Glioma-Associated Proteases

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Abstract

Proteolytic enzymes constitute 2–3 % of all known human genes and represent an important tool for the control of the biological functions of proteins. During gliomagenesis, the complex regulation of proteases in transformed and stromal cells is impaired as a result of several factors, and proteases critically contribute to the hallmarks of gliomas. Proteins regulated by proteases include components of the extracellular matrix, local mediators, cell surface receptors, ion channels and adhesion molecules, cytoskeletal proteins, components of the intracellular signaling cascades, and regulators of the cell cycle. Via the proteolytic modifications of these substrates and/or by non-proteolytic mechanisms, the extracellular as well as intracellular proteases contribute to the increased invasiveness of glioma cells, promote the self-renewal and proliferation of glioma stem-like cells, and facilitate tumor neovascularization. The role of proteases in glioma progression is therefore multifaceted and complex. Glioma-associated proteases represent attractive therapeutic targets and several approaches were proposed including the inhibition of the extracellular proteases involved in glioma invasiveness as well as the inhibition of the proteasome and γ -secretase. However, a more precise understanding of the pathogenetic role of proteases in individual glioma patients at different stages of the disease is necessary as indicated by the relatively low therapeutic efficacy of the protease inhibitors in the initial clinical trials. Identification of the key protease-dependent processes in individual glioma patients, the most effective modes of protease targeting, and optimal delivery schedules and routes seem to be crucial to improve the therapeutic outcomes.

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Keywords

Glioma • Tumorigenesis • Angiogenesis • Invasion • Apoptosis • Microenvironment • Therapeutic targeting • Tumor stroma

Abbreviations

ADAM	A disintegrin and metalloproteinase
ADAMTS	A disintegrin and metalloproteinase with thrombospondin motifs
bFGF	Basic fibroblast growth factor
BDNF	Brain-derived neurotrophic factor
BMP	Bone morphogenic protein
CAM	Cell adhesion molecule
CDKN2A	Cyclin-dependent kinase inhibitor 2A
CXCL12	Chemokine (C-X-C Motif) Ligand 12 (SDF stromal cell-derived
	factor)
CXCL16	Chemokine (C-X-C Motif) Ligand 16
DISC	Death-inducing signaling complex
ECE	Endothelin converting enzyme
ECM	Extracellular matrix
EGFR	Epidermal growth factor receptor
ERK	Extracellular signal-regulated kinase
FAK	Focal adhesion kinase
GCP-II	Glutamate carboxypeptidase-II (N-acetyl-L-aspartyl-L-glutamate pep-
	tidase I, NAALADase I, PSMA, prostate-specific membrane antigen)
GrB	Granzyme-B
HB-EGF	Heparin-binding EGF-like growth factor
HGF	Hepatocyte growth factor
HIF	Hypoxia inducible factor
IDH	Isocitrate dehydrogenase
IFN	Interferon
IGF	Insulin-like growth factor
MAPK	Mitogen-activated protein kinase
miRNA	Micro RNA
MMP	Matrix metalloproteinase
MT-MMP	Membrane-type MMP
PAI	Plasminogen activator inhibitor
PAR	Protease-activated receptor
PI3K	Phosphatidylinositol-4,5-bisphosphate 3-kinase
PTEN	Phosphatase and tensin homolog
RNAi	RNA interference
RTK	Receptor tyrosine kinase
Shh	Sonic hedgehog

SUMO	Small ubiquitin-like modifier
TF	Tissue factor (fIII)
TFPI	Tissue factor pathway inhibitor
TGF	Transforming growth factor
TIMP	Tissue inhibitor of matrix metalloproteinase
TNF	Tumor necrosis factor
tPA	Tissue-type plasminogen activator
TRAIL	TNF-related apoptosis-inducing ligand
uPA	Urokinase-type plasminogen activator
uPAR	Urokinase-type plasminogen activator receptor
USP	Ubiquitin-specific protease
VEGF	Vascular endothelial growth factor
VEGFR	Vascular endothelial growth factor receptor

12.1 Proteolytic Enzymes: General Overview

With a total of 585 proteases listed in the degradome database (http://degradome. uniovi.es/dindex.html), proteases constitute approximately 2–3 % of all known human genes (Puente et al. 2003). Biochemically, proteases belong to hydrolases that cleave the covalent bonds linking amino acids in the polypeptide backbone releasing smaller protein fragments and/or individual amino acids (Hooper 2002), or removing posttranslationally attached proteins such as ubiquitin or SUMO (Clague et al. 2012; Hickey et al. 2012). Based on the nature of their active site and the mechanism of action, five main classes of proteases are distinguished, i.e., aspartic, cysteine, metallo, serine, and threonine, with additional classes found in lower organisms (http://merops.sanger.ac.uk/, Rawlings et al. 2012). The specificity of the peptide bond cleavage varies widely: some proteases are highly specific (e.g., blood coagulation proteases, caspases) whereas others (e.g., proteasome, cathepsins, proteinase K) cleave a wide variety of substrates at several positions.

Besides its role in protein digestion and catabolism, the proteolytic cleavage represents a very important and mostly irreversible mechanism of protein function regulation on the posttranslational level (Clague et al. 2012; Hickey et al. 2012; Turk et al. 2012a). Proteolysis can lead to

- 1. Protein activation [e.g., zymogen activation, protein maturation by proprotein convertases such as furin (Seidah and Chretien 1999; Maret et al. 2012)],
- 2. Protein inactivation [e.g., cleavage of a specific inhibitor of caspase-activated DNAse by caspase-3 during apoptosis (Enari et al. 1998)],
- 3. Adjustment of the biological activity of the protein [e.g., chemokine processing by matrix metalloproteinases or aminopeptidases (Wolf et al. 2008)],

4. Changes affecting the turnover of the protein (e.g., changed susceptibility to degradation after the removal of ubiquitin by deubiquitinating enzymes (Wilkinson 2009), or protein cleavage that enables further proteolytic processing).

Proteolysis thus determines the spatiotemporal bioavailability of proteins either quantitatively (e.g., degradation of structural or nutritive proteins) or qualitatively by highly specific ("limited") proteolysis of particular peptide bonds, fine-tuning the biological activities of regulatory peptides (Konkoy and Davis 1996).

