential membrane-bound MMP and MP substrates (Continued)

Substrate ¹	CD	Inhibitor	Specificity ²	Reference
NGF-R	1	EDTA, O-phen	MP	(Diaz-Rodriguez <i>et al.,</i> 1999)
		TAPI-2	Zn ²⁺ -dependent MP	
NKR BY55	CD160	O-phen	MP	(Giustiniani et al., 2007)
PECAM-1	CD31	llomastat (GM6001)	Broad spectrum MMP and TACE	(Ilan et al., 2001)
		MMP-2/MMP-9 Inhibitor I*	MMP-2, MMP-9	
		NNGH (MMP-3 Inhibitor II*)	MMP-3	
		MMP-8 Inhibitor*	MMP-8	
PSGL-1	CD162	EDTA Not inhibited by: O-phen, Batimastat and Marimastat	MP	(Davenpeck <i>et al.</i> , 2000)
Sialophorin	CD43	O-phen	MP	(Bazil and Strominger, 1994)
SorLA	1	BB-3103	Broad spectrum MMP and TACE	(Hampe <i>et al.</i> , 2000)
SRCR M130	CD163	TAPI-0	MMP-1, MMP-9, TACE	(Hintz et al., 2002)
Syndecan-3	1	BB-3103	Broad spectrum MMP and TACE	(Asundi <i>et al.</i> , 2003)
		Batimastat (BB-94)	Broad spectrum MMP and TACE	
pro-TGF- $lpha$	1	RU36156	MMP-8, MMP-9 and TACE	(Gallea-Robache et al., 1997)
		TAPI-2	Zn ²⁺ -dependent MP	(Arribas <i>et al.</i> , 1996)
		TAPI(-1)	Collagenase, gelatinase, ADAM-10, TACE	(Shao et al., 2004)
		O-phen	MP	(Arribas et al., 1996)
		Batimastat (BB-94)	Broad spectrum MMP and TACE	(Merlos-Suarez <i>et al.</i> , 2001)
		llomastat (GM6001)	Broad spectrum MMP and TACE	(Yoshisue and Hasegawa, 2004; Shao <i>et al.</i> , 2004)
		Marimastat (BB-2516)	Broad spectrum MMP and TACE	
Tie-1	/	EGTA	Ca ²⁺ -dependent MP	(Yabkowitz et al., 1999)
		BB-24	Zn ²⁺ -dependent MP	
		Not inhibited by: TIMP-2	·	
TNF-R55/60	CD120a	TAPI(-1)	Collagenase, gelatinase, ADAM-10, TACE	(Mullberg <i>et al.</i> , 1995)
		RU36156	MMP-8, MMP-9 and TACE	(Gallea-Robache <i>et al.,</i> 1997)
		BB-2275	Zn ²⁺ -dependent MP	(Williams et al., 1996)
TNF-R75/80	CD120b	TAPI(-1)	Collagenase, gelatinase, ADAM-10, TACE	(Crowe et al., 1995)



TABLE 4 Potential membrane-bound MMP and MP substrates (Continued)

Substrate ¹	CD	Inhibitor	Specificity ²	Reference
		RU36156	MMP-8, MMP-9 and TACE	(Gallea-Robache <i>et al.</i> , 1997)
TSHR	/	BB2116	MMP-3, -7, -2, -9	(Couet et al., 1996; Misrahi and Milgrom, 1997;
				de Bernard <i>et al.</i> , 1999)
		Not inhibited by TIMP-1, TIMP-2		(de Bernard <i>et al.</i> , 1999)
ULBP2	1	Batimastat (BB-94)	Broad spectrum MMP and TACE	(Waldhauer and Steinle, 2006)
		MMP inhibitor III*	Broad spectrum	(Waldhauer and Steinle, 2006)
VCAM-1	CD106	Marimastat (BB-2516)	Broad spectrum MMP and TACE	(Hummel et al., 2001)
VPR V2	1	O-phen	MP	(Kojro and Fahrenholz, 1995)