The activity of proteases can be controlled at several levels. In addition to the regulation of the expression level via transcriptional and posttranscriptional mechanisms and protein degradation, several proteases are synthesized in an inactive form (zymogen) that requires proteolytic cleavage in order to be converted to the active form. This activation is frequently accomplished by proteolysis in a multiprotein complex and represents a well-established regulatory step for. e.g., matrix metalloproteinases (MMPs) (Kessenbrock et al. 2010), plasminogen, urokinase-type plasminogen activator (uPA), and caspases (Donepudi and Grutter 2002). The activity of proteases is further regulated by their sequestration to specialized cellular compartments such as nucleus (Clague et al. 2012; Geng et al. 2012), endoplasmic reticulum, Golgi apparatus, endosomes, lysosomes, or secretory granules (Shen and Prywes 2004; Colbert et al. 2009; Lemberg 2011; Krzewski and Coligan 2012; Turk et al. 2012b; Bergbold and Lemberg 2013; Hattori and Tsujimoto 2013; Repnik et al. 2013; Seidah et al. 2013), mitochondria (Bulteau and Bayot 2011; Anand et al. 2013), and invadosomes (Brisson et al. 2012), where they meet with a stabilizing and optimal reaction microenvironment as well as with the target substrates. Besides this, proteases are controlled by a number of endogenous extracellular (secretory) and intracellular inhibitors. While α 2-macroglobulin and α 1-antitrypsin have the ability to inhibit a broad range of proteases, other endogenous inhibitors are more selective for individual proteases or protease classes, although there is some overlap in their specificities (Turk 2006; Mason and Joyce 2011). The serpins such as plasminogen activator inhibitors (PAI) 1 and 2 or α 2-antiplasmin (Law et al. 2006) or the Kunitz-type inhibitors such as tissue factor pathway inhibitor (TFPI) predominantly inhibit serine proteases, whereas cystatins (Turk et al. 2008) and calpastatin inhibit the cysteine proteases cathepsins and calpains, respectively (Turk 2006; Turk et al. 2008; Cox 2009; Mason and Joyce 2011; Campbell and Davies 2012). Some intracellular serpins, such as serpinB3, serpinB4, and serpinB9, can function as cross-class inhibitors inhibiting serine as well as cysteine proteases (Law et al. 2006; Izuhara et al. 2008). The activity of MMPs, ADAMs ("A Disintegrin And Metalloproteinase"), and ADAMTS ("A Disintegrin And Metalloproteinase with Thrombospondin Motifs") is regulated by the four members of the tissue inhibitor of matrix metalloproteinase (TIMP) family TIMP1-4, which form tight 1:1 complexes with the target proteases (Murphy 2011). TIMP1-4 differ somewhat in their ability to inhibit individual metalloproteases and in their expression pattern. TIMP1 has a restricted inhibitory potential as it does not inhibit the membrane-type MMPs (MT-MMPs); it is widely expressed extracranially, but its expression in the brain is confined to the regions with persistent neuronal plasticity such as the hippocampus, the olfactory bulb, and the cerebellum (Rivera et al. 2010; Murphy 2011). TIMP2 is constitutively expressed in many tissues and is the most abundantly expressed TIMP in the brain at least in the rat (Fager and Jaworski 2000). TIMP2 plays a dual role in regulating metalloproteases; besides being a protease inhibitor, TIMP2 is critically involved in the complex process of MMP2 activation. TIMP2 forms a trimolecular complex with MMP2 and MT1-MMP (MMP14) thereby enabling efficient activation of MMP2 by MMP14 on the cell surface (Strongin et al. 1995). These results of in vitro studies are further supported by the observation that TIMP2 knockout mice have impaired MMP2 activation, which can be rescued by exogenous TIMP2 (Caterina et al. 2000; Wang et al. 2000). TIMP3 is expressed in several tissues and its ablation in mice leads to emphysema-like damage of the lungs and increased apoptosis in the mammary gland suggesting its important role in regulating metalloproteases (Murphy 2011). Expression of the recently described TIMP4 is restricted to heart, kidney, pancreas, colon, testes, adipose tissue, and brain (Melendez-Zajgla et al. 2008). The data on TIMP4 function are limited, but the protein is suspected to have pro-tumorigenic activities (Melendez-Zajgla et al. 2008). It is important to stress that the majority of the endogenous protease inhibitors exhibits several physiological and pathological roles that are independent of their ability to inhibit the activity of proteases (Rivera et al. 2010), which must be considered when interpreting their effects on protease-mediated processes in the experimental models.

In addition to the protease genes, several proteins highly homologous to proteases but devoid of the proteolytic activity due to amino-acid substitution (s) in the active site are encoded in the human genome (Puente et al. 2003). For example, human ADAMs from the metzincin subgroup of the zinc protease superfamily comprise 19 members, of which approximately half are enzymatically inactive (Seals and Courtneidge 2003; Klein and Bischoff 2011). The inactive protease homologues may have important regulatory functions in sequestering inhibitors or protease substrates, or participate on protein-protein interactions that are unrelated to their "evolutionary original" proteolytic role. This latter aspect is also typical for several "bona fide" proteases, as they frequently contain non-protease domains that enable non-hydrolytic protein-protein interactions (Del Rosso et al. 2002; Rozanov et al. 2004; Mina-Osorio 2008; Sakamoto and Seiki 2009; Dufour et al. 2010; Redondo-Munoz et al. 2010). Thus, a number of proteases can serve as receptors (Mina-Osorio 2008; Klein and Bischoff 2011; Raj et al. 2013), signaling molecules (Rogove et al. 1999; Sower et al. 1999; Beffert et al. 2006; LaRusch et al. 2010; Strongin 2010), or modulator molecules directly interacting with and influencing other components of the signal transduction pathways (Sumitomo et al. 2000).

Proteases act intracellularly, in the extracellular space as well as in body fluids and secretions. The intracellular proteases are indispensable for proper protein maturation [e.g., proprotein convertases (Seidah and Chretien 1999)], contribute to the cytoskeletal remodeling [e.g., calpains (Franco and Huttenlocher 2005)] and regulation of transcription (Best et al. 2002; Chapman 2004), remove misfolded, damaged, or unneeded proteins (lysosomal proteases, proteasomes) (Das et al. 2012; Kaminskyy and Zhivotovsky 2012; Viry et al. 2014), and initiate and execute apoptosis (Pop and Salvesen 2009; Goldschneider and Mehlen 2010). Proteolysis also takes place within biological membranes (Lemberg 2011; Bergbold and Lemberg 2013). This unique mechanism mediated by, e.g., presenilins or rhomboids frequently leads to the release of effector peptides, often with a signaling or transcription factor activity, from transmembrane proteins such as Notch (Lemberg 2011). Proteases acting in the extracellular space are either secreted (e.g., uPA, MMPs 2 and 9, cathepsins, ADAMTS) or plasma membrane bound (e.g., MT1-MMP, ADAMs). Nevertheless, the secreted proteases can also associate with the cell surface by binding to specific membrane receptors as demonstrated for uPA, MMP2, MMP9, and procathepsin-B and their respective receptors uPAR. α -v- β -3 integrin, CD44, and annexin II (Brooks et al. 1996; Yu and Stamenkovic 1999: Mohamed and Sloane 2006: Eden et al. 2011). This binding enhances the proteolytic activity not only by the spatial concentration of the protease but frequently also decreases the effects of endogenous inhibitors.

The widespread distribution of proteases reflects their participation in almost every physiological process on the level of individual cells as well as on the level of the whole organism. Proteases exert control of cell behavior including its metabolism, signal sensing and transduction, proliferation and death, as well as participate among others in angiogenesis, blood clotting, and immune defense (see Lopez-Otin and Bond (2008) for review).

Proteases from various classes are expressed in the brain and fulfil numerous biological functions. The serine proteases neurotrypsin and neuropsin were originally identified due to their abundant expression in the neural tissue, but other more "traditional" serine proteases such as thrombin, plasmin, tPA, and trypsin 4 are also locally produced in the brain (see Wang et al. (2008b), Almonte and Sweatt (2011) and references therein). Similarly, metalloproteases such as MMP2, MMP9, several ADAMs, and ADAMTS4 and 5 are expressed in the central nervous system (for review see Yang et al. 2006; Rivera et al. 2010). Extracellular as well as intracellular brain proteases play an important role in neuronal signaling. Besides the processing, conversion, and inactivation of neuropeptides and growth factors such as pro-BDNF (brain-derived neurotrophic factor) (Hallberg et al. 2005; Almonte and Sweatt 2011), proteases trigger intracellular signaling cascades through "protease-activated receptors" (PAR) 1-4. These receptors are expressed on the surface of neurons, microglia, and astrocytes and their proteolytic cleavage exposes an amino-terminal part of the molecule that acts as a tethered intramolecular ligand for the same receptor and activates signal transduction through G proteins (see Noorbakhsh et al. (2003) for review). Ligand-gated ion channels may also be cleaved by proteases with subsequent changes in their turnover or signaling. For example, the intracellular calcium-activated cysteine proteases calpains cleave the NR2A subunit of the NMDA receptors (Guttmann et al. 2002) as well as degrade GRIP (glutamate receptor-interacting protein), a molecule important for the morphological and functional organization of the synapses (Lu et al. 2001). Likewise, the extracellular serine protease tPA is thought to be directly involved in

glutaminergic transmission as it is induced by neuronal activity (Qian et al. 1993) and facilitates NMDA receptor-mediated signaling by cleaving the NR1 subunit (Nicole et al. 2001). Neuronal neurotransmitter receptors are also regulated by a spatiotemporally limited activation of caspases. In hippocampal neurons, NMDA receptor signaling causes caspase-3 activation by the mitochondrial pathway. The activated caspase-3 subsequently cleaves and inactivates the serine-threonine protein kinase Akt1, which blocks AMPA receptor internalization and inhibits long term depression (LTD) (Li et al. 2010b; Li and Sheng 2012). Similarly, caspase-1 was demonstrated to function as a negative regulator of the AMPA receptor signaling, resulting in the inhibition of long term potentiation (LTP) (Lu et al. 2006a). Other proteases with signaling roles in the brain include secretases that are indispensable for the Notch-1 signaling by liberating its C-terminal intracellular domain (Prox et al. 2012) and the ubiquitin-proteasome system, which impacts, e.g., on the Notch, Wnt, BMP, or Shh signal transduction pathways by regulating their intracellular effectors (Lehman 2009). The neuropsin-mediated cleavage of fibronectin (Almonte and Sweatt 2011) and of the L1 cell adhesion molecule (L1CAM, Shimizu et al. 1998) as well as the processing of betadystroglycan and N-cadherin by MMP9 (Dziembowska and Wlodarczyk 2012) are other examples of the remodeling of the extracellular matrix and the cleavage of cell adhesion molecules by which several proteases play an important role in LTP, synapse remodeling, and neuronal plasticity [for further details see, e.g.,

LTP, synapse remodeling, and neuronal plasticity [for further details see, e.g., Tomimatsu et al. (2002), Reif et al. (2007), Stephan et al. (2008), Wright and Harding (2009), Shiosaka and Ishikawa (2011), Dziembowska and Wlodarczyk (2012), Li and Sheng (2012)].

In addition, proteases are essential factors during brain development. MMPs such as MMP3 and MMP9 contribute to neurite outgrowth, axon guidance, and neuronal migration (Vaillant et al. 1999, 2003; Van Hove et al. 2012). A similar role was proposed for the plasminogen activator-plasmin system (Seeds et al. 1997) and caspases (Williams et al. 2006; Westphal et al. 2010). ADAMs, most notably ADAM 10, 22, and 23, seem to have a complex role during central nervous system (CNS) development affecting the proliferation, neuronal migration, axon growth, and differentiation of neuronal progenitors, and their absence in mice results in serious CNS defects and early mortality (reviewed in Yang et al. 2006). Likewise, cathepsins were demonstrated to be indispensable for the proper development of the CNS. Combined deletion of the cysteine cathepsins B and L leads to neuronal loss with profound brain atrophy as well as early mortality in mice (Felbor et al. 2002). The deficiency of the aspartate protease cathepsin-D in mice was reported to cause disturbed myelin structure (Mutka et al. 2010), accumulation of ceroid, astrogliosis, and early mortality (Shevtsova et al. 2010) paralleling the phenotype of the congenital neuronal ceroid lipofuscinosis caused by cathepsin-D deficiency in humans (Siintola et al. 2006; Fritchie et al. 2009). The phenotype in cathepsin-K knockout mice is less severe and involves changes in hippocampal cytoarchitecture as well as learning and memory deficits (Dauth et al. 2011).

Imbalances in the proteolytic activities lead to several pathologies (Lopez-Otin and Bond 2008) including inflammatory, neurodegenerative, and malignant

diseases affecting the CNS. Proteases were thus shown to participate on the pathogenesis of Alzheimer's (Bernstein 2005) and Parkinson's disease (Crocker et al. 2005) as well as the pathogenesis of ischemic (Morancho et al. 2010), traumatic (Knoblach and Faden 2005), inflammatory, and infectious (Kieseier and Bernal 2005) states.

The concept of the role of proteolytic enzymes in malignant diseases dates back to the half of the last century (Fischer 1946). At that time, proteases were viewed as effectors facilitating tumor cell dissemination by cleaving the protein components of the extracellular matrix. This is certainly the case for some of the proteases localized extracellularly or concentrated in the specialized regions of plasma membrane where their activity, together with the adhesion molecules, mediates interactions of the cancer cells with their surroundings (Stylli et al. 2008). However, experimental work in the ensuing years led to a more complex picture emphasizing the importance of proteases for several aspects of malignancy (reviewed in Nomura and Katunuma 2005; van Hinsbergh et al. 2006; Lopez-Otin and Matrisian 2007; Kessenbrock et al. 2010). For example, the membrane-bound MT1-MMP (MMP14) can mediate intracellular proteolysis of a centrosomal protein pericentrin-2, which leads to chromosomal instability and aneuploidy (Golubkov and Strongin 2007). Similar role at the early stages of tumor development was suggested for other proteases as well. Caspases, the initiators and executors of apoptotic cell death, are generally viewed as "guardians" protecting the organism from cancer. However, the activation of the DNA fragmentation factor by caspase-3 may lead to increased mutation frequency, genome instability, and chromosomal translocations when the apoptotic program is not completed (Aplan 2006; Lovric and Hawkins 2010). In addition, the caspase-3-mediated activation of prostaglandin E2 production and secretion by the tumor cells exposed to cytotoxic therapies can in fact enhance tumor repopulation by the surviving tumor cells (Huang et al. 2011) and thus eventually contribute to the cancer recurrence and progression. This together with other reports supports the notion that proteases in addition to tissue invasion and metastasis participate in cancer initiation, generation of genomic instability in tumor cells (Radisky et al. 2005), tumor angiogenesis, immune escape, dysregulation of apoptosis (Abraham et al. 2005), and cell proliferation, as well as on the infiltration of the tumors by immune cells (reviewed in McCawley and Matrisian 2001; Kessenbrock et al. 2010).

On the other hand, several proteases have rather anti-tumorigenic effects, e.g., by inactivating bioactive peptides, generating anti-angiogenic fragments from the extracellular matrix, inhibiting cell growth or modulating the inflammatory response (Lopez-Otin and Matrisian 2007). In other cases the net pro- or anti-oncogenic activity of a protease may critically depend on its cellular source as well as on other microenvironmental factors. For example, MMP9 may promote tumor growth and invasiveness as well as enhance angiogenesis by liberating VEGF (vascular endothelial growth factor) (Bergers et al. 2000), whereas the MMP9 mediated degradation of other extracellular matrix proteins such as type IV collagen or plasminogen produces potent suppressors of angiogenesis tumstatin and angiostatin, respectively (Hamano et al. 2003; Rege et al. 2005).

The role of proteases in cancer progression is therefore multifaceted and only partially elucidated. In this chapter we summarize the current knowledge of the expression of proteases in gliomas and discuss their regulation and potential mechanisms whereby they contribute to several aspects of glioma pathogenesis. Finally, the possible exploitation of proteases as therapeutic targets is also reviewed.