¹Substrate acronyms: ACE, angiotensin-converting enzyme; ANF-R, atrial natriuretic factor receptor; C1qRp, complement component 1 q subcomponent receptor 1; AR, amphiregulin; c-Met, met proto-oncogene TKR; CXCL16, transmembrane chemokine CXCL16; FcyRIII, low affinity $\lg \gamma$ Fc receptor III; Fc $_{\epsilon}$ RII, low affinity Ig $_{\epsilon}$ Fc receptor II; GHR, growth hormone receptor; GM-CSF-R $_{\alpha}$, granulocyte-macrophage colony-stimulating factor receptor $_{\alpha}$ chain; GP VI, alycoprotein VI; HER4, Tyrosine kinase-type cell surface receptor HER4; IL-R, interleukin receptor; LDL-R, low-density lipoprotein receptor; LIGHT, homologous to lymphotoxins, exhibits inducible expression, and competes with herpes simplex virus glycoprotein D for herpes virus entry mediator, a receptor expressed by T lymphocytes; M-CSF, macrophage-colony stimulating factor; MICA/B, MHC class I chain-related gene A/B; MMR-1, Macrophage mannose receptor-1; N-CAM L1, neural cell adhesion molecule L1; NGF-R, nerve growth factor receptor; NKR BY55, NK cell receptor BY55; NNGH, N-Isobutyl-N-(4methoxyphenylsulfonyl)-glycylhydroxamic acid; O-phen, 1,10-phenantroline; PECAM-1, platelet endothelial cell adhesion molecule-1; PSGL-1, P-selectin glycoprotein ligand-1; -R, receptor; SorLA, sorting protein-related receptor containing LDL-R class A repeats; SRCR M130, scavenger receptor cysteine-rich type 1 protein M130; TAPI, TNF-α Protease Inhibitor; Tie-1, tyrosine kinase receptor tie-1; TSHR, thyrotropin receptor; ULBP2, UL16-binding protein 2; VCAM-1, Vascular cell adhesion molecule-1; VPR V2, V2 vasopressin receptor. Additional acronyms can be found in the list of abbreviations

²Inhibitor specificities: for detailed information, the reader is referred to the reviews (Kontogiorgis et al., 2005), (Sang et al., 2006) and (Whittaker

occludin degradation and increased permeabilization of endothelial cell and epithelial sheets (see Section 2.2 and Figures 14 to 16). Treatment of human normal vaginal-cervical cells with natural doses of 17β estradiol upregulated activation of MMP-7 intracellularly, in the Golgi network, and augmented secretion of activated MMP-7. This MMP-7 was shown to be necessary and sufficient to produce estrogen-mediated decrease of tight junctional resistance and extracellular modulation of occludin. Hence, MMP-7-mediated proteolysis of occludin might be an essential step in the estrogen modulation of paracellular permeability in vivo (Gorodeski, 2007).

6. POTENTIAL CELL SURFACE-ASSOCIATED MMP **SUBSTRATES**

Processing of various membrane-bound molecules is inhibited by metalloproteinase-specific inhibitors, although the involved metalloproteinase has not been

identified yet. These substrates have been grouped in Table 4 with the protease inhibitor profiles and the inhibitor specificities. As discussed before, the inhibition pattern of a proteolytic process yields information on the involved enzyme(s) or protease class(es). Ectodomain shedding of a whole array of membranebound molecules is inhibited by the non-specific cation chelators EDTA, EGTA, and 1,10-phenantroline (e.g., ANF-R, IL-4R, leukosialin). It is relevant to notice that the affinity of EDTA is higher for light metal cations, whereas 1,10-phentroline favours the binding of heavy metal cations. In addition, EGTA preferentially chelates Ca²⁺ ions, thus inhibiting Ca²⁺-dependent proteases. Broad-spectrum MMP inhibitors, such as most hydroxamates, also inhibit TACE and other ADAMs. Hence, a shedding process inhibited by batimastat, marimastat, GM6001, etc. is not necessarily mediated by an MMP and requires further investigation of the protease(s) in charge (e.g., desmoglein-1, HER4, megalin, VCAM-1). Along this line, inhibition by TIMPs does not guarantee that the cleaved molecule is an MMP substrate, as



^{*}Additional information on the inhibitor structure and characteristics can be found at http://www.merckbiosciences.co.uk/home.asp.