12.2 Dysregulation of Proteolytic Enzymes in Gliomas

Several studies (summarized in Table 12.1) addressed the expression and possible function of proteolytic enzymes in gliomas. Of these, the extracellularly localized proteases participating on glioma invasiveness and angiogenesis were most extensively studied and were the subject of a number of excellent reviews (Chintala et al. 1999; Fillmore et al. 2001; VanMeter et al. 2001; Binder and Berger 2002; Levicar et al. 2003; Rao 2003; Lakka et al. 2005; Mentlein et al. 2012).

A very comprehensive view of the differential protease expression in gliomas can be obtained from the data in The Cancer Genome Atlas Research Network (2008). These data clearly show a consistent signature of up- or downregulated proteases and their homologues (Fig. 12.1a) corroborating the over- (e.g., MMP14, MMP2, MMP7, MMP9, tPA, uPA) or under-expression (e.g., kallikreins, ADAMTS8) observed in previous smaller studies. Importantly, it reveals the dysregulation of expression of numerous proteases that have been little or not at all explored in relation to glioma pathogenesis so far, making them candidates for future studies (e.g., CFI, CPVL, DPEP1, ENPEP, LTF, MEST, MAP1D, ubiquitin-specific proteases).

Several of the consistently upregulated proteases are implicated in the immune response (ADAMDEC1, C1RL, C1S, CFI, CPVL, LTF, PSMB8, PSMB9, SPPL2A) probably reflecting the proinflammatory state induced by gliomas and high infiltration by microglia/macrophages (Gabrusiewicz et al. 2011) and other immune cells. Similarly, proteases involved in the remodeling of the extracellular matrix and angiogenesis (ADAMTS5, MMP14, MMP2, MMP7, MMP9, tPA, uPA) are highly upregulated. The consistently downregulated proteases on the other hand comprise proteases or their homologues typical for the normally functioning neuronal tissue, i.e., involved in neurotransmission, ion channel regulation, and axonal growth (e.g., AMZ1, ASPA, DPP10, PCSK2, TRHDE, AGTPBP1, CPE, KLK8, PCSK1, ACY3, ASRGL1, DPP6, DPYSL2, DPYSL4, FOLH1, NELF, THOP1). In addition, several proteases with a proposed tumor suppressor function (e.g., ADAM11, PRSS3, ADAM23, ADAMTS8, CRMP1, KLK10) are downregulated.

Interestingly, a subset of proteases seems to be preferentially dysregulated in association with the individual glioblastoma molecular subtypes that were recently proposed by Verhaak et al. (2010) (Fig. 12.1b). Indeed, several proteases and protease inhibitors (e.g., ADAM12, caspases, cathepsins, uPA, cystatin A, serpins) are part of the Verhaak mesenchymal transcriptomic signature (Verhaak et al. 2010). In addition, a number of proteases are in fact upregulated solely or most markedly in this subtype (Fig. 12.1b), which might correspond to the higher

Table 12.1 Proteases with possible path	nogenetic role in gliomas	
Protease	Expression compared to nontumorous brain	Note, reference(s)
Aspartic proteases		
Cathepsin-D	Increased	(Robson et al. 1990; Sivaparvathi et al. 1996b); expressed in reactive macrophages (Robson et al. 1990); higher expression correlates with shorter patient survival (Fukuda et al. 2005); in contrast, Warich et al. observed decreased expression with increased anaplasia (Warich et al. 1995); may act as a mitogen and contribute to glioma invasiveness (Levicar et al. 2002).
Presenilin-1	Expression detected by IHC	(Miake et al. 1999), presentlin-1 is the enzymatic component of the γ -secretase complex, cleaves CD44 in glioma cells (Murakami et al. 2003), inhibitors interfere with the Notch and neurotrophin signaling and inhibit glioma growth (Fan et al. 2010; Gilbert et al. 2010; Chen et al. 2010; Hu et al. 2011; Chu et al. 2013; Kristoffersen et al. 2013; Zou et al. 2013; Forsyth et al. 2014; Saito et al. 2014).
Presenilin-2	Increased	Enzymatic component of the <i>y</i> -secretase complex, depletion by RNAi in glioma cells leads to decreased growth and invasiveness (Liu et al. 2012).
Renin	Increased	(Ariza et al. 1988); inhibition of renin leads to decreased cell growth in vitro (Juillerat-Jeanneret et al. 2004).
Cysteine proteases		
Calpain-1	Increased	(Ray et al. 2002)
Calpain-2	Increased	(Ray et al. 2002); calpain-2 is required for the invasion of glioma cells (Jang et al. 2010).

(Rempel et al. 1994; Mikkelsen et al. 1995; Sivaparvathi et al. 1995; Demchik et al. 1999; Strojnik et al. 2000; Konduri et al. 2001; Wang et al. 2005; Colin et al. 2009; Gole et al. 2009, 2012); glioblastoma cells secrete cathepsin-B (McCormick 1993; Formolo et al. 2011); endothelial cells of blood vessels also express cathepsin-B (Mikkelsen et al. 1995; Sivaparvathi et al. 1995; Wang et al. 2005); cathepsin-B activity is higher in the invasive vs. noninvasive glioma cells and is expressed at the invasive front of the cells (Gole et al. 2009); expression of its inhibitor cystatin E/M is silenced by promoter methylation in gliomas (Qiu et al. 2008). Downregulation of cathepsin-B expression impairs the tumorigenic and invasive potential of glioblastoma cells (Mohanam et al. 2001) and suppresses the glioblastoma-induced neoangiogenesis (Yanamadra et al. 2004). Higher expression of cathepsin-B correlated with shorter patient survival (Strojnik et al. 2000, 2005; Colin et al. 2009).	Anti-cathepsin-H antibodies inhibit invasion of glioblastoma cells in vitro (Sivaparvathi et al. 1996b).	(Sivaparvathi et al. 1996b; Strojnik et al. 2005; Gole et al. 2012); glioblastoma cells secrete cathepsin-L (Formolo et al. 2011); VEGF transcriptionally upregulates the expression of cathepsin-L in glioblastoma cells (Keerthivasan et al. 2007). Anti-cathepsin-L antibodies inhibit in vitro invasion of glioblastoma cells (Sivaparvathi et al. 1996b); downregulation of cathepsin-L expression impairs invasion and promotes apoptosis of glioma cells (Levicar et al. 2003b).	(Flannery et al. 2003, 2006); higher expression of cathepsin-S correlated with shorter patient survival (Flannery et al. 2006). (continued)
Increased	Increased	Increased	Increased
Cathepsin-B	Cathepsin-H	Cathepsin-L	Cathepsin-S

	Expression compared to nontumorous	
Protease	brain	Note, reference(s)
Procaspase-3	Increased	(Ray et al. 2002; Bodey et al. 2004; Tirapelli et al. 2010); higher expression of cleaved caspase-3 correlated with longer patient survival (Kobayashi et al. 2007); basal caspase-3 activity promoted migration and invasiveness of glioblastoma cells (Gdynia et al. 2007).
Procaspase-8	Equivocal results	(Xiao et al. 2002; Bodey et al. 2004; Ashley et al. 2005; Bellail et al. 2010); basal caspase-8 activity promoted migration of and invasiveness glioblastoma cells (Gdynia et al. 2007); possible association between a polymorphism of propaspase-8 and increased risk of glioma (Bethke et al. 2008).
Ubiquitin-specific protease (USP) 2a	Increased	(Tao et al. 2013)
USP7	Decreased	(Ruano et al. 2008)
USP8	Expression detected by IHC	USP8 deubiquitinates AIP4, an ubiquitin E3 ligase, which ubiquitinates and destabilizes FLIPs (CASP8 and FADD-like apoptosis regulator) to confer TRAIL sensitivity of glioma cells (Panner et al. 2010).
USP9x	Expression detected by WB and qRT-PCR	USP9x, as an interactant of SOX-2, is required for the growth and survival of glioma cells (Cox et al. 2013).
USP10	Increased	Higher expression of USP10 is correlated with shorter patient survival (Grunda et al. 2006).
USP15	Increased	<i>USP15</i> gene amplification observed in 2 % of glioblastomas confers poor prognosis (Eichhorn et al. 2012); USP15 binds to the type I TGF- β receptor complex, deubiquitinates, and stabilizes the type I TGF- β receptor, leading to an enhanced TGF- β signaling and oncogenic capacity of glioma-initiating cells (Eichhorn et al. 2012).
USP22	Expression detected by WB and RT-PCR	USP22 is required for the proliferation and survival of glioma cells (Li et al. 2013).

Table 12.1 (continued)

Metalloproteases		
ADAM3A		Homozygous deletion of <i>ADAM3A</i> gene in 16 % pediatric high grade gliomas (Barrow et al. 2011).
ADAM8	Increased	Expression associated with worse clinical outcome (He et al. 2012a); ADAM8 enzymatic activity promotes glioma invasion through matrigel (Wildeboer et al. 2006).
ADAM10	Increased	Acts as a sheddase for membrane-bound molecules such as N-CAM (Kohutek et al. 2009), CD44 (Murai et al. 2004), L1CAM (Mohanan et al. 2013), CXCL16 (Ludwig et al. 2005), and Coxsackievirus and Adenovirus Receptor (CAR) (Houri et al. 2013), thereby promoting glioma motility and growth; important for the renewal of glioma stem-like cells (Bulstrode et al. 2012); involved in the impaired immune recognition of glioma stem cells (Wolpert et al. 2014).
ADAM12	Increased	Expressed by oligodendrocytes and oligodendrogliomas (Kanakis et al. 2013), may be involved in proHB-EGF (heparin-binding EGF-like growth factor) release in glioblastoma (Kodama et al. 2004).
ADAM17	Ambiguous data	Decreased expression reported by Comincini et al. (2009), increased according to TCGA data; mediates hypoxia-induced glioma invasiveness (Zheng et al. 2007); may contribute to stemness maintenance through the Notch signaling (Chen et al. 2013b); promotes the malignant phenotype of glioma cells (Zheng et al. 2012); introduction into astrocytes induced a neoplastic phenotype by deregulating EGFR signaling (Katakowski et al. 2009); involved in the impaired immune recognition of glioma stem cells (Wolpert et al. 2014).
ADAM19	Increased	ADAM19 enzymatic activity promotes glioma invasion through matrigel (Wildeboer et al. 2006).
ADAM22	Decreased	Enzymatically inactive, inhibits glioma proliferation via its disintegrin domain (D'Abaco et al. 2006), receptor for the Leucine-Rich Glioma-Inactivated (LGI) proteins (Kegel et al. 2013).
		(continued)

Table 12.1 (continued)		
Protease	Expression compared to nontumorous brain	Note, reference(s)
ADAM33		An association between ADAM33 polymorphisms and the risk of glioma was reported (Schwartzbaum et al. 2005; Backes et al. 2013).
ADAMTS4	Increased	(Held-Feindt et al. 2006); cleaves brevican in vitro (Matthews et al. 2000).
ADAMTS5/11	Increased	Cleaves brevican in vitro (Held-Feindt et al. 2006).
ADAMTS8	Decreased	(Dunn et al. 2006), proposed tumor suppressor (Choi et al. 2014) and angiogenesis inhibitor in other systems (Vazquez et al. 1999).
ATP23 peptidase (XRCC6BP1)		Lack of amplification associated with better glioma patient survival (Fischer et al. 2010).
Carboxypeptidase-E	Decreased	Lower immunohistochemical staining associated with shorter patient survival; downregulated by hypoxia; overexpression promotes glioma cell proliferation but inhibits migration in vitro (Horing et al. 2012).
CSN5/JAB1	Increased	Probable protease subunit of the COP9 signalosome complex, possible prognostic factor (He et al. 2012b).
Endothelin-converting enzyme-1 (ECE-1)	Expression detected	Glioma and endothelial cells express ECE-1 together with other components of the endothelin system in situ suggesting local endothelin synthesis in gliomas (Egidy et al. 2000; Naidoo et al. 2005).
Glutamate carboxypeptidase II (GCP-II, PSMA)		Expressed by endothelial cells in gliomas (Chang et al. 1999; Wemicke et al. 2011).
Matrix metallopeptidase (MMP)1 (collagenase-1)	Increased	(Stojic et al. 2008; Hagemann et al. 2012), expression associated with worse survival (Zhang et al. 2011; Xu et al. 2013), polymorphism in the promotor region linked to glioblastoma (McCready et al. 2005), possible role in glioma invasion (Gessler et al. 2011); mediates the NO-induced increase of glioma cell motility (Pullen and Fillmore 2010), promotes tumor-induced angiogenesis (Pullen et al. 2012).

MMP2 (gelatinase-A)	Increased	(Sawaya et al. 1996; Forsyth et al. 1999; Munaut et al. 2003), expressed by glioma and less by endothelial cells (Raithatha et al. 2000), increased expression at the invasive edge compared to tumor core in 40 % of glioblastoma cases in a study by Kim et al. (2011). See main text for further details.
MMP3 (stromelysin-1)	High in childhood astrocytoma (Bodey et al. 2000)	Variable expression reported in small cohorts of glioblastoma patients (Nakagawa et al. 1994; Vince et al. 1999); may be involved in glioma invasion (Laurent et al. 2003; Mercapide et al. 2003; Jin et al. 2013; Zheng et al. 2013); may activate MMP2 (Miyazaki et al. 1992).
MMP7 (matrilysin)	Variable expression	(Vince et al. 1999; Thoms et al. 2003; Rome et al. 2007; Xie et al. 2011); weak expression in oligodendrocytic regions (Thoms et al. 2003), expressed in some glioma cell lines in vitro (Nakano et al. 1993, 1995); polymorphism in the promoter region possibly associated with astrocytoma development (Lu et al. 2006b).
MMP9 (gelatinase-B)	Increased	(Rao et al. 1993b; Komatsu et al. 2004); expressed by glioma and various stromal cells, plays role in angiogenesis, glioma proliferation, and invasiveness (Rao et al. 1993b, 1996; Forsyth et al. 1999; Vince et al. 1999; Pagenstecher et al. 2001; Munaut et al. 2003; Bhoopathi et al. 2010; Sun et al. 2013); induces vascular remodeling via VEGF liberation (Du et al. 2008); possible cerebrospinal fluid marker for primary and secondary CNS cancers (Friedberg et al. 1998); higher expression associated with shorter survival in glioblastoma patients.
MMP10 (stromelysin-2)		Higher expression in gemistocytic astrocytes compared to oligodendrocytic regions (Thorns et al. 2003).
MMP11 (stromelysin-3)	Increased	Expressed by tumor infiltrating macrophages, endothelial cells, and some glioma cells (Thorns et al. 2003; Stojic et al. 2008).
MMP12 (macrophage elastase)		Mediates tenascin C-induced increase in glioma invasiveness (Sarkar et al. 2006); upregulated during bevacizumab treatment (Lucio-Eterovic et al. 2009).
		(continued)