TABLE 5 Cell surface MMP substrates without transmembrane domain

Substrate	Type of cell membrane association	Cleaving MMP	Reference
ADAMTS-4	Association with chondroitin and heparan sulfate chains on syndecan-1	MMP-9, MMP-13	(Tortorella <i>et al.</i> , 2005)
		MT4-MMP	(Gao <i>et al.</i> , 2002; Gao <i>et al.</i> , 2004)
C3b	Amide and ester bonds with cell surface molecules	MT1-MMP	(Rozanov <i>et al.</i> , 2004b)
C4b	Amide and ester bonds with cell surface molecules	MT1-MMP	(Rozanov et al., 2004b)
Galectin-3	Binding to IgE and multiple cell surface molecules	MMP-2, MMP-9	(Ochieng <i>et al.</i> , 1994; Ochieng <i>et al.</i> , 1998)
Galectin-9	Binding to cell surface molecules	ND MMP	(Chabot <i>et al.</i> , 2002)
KiSS protein	Complex with pro-MMP-2,-9	MMP-2,-9	
		MT1-, MT3-, MT5-MMP	(Takino <i>et al.</i> , 2003)
pro-TGF- $oldsymbol{eta}$	ECM association	MMP-2,-3,-9	
. ,		MT1-MMP	(Yu and Stamenkovic, 2000)
tTG	Binding to integrins	MT1-MMP, MMP-2	
	-	MT2-, MT3-MMP	(Belkin <i>et al.</i> , 2001;
			Belkin <i>et al.</i> , 2004)
ApoE	Complex with pro-MMP-2	MT1-MMP, MMP-7	(Aoki <i>et al.</i> , 2005)
gC1qR	Binding to the hemopexin domain of MT1-MMP	MT1-MMP	(Rozanov <i>et al.</i> , 2002)

apoE, apolipoprotein E; C3b, complement component 3b; C4b, complement component 4b; gC1qR, receptor of complement component 1q

TIMP-3 inhibits various ADAMs and some proteases of the ADAMTS family (see Table 1). However, some conclusions can be drawn from a TIMP inhibition pattern. As TIMP-2 and TIMP-4 only inhibit MMPs, inhibition or absence of inhibition by these TIMPs, respectively, identifies or rejects MMPs as the operating sheddases (e.g., c-Met, tie-1, TSHR). A metalloprotease inhibited by TIMP-1 is likely to be an (MT-)MMP, as ADAM-10 is the only non-MMP to be inhibited (e.g., HER2). Thus, as long as few specific MMP inhibitors exist, particular care must be taken when drawing conclusions about the identity of the sheddase. Additional cell surface molecules that are modulated by ectodomain shedding have been described (Hooper et al., 1997; Blobel, 2000; Dello and Rovida, 2002; Arribas and Borroto, 2002; Garton et al., 2006).

Finally, some MMP substrates without transmembrane domain are located at the cell surface by receptor binding, by a membrane vesicle, a membrane-bound proteoglycan or another transmembrane protease. For that reason, these have not all been discussed in detail in the above survey. Some examples of such cell surfaceassociated proteins are galectin-3 and -9 (Ochieng et al., 1994; Ochieng et al., 1998; Chabot et al., 2002); tTG (Belkin et al., 2001; Belkin et al., 2004); the KiSS protein/metastin (Takino et al., 2003); pro-TGF-β (Yu and Stamenkovic, 2000); ADAMTS-4 (Gao et al., 2004); the complement components C3b and C4b (Rozanov et al., 2004b); apolipoprotein E (Aoki et al., 2005) and gC1qR, the receptor of complement component 1q (Rozanov et al., 2002) (Table 5).

CONCLUSION

Due to the rapid development of innovative biochemical techniques and the expanding use of transgenic and knockout animals, it became obvious that the action radius of MMPs is not restricted to massive ECM destruction in physiological tissue remodelling and pathological tissue degradation. Identification of specific matrixas well as non-matrix-components as MMP substrates showed that MMPs also play significant roles in highly complex processes such as the regulation of cellular behavior, cell-cell communication and tumor progression (McCawley and Matrisian, 2001). An extended variety of bioactive molecules is modified by MMPs in particular physiopathological processes (Sternlicht and Werb, 2001).