(continued)
12.1
Table

	Expression compared to nontumorous	
Protease	brain	Note, reference(s)
MMP13 (collagenase-3)	Increased	Higher expression associated with worse prognosis in glioma (Wang et al. 2012), involved in glioma invasiveness (Inoue et al. 2010), mediates promigratory effects of GDNF (glial cell line-derived neurotrophic factor) and leptin (Yeh et al. 2009; Lu et al. 2010).
MMP14 (MT1-MMP)	Increased	(Yamamoto et al. 1996; Lampert et al. 1998; Fillmore et al. 2001; Guo et al. 2005; Wang et al. 2013b); cleaves and activates proMMP2 (Fillmore et al. 2001), promotes neovascularization (Hiraoka et al. 1998; Deryugina et al. 2002), important for the infiltration of glioma cells along white matter (Belien et al. 1999); increased expression at the invasive front in gliomas (Guo et al. 2005); induces COX-2 expression in glioma cells (Annabi et al. 2009); associated with glioma patient survival (Wang et al. 2013b), expressed in microglia (Markovic et al. 2009).
MMP15 (MT2-MMP)	Increased	(Lampert et al. 1998; Nakada et al. 1999a; Fillmore et al. 2001); mediates increased invasiveness of glioma cells exposed to CXCL12 (Zhang et al. 2005).
MMP16 (MT3-MMP)	Increased	(Fillmore et al. 2001); involved in glioma invasiveness (Li et al. 2013a).
MMP19	Increased	More expressed at the invasion margin of human glioblastomas (Stojic et al. 2008), involved in glioma invasiveness (Lettau et al. 2010).
Neprilysin	Increased	(Monod et al. 1992), expressed by glioma cells in vitro (Monod et al. 1989), cleaves brain natriuretic peptide (Medeiros Mdos et al. 1991), substance P (Endo et al. 1989) and basic fibroblast growth factor (bFGF) (Goodman et al. 2006).
YME1-like 1 (YME1L1)	Decreased	Associated with patient survival, identified as a landscape gene consistently altered in the TCGA glioma dataset (Bredel et al. 2009).

Serine proteases		
Dipeptidyl peptidase IV	Increased	Expressed by vascular and scattered mononuclear-like cells in gliomas, by glioma cells in glioblastomas (Mares et al. 2012); variable expression in glioma cell lines, may inhibit glioma cell growth through an enzymatic activity independent mechanism (Stremenova et al. 2007; Busek et al. 2012).
Furin	Increased	Necessary for the Bcl2-mediated increase of glioma invasiveness (Wick et al. 2004); decreased growth and invasiveness after inhibition of furin in glioma cells, role in the activation of MT1-MMP (MMP14), TGF- β and IGF-1 receptor (Mercapide et al. 2002); in contrast, processing of N-cadherin by furin leads to decreased migration (Maret et al. 2012).
Hepatocyte growth factor activator		Promotes glioma migration, enhances growth, and increases vascular density of experimental tumors (Uchinokura et al. 2006); expression of its endogenous inhibitor (hepatocyte growth factor activator inhibitor type-2/placental bikunin, HAI-2/PB) is decreased in glioblastomas (Hamasuna et al. 2001).
Kallikrein related peptidases (KLK)	Decreased	Dysregulated KLK1, 13, and 15 may predict worse overall-survival in glioblastoma (Girgis et al. 2012); KLK7 detected by RT-PCR in 50 % glioblastomas, may contribute to glioma cell invasion (Prezas et al. 2006); ambiguous data for KLK6 expression-decreased in glioblastoma compared to low grade tumors (IHC) (Strojnik et al. 2009), increased KLK6 (qRT-PCR) (Talieri et al. 2012); higher KLK6 IHC staining associated with worse patient survival, KLK6 promotes the resistance of glioma cells to apoptosis in vitro (Drucker et al. 2013).
Matriptase	Increased	(Clark et al. 2010); overexpression of an endogenous matriptase inhibitor decreased glioma invasion (Miyata et al. 2007).
Neutrophil elastase	Increased	Elastase-positive polymorphonuclear neutrophils are recruited to the infiltrative margin of high grade gliomas (Iwatsuki et al. 2000). (continued)

Table 12.1 (continued)		
	Expression compared to nontumorous	
Protease	brain	Note, reference(s)
PCSK5A		Increases migration of glioma cells in vitro by cleaving N-cadherin (Maret et al. 2012).
PCSK6		Increased in infiltrating glioma cells, may contribute to the invasive phenotype of glioma cells (Delic et al. 2012).
Plasminogen		Produced by glioma cells, contributes to MMP activation (Le et al. 2003, Tsatas and Kaye 2003).
Prolyl oligopeptidase		Possible role in protein secretion in glioma cells (Schulz et al. 2005).
Rhomboid domain containing 1		Silencing by RNAi inhibits glioma cell growth in vitro (Wei et al. 2014).
Seprase (FAP)	Increased	Expressed in gliomas in vivo (Stremenova et al. 2007; Mentlein et al. 2011) and glioma cell lines in vitro (Rettig et al. 1986; Mentlein et al. 2011; Busek et al. 2012); possible role in the migration of glioma cells within the brain extracellular matrix (Mentlein et al. 2011).
Thrombin		Thrombin-positive glioma cells detected in glioblastomas by IHC; thrombin induces proliferation of glioma cells (Ogiichi et al. 2000) and induces VEGF expression in vitro (Yamahata et al. 2002); a direct thrombin inhibitor argatroban reduces glioma growth in animal models (Hua et al. 2005b; Yamaguchi et al. 2013).
Tissue-type plasminogen activator (tPA)	Equivocal results	(Sawaya et al. 1991; Kinder et al. 1993; Caccamo et al. 1994; Landau et al. 1994; Arai et al. 1998; Goh et al. 2005; Salmaggi et al. 2006)
Urokinase-type plasminogen activator (uPA)	Increased	(Kinder et al. 1993; Caccamo et al. 1994; Landau et al. 1994; Arai et al. 1998); possible prognostic factor in glioma (Hsu et al. 1995); uPA is expressed in tunnor and vasculature cells in high grade gliomas (Yamamoto et al. 1994; Zhang et al. 2000), activates other proteases directly (Zhao et al. 2008a) or via plasminogen activation; activates hepatocyte growth factor (HGF) (Naldini et al. 1992); binding of uPA to its cellular receptor uPAR promotes its proteolytic activation as

		well as triggers signaling through uPAR (reviewed in Tsatas and Kaye 2003; Eden et al. 2011); mediates the proinvasive effect of basic
		fibroblast growth factor and transforming growth factor (TGF)- α (Mori et al. 2000).
Threonine proteases		
Gamma-glutamyltransferase	Increased	Expressed in the vasculature and glioma cells (Mares et al. 2012), possible role in glioma growth and GSH metabolism (Schafer et al. 2001).
Proteasome		Decreased chymotrypsin-like and peptidylglutamyl peptide hydrolyzing activity of purified S20 proteasome in 67 % tumors compared to peritumoral tissue, changed subunit composition (Piccinini et al. 2005); decreased LMP2 subunit (Mehling et al. 2007); excessive proteasome-mediated degradation of NF1 (Neurofibromin 1) contributes to its functional inactivation in gliomas (McGillicuddy et al. 2009); decreased proteasome activity in glioma cancer stem cells may promote Notch signaling by stabilizing the Notch intracellular domain (Lagadec et al. 2014) and may be useful for tracking and possibly targeting of glioma stem-like cells (Vlashi et al. 2009); proteasome inhibitors are tested in clinical trials in glioma patients (see Sect. 12.5; Vlachostergios et al. 2013).
Taspase	Increased	(Scrideli et al. 2008); functional role not yet determined, cleaves MLL (mixed lineage leukemia; Lysine (K)-Specific Methyltransferase 2A), a protein required for the maintenance of HOX gene expression in glioma stem cells (Gallo et al. 2013).
<i>Note</i> : Increased expression of procas expression of other procaspases [proc cell lines <i>IHC</i> immunohistochemistry, <i>WB</i> wes	asse-9 (Ray et al. 2002; Waltereit and Weller 2 aspase-10 (Xiao et al. 2002; Ashley et al. 2005) tern blot, <i>qRT-PCR</i> real-time reverse transcripter.	2002; Bodey et al. 2004; Johnson et al. 2007; Fukushima et al. 2008) and), procaspase-6 (Bodey et al. 2004)] were detected in gliomas and glioma tion PCR



overall necrosis with ensuing inflammatory infiltrate and expression of angiogenic genes in the mesenchymal subtype (Verhaak et al. 2010).