The above survey points out that MMPs do not only cleave multiple soluble substrates, but also process a



whole array of membrane-bound proteins. These proteolytic events on the cell surface may have extremely diverse biological implications (see Table 2), ranging from maturation (e.g., pro- α integrin subunits), activation (e.g., PAR1) and potentiation (HER2) of a cell surface component, to its inactivation (e.g., syndecan-1) or even its degradation (e.g., NG2 proteoglycan and β dystroglycan). Besides the regulation of cell-bound activity, ectodomain proteolysis of substrates may also be required for the diffusion of the reaction product(s) into the extracellular environment to facilitate receptor activation on adjacent or even more distal cells (e.g., pro-TNF- α and RANKL). In addition, a liberated receptor fragment might as well possess inhibitory power by acting as a soluble decoy receptor that binds soluble ligands, preventing their interaction with the cell-bound, signal-transducing receptor (e.g., FGFR-1).

Through these distinct effects on the biological activity of the substrates, proteolysis of cell surface proteins by MMPs has a major impact on a multitude of physiological functions, as well as on onset and evolution of many diseases. In addition, MMP activity itself can be directly regulated by proteolysis of cell surface proteins. For instance, MMPs cleave their membrane-bound inducer, EMMPRIN, allowing the active fragment to induce MMP activity in adjacent cells or in more distal tissues. Conversely, they also modulate their own internalization and degradation by degrading their scavenger receptor, LRP, assuring sustained MMP activity. Finally, MMPs can terminate their own activity by autocatalytic proteolysis.

Inhibition of MMPs seems to be the ideal solution in many pathologies. However, the enthusiasm generated by a large number of in vitro and in vivo studies has been dramatically mitigated in recent years by the failure of MMP inhibitors to block tumor progression in clinical trials (Coussens et al., 2002). This fiasco could be explained partly by the fact that inhibitors were administered only to late-stage cancer patients, whereas proteases are often involved in early stages of tumor progression. In addition, the lack of selectivity and specificity of inhibitors is a problem, as tumor invasion and metastasis require the concerted action of particular MMPs. However, as stated by Del Rosso and coworkers (2005), our understanding of protease-environment interactions is far from exhaustive. The initial, naïve view of proteases acting in the soluble phase has evolved into a kaleidoscope of images in which proteolytic reactions in tissue remodelling mostly occur at, and are modulated by, the cell surface. As a consequence, insight in the modification of cell surface proteins by MMPs and the associated implications, is essential to elucidate the cross-talk between proteases at the cell surface and with the extracellular environment. In conclusion, starting with the exploration of the cell surface could become a prerequisite in the successful development of new MMP inhibitors and innovative therapeutic approaches for cancer and inflammatory diseases.

ABBREVIATIONS

 $A\beta$, β -amyloid protein; ACE, angiotensin-converting enzyme; ADAM, a disentegrin and metalloproteinase; ADAMTS, a disentegrin and metalloproteinase with thrombospondin-like motif; ANF-R, atrial natriuretic factor receptor; AP, alkaline phosphatise; ApoE, apolipoprotein E; APP, amyloid precursor protein; AR, amphiregulin; ARF, acute renal failure; BBB, blood-brain barrier; BP, bullous pemphigoid; BP-**180,** BP antigen-2; **BRB,** blood-retinal barrier; **C1qRp,** complement component 1 q subcomponent receptor 1; C3b/4b, complement component 3b/4b; CD, cluster of differentiation of human (glyco)proteins; CD44ICD, intracellular domain of CD44; c-Met, met proto-oncogene TKR; CNS, central nervous system; **CTL**, cytotoxic T cell; **EAE**, experimental autoimmune encephalomyelitis; **E-cadherin**, epithelial cadherin; **ECM**, extracellular matrix; **EDTA**, ethylenediaminetetraacetic acid; EGF(R), epidermal growth factor (receptor); **EGTA**, ethylene glycol-bis(2-aminoethylether)-N,N,N',N'-tetraacetic acid; **EMMPRIN**, extracellular matrix metalloproteinase inducer; FasL, Fas ligand; **FcyRIII,** low affinity Ig γ Fc receptor III; **Fc** ε **RII,** low affinity Ig ε Fc receptor II; **FGF**, fibroblast growth factor; **FGFR-1**, FGF receptor-1; **gC1qR**, receptor of complement component 1q; GHR, growth hormone receptor; **GM-CSF-R** α , granulocyte-macrophage colony-stimulating factor receptor α chain; **GnRH**, gonadotropin-releasing hormone; GP VI, glycoprotein VI; GPCR, G protein-coupled receptor; GPI, glycosyl phosphatidylinositol; HB-EGF, heparin-binding epidermal growth factor-like growth factor; HER2/4, tyrosine kinase-type cell surface receptor HER2/4; ICAM-1, intercellular adhesion molecule-1; ICE, IL- 1β -converting enzyme; **Ig**, immunoglobulin; **IL-** (**R**), interleukin- (receptor); **IL-1** β , interleukin-1 β ; **KitL**, Kit ligand; KS, keratoconjunctivitis sicca; LDL(-R), low density lipoprotein (receptor); LIGHT, homologous to



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lymphotoxins, exhibits inducible expression, and competes with herpes simplex virus glycoprotein D for herpes virus entry mediator, a receptor expressed by T lymphocytes; LPS, lipopolysaccharide; LR, 34/67 kDa laminin receptor; **LRP**, low-density lipoprotein receptor-related protein; **L-selectin**, leukocyte-selectin; m-, membrane-bound; MBP, myelin basic protein; M-CSF, macrophage-colony stimulating factor; MEVC, microvascular endothelial cell; MICA/B, MHC class I chain-related gene A/B; MMP, matrix metalloproteinase; MMR-1, macrophage mannose receptor-1; MP, metalloproteinase; MT-MMP, membrane-type MMP; MUC1, mucin-1; N-cadherin, neuronal cadherin; **N-CAM L1**, neural cell adhesion molecule L1; NE, neutrophil elastase; NGF-R, nerve growth factor receptor; **NK cell,** natural killer cell; **NKR BY55,** NK cell receptor BY55; PAR1, protease-activated receptor-1; **PC**, proprotein convertase; **PDGF**, platelet-derived growth factor; **PDR**, proliferative diabetic retinopathy; **PECAM-1**, platelet endothelial cell adhesion molecule-1; **PLAD**, preligand assembly domain; **PMA**, phorbol 12-myristate 13-acetate; **PSGL-1**, P-selectin glycoprotein ligand-1; **PVR**, proliferative vitreoretinopathy; -**R**, receptor; RANK(L), receptor activator of nuclear factor κ B (ligand); **s-,** soluble; **SDF-1,** stromal cell-derived factor-1; SorLA, sorting protein-related receptor containing LDL-R class A repeats; **SP-D**, surfactant protein-D; **SRCR M130**, scavenger receptor cysteine-rich type 1 protein M130; **Ssc,** systemic sclerosis; **TACE,** TNF- α -converting enzyme; **TAPI,** TNF- α protease inhibitor; **TGF-** α/β , transforming growth factor- α/β ; **Tie-1**, tyrosine kinase receptor tie-1; TIL, tumor infiltrating lymphocyte; **TIMP**, tissue inhibitor of metalloproteinases; **TKR**, tyrosine kinase receptor; **TMD**, transmembrane domain; **TMPS**, triple membrane-passing signal mechanism; **TNF**- α , tumor necrosis factor- α ; **t-PA**, tissue-type plasminogen activator; TSHR, thyrotropin receptor; tTG, tissue transglutaminase; ULBP2, UL16-binding protein 2; u-PA, urokinase-type plasminogen activator; **uPAR**, urokinase-type plasminogen activator receptor; VCAM-1, vascular cell adhesion molecule-1; VEcadherin, vascular endothelial-cadherin; VEGF, vascular endothelial growth factor; VPR V2, V2 vasopressin receptor; X, Xenopus.

ACKNOWLEDGMENTS

The present study was supported by The Fund for Scientific Research-Flanders (FWO-Vlaanderen), the Geconcerteerde OnderzoeksActies (GOA 2007-2011), The Rega Centre of Excellence (COE 05/015), the Charcot Foundation and the Belgian Foundation against Cancer. PVDS is a postdoctoral fellow of the FWO-Vlaanderen.

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Editor: Michael M. Cox