Albeit the transcriptomic TCGA data give very rich and complex information on the dysregulation of proteolytic systems based on over 500 glioblastoma cases, it is important to realize their limitations. As detailed above, the transcriptional regulation of protease expression represents only one possible level of control mechanisms, as proteolytic systems are often regulated on the posttranscriptional and posttranslational levels. In addition, although the TCGA data corroborate the heterogeneity of glioblastomas also with respect to the expression of proteases, they do not allow distinguishing the contribution of transformed and stromal cells and may therefore point to a changed cellular composition in different glioma subtypes rather than differential expression in the transformed cells. Irrespective of these limitations, they are a valuable source for selecting proteases for studies of glioma pathogenesis and identification of future therapeutic targets.

12.3 Signals and Mechanisms Affecting Expression and Activity of Proteases in Gliomas

The mechanisms leading to protease dysregulation in gliomas are complex and still only partially understood. However, several aberrant signaling pathways and mechanisms characteristic for gliomagenesis drive the tumor progression in part by affecting the proteolytic machinery (Fig. 12.2).



Fig. 12.2 Examples of gliomagenesis relevant factors and events affecting the local proteolytic balance, and the biological consequences of dysregulated protease expression. *PTEN* phosphatase and tensin homolog, *IDH* isocitrate dehydrogenase, *RTK* receptor tyrosine kinase

12.3.1 Mechanisms Leading to Dysregulation of Protease Expression

The receptor tyrosine kinase (RTK)/Ras/PI3K signaling pathway is dysregulated in over 80 % of gliomas (Van Meir et al. 2010) and promotes cell proliferation, survival, and invasion. The most frequent alteration is EGFR gene amplification, overexpression, or the presence of a constitutively active mutant EGFRvIII variant; these are present in approximately half of the patients and are a characteristic phenotypic feature of the primary glioblastomas (Ohgaki and Kleihues 2007; Van Meir et al. 2010). It is worth mentioning that the active MMP9 was detected in 69 % of primary and just 14 % of secondary glioblastomas and its expression was strongly associated with the expression of EGFRvIII (Choe et al. 2002). Indeed, the EGFR signaling was demonstrated to increase the expression of several proteases in glioma cells in vitro including MMP9 (Kang et al. 2005; Zhao et al. 2010), MMP1 (Anand et al. 2011; Li et al. 2011), MMP2 (Lal et al. 2002; Park et al. 2006), MMP14 (Van Meter et al. 2004), and uPA (Amos et al. 2010). Besides that, EGFR signaling influences the subunit composition of the proteasome which was speculated to be associated with the radioresistance of glioma cells (Kim et al. 2008b). Protease expression can also be influenced by other alterations in the abovementioned RTK/Ras/PI3K signaling pathway such as PTEN (phosphatase and tensin homolog) deletion or Ras mutations, which occur in 37 % and 2 % of gliomas, respectively (Van Meir et al. 2010). PTEN inactivation in gliomas correlates with higher MMP9 expression (Comincini et al. 2009) and in a similar way as the activation of the downstream PI3K promotes the production of MMP2 and MMP9 in glioma cells in vitro (Koul et al. 2001; Kubiatowski et al. 2001; Park et al. 2002; Furukawa et al. 2006; Kwiatkowska et al. 2011). Similarly, constitutively active form of Ras was demonstrated to increase uPA expression and promote cell invasiveness in normal human astrocytes transformed by the introduction of human telomerase in combination with inactivation of p53/pRb by E6/E7 (Zhao et al. 2008b). The aberrant EGFR/Ras/PI3K pathway is also associated with the increased expression of tissue factor, a crucial cofactor for the initiation of the proteolytic blood clotting cascade (Rong et al. 2009; Magnus et al. 2010).

Glioblastoma microenvironment typically contains increased concentration of a number of cytokines including growth factors and chemokines, as well as local mediators such as adenosine or NO, which were demonstrated to influence the expression of proteases in glioma cells (Table 12.2).

Protease expression with the subsequent promotion of invasiveness is also affected by the interaction of glioma cells with the components of the extracellular matrix (ECM). Park et al. (2002) showed that binding of the hyaluronic acid to glioma cells activates the focal adhesion kinase (FAK)-ERK 1/2 signaling pathway and leads to increased MMP9 secretion. Similarly, tenascin C increases the invasiveness of glioma cells by stimulating the expression of MMP12 (Sarkar et al. 2006).

Local	
mediator	Upregulated protease(s)
VEGF	Cathepsin-L (Keerthivasan et al. 2007)
HGF	uPA (Moriyama et al. 1999), MMP2, MMP14 (Moriyama et al. 1996; Hamasuna et al. 1999)
CXCL12	MMP15 (Zhang et al. 2005), MMP9 (Kenig et al. 2010)
CXCL1	MMP2 (Zhou et al. 2005)
TGF-β	MMP19 (Lettau et al. 2010), MMP9 (Dziembowska et al. 2007; Ye et al. 2012), MMP7 (Nakano et al. 1993), ADAMTS4, ADAMTS5 (Held-Feindt et al. 2006)
bFGF	uPA (Mori et al. 2000)
TNF-α ^a	MMP9 (Esteve et al. 1998, 2002), MMP19 (Lettau et al. 2010)
IL-1	MMP9 (Esteve et al. 1998, 2002), uPA (Kasza and Koj 2002), ADAMTS4 (Held-Feindt et al. 2006)
IL-6	MMP2 (Li et al. 2010b)
Oncostatin M	uPA (Krona et al. 2007)
IFN-γ	MMP19 ^a (Lettau et al. 2010)
TRAIL	MMP9 (Kim et al. 2008a)
Adenosine	MMP9 (Gessi et al. 2010)
NO	MMP1 (Pullen and Fillmore 2010)

Table 12.2 Examples of local mediators affecting the expression of proteases in glioma cells

^aSuppression of constitutive MMP2 expression was reported by Qin et al. (1998)

The Sp1 transcription factor promotes the expression of MMP2 (Qin et al. 1999; Guan et al. 2012), ADAM17 (Szalad et al. 2009), and cathepsin-B (Yan et al. 2000) in glioma cells and is highly expressed in the majority of gliomas. Similarly, the Ets-1 transcription factor (Oikawa and Yamada 2003) is overexpressed in glioblastomas (Kitange et al. 1999a) and mediates the transcription of MMP9 (Sahin et al. 2005), cathepsin-B (Yan et al. 2000) and uPA (Kitange et al. 1999b; Nakada et al. 1999b). Several MMP genes also contain the AP-1 element and their transcription may therefore be activated by Jun and Fos transcription factors (Westermarck and Kahari 1999) in response to a variety of signals from the extracellular milieu (Chakraborti et al. 2003).

Intratumoral hypoxia, a typical feature of glioblastoma microenvironment affecting multiple signaling pathways, as well as mutations of IDH (isocitrate dehydrogenase) lead to the stabilization and thereby activation of the HIF1- α subunit of the transcription factor HIF (hypoxia inducible factor), which accelerates glioma progression in part through the upregulation of MMP2, MMP9, and ADAM17 (Brat et al. 2004; Fujiwara et al. 2007; Zheng et al. 2007; Fu et al. 2012).

Recently (see also Chap. 4) alterations in the expression of microRNAs (miRNAs) were described in glioblastomas (Moller et al. 2013) and the mechanisms by which miRNAs may influence the phenotype of glioma cells may also involve the regulation of proteases. miRNAs may directly target the protease mRNA, or exert an indirect effect by modulating the pathways regulating the expression of proteases or their inhibitors. In glioblastoma specimens, miR-211

expression is silenced by promotor hypermethylation and its expression level inversely correlates with MMP9 expression (Asuthkar et al. 2012). Similar negative correlation was also observed between MMP9 and miR-491-5p (Yan et al. 2011). Importantly, both miRNAs were demonstrated to downregulate MMP9 in glioma cells in vitro resulting in decreased invasiveness (Yan et al. 2011; Asuthkar et al. 2012). Other examples of the effects of miRNAs on the proteolytic balance include the negative regulation of MMP16 by miR-146b-5p (Xia et al. 2009; Li et al. 2013a), MMP3 by miR-152 (Zheng et al. 2013), and ADAM17 by miR-145 (Lu et al. 2013). The expression of MMP2 and MMP9 in glioma cells in vitro is further influenced by miR-7, which is downregulated in gliomas, and affects the proteases indirectly by downregulating FAK (Wu et al. 2011). In addition to these tumor suppressor miRNAs, protease targets were also demonstrated for the oncogenic miRNAs. miR-10b is overexpressed in gliomas (Moller et al. 2013) and induces glioma cell invasiveness by targeting the homeobox DNA-binding domain containing transcription factor HOXD10, a negative regulator of MMP14 and uPAR (Sun et al. 2011).

Interestingly, the expression of proteases involved in the remodeling of ECM was recently demonstrated to be induced by the therapeutic interventions used to treat gliomas, thereby somewhat paradoxically contributing to the tumor recurrence. Glioma cells exposed to ionizing radiation exhibit enhanced invasiveness caused by several mechanisms including the upregulation of proteases (Wild-Bode et al. 2001; Park et al. 2006; Badiga et al. 2011; Shankar et al. 2014). A rapid increase in the expression and activation of MMP2, MMP9, and MMP14 after sublethal irradiation was demonstrated in glioma cells in vitro and an MMP inhibitor o-phenantroline was able to reduce the increased invasiveness of the irradiated glioma cells (Wild-Bode et al. 2001). Similarly, treatment with a plasmid silencing the expression of MMP2 resulted in the reversal of the proinvasive effects of irradiation and increased the radiosensitivity of glioma cells (Badiga et al. 2011). The radiation-mediated enhancement of protease expression is probably p53 independent (Wild-Bode et al. 2001) and is suppressed in the presence of the active PTEN (Park et al. 2006). In the case of MMP2, radiation increases its transcription as a result of the activation of the Src and EGFR signaling with the ensuing activation of p38, PI3K, and Akt (Park et al. 2006). Bevacizumab, a monoclonal antibody targeting VEGF, was similarly shown to promote the invasiveness of glioma cells (Lucio-Eterovic et al. 2009; de Groot et al. 2010). Glioma cells exposed to bevacizumab upregulated MMP12, MMP9, MMP2, as well as plasminogen in vitro and a similar upregulation was observed in experimental tumors in mice treated with bevacizumab contributing to their more infiltrative growth (Lucio-Eterovic et al. 2009). This increase of MMP2 and MMP14 expression was also detected in glioma patients treated with bevacizumab (de Groot et al. 2010; Furuta et al. 2014) and the increase of MMP9 in the urine was in fact suggested as a marker for bevacizumab failure in glioma patients (Takano et al. 2010).

12.3.2 Mechanisms Leading to Dysregulation of Protease Activation

Besides the dysregulation of the protease gene expression, the increased activity of extracellular proteases is frequently a result of an inappropriate zymogen activation caused by the protease cofactor overexpression. The cell surface receptors urokinase-type plasminogen activator receptor (uPAR, CD87) (Yamamoto et al. 1994b) and tissue factor (TF, fIII) (Hamada et al. 1996), a crucial cofactor for the initiation of blood coagulation cascade, are both upregulated in gliomas. uPAR is a multifunctional glycosylphosphatidylinositol (GPI)-linked membrane protein that binds several extracellular ligands including uPA (Eden et al. 2011). The binding of uPA to uPAR not only promotes the activation of uPA leading to enhanced pericellular proteolysis but also directly regulates glioma cell adhesion and migration through uPAR (see Mohanam et al. (1999), Eden et al. (2011) and Sect. 12.4.1.3). TF is a transmembrane receptor and cofactor of the coagulation factor VIIa and its overexpression contributes to the procoagulative state in gliomas (Rong et al. 2006). Similarly to uPAR, TF promotes the malignant phenotype of glioma cells by activating intracellular signaling independent of its role in protease activation (Dutzmann et al. 2010; Gessler et al. 2010).

Zymogens may further be inappropriately activated as a result of the dysregulation of the local "proteolytic context" (reviewed in Mason and Joyce 2011). Interestingly, some aspects of the complex proteolytic systems resemble the basic features of the signaling cascades such as signal amplification, cross talk, and a purposeful adaptation. Within the broader, functionally interrelated proteolytic networks, the interactions of individual proteases are frequently reciprocal (Fig. 12.3). For example, uPA can both activate and be activated by plasmin and cathepsin-B (Mason and Joyce 2011) and some proteases facilitate the activity of other proteases by inactivating their inhibitors [e.g., MMPs can inactivate a range of serpins (Kessenbrock et al. 2010) and cathepsin-B cleaves some TIMPs and serpins (Mason and Joyce 2011)]. The glioma proteases cathepsin-B, uPA, and a number of the MMPs seem to occupy critical nodes within the complex proteolytic systems due to the broad range of their respective activators, the ability to activate numerous other proteases and to inactivate several protease inhibitors (Mason and Joyce 2011).

Altered availability of the endogenous protease inhibitors may be another mechanism contributing to the dysregulation of proteolytic activity in gliomas, the best example being the imbalance between the cysteine cathepsins and cystatins that is thought to contribute to tumor invasion. In gliomas, cystatin-E/M downregulation was reported in 78 % of cases and the reduced expression correlated with its promoter hypermethylation (Qiu et al. 2008). Cystatin-C is also downregulated in glioblastomas compared to the low grade tumors and may be a predictive factor for patient survival (Nakabayashi et al. 2005). Further, Gole et al. (2012) showed that at the tumor margin the expression of cystatin-B is decreased, while cathepsin-B is, compared to the central part of the tumor, redistributed into the extracellular space. Such pathologic regulation of the availability of the cathepsin activity may lead to increased invasiveness (Gole



Fig. 12.3 The proteolytic network of extracellular proteases implicated in glioma progression. Proteases from various classes interact in a multidirectional network through the proteolytic activation of zymogens (*green lines*) and inactivation (*red lines*) of endogenous protease inhibitors. Cysteine proteases in *black*, metalloproteases in *red*, serine proteases in *green*, aspartate proteases in *blue*; the protease inhibitors of individual protease classes are shown in the corresponding shades. *MMP* matrix metalloproteinase, *uPA* urokinase-type plasminogen activator, *uPAR* urokinase-type plasminogen activator receptor

et al. 2012). These results are supported by the findings that ectopic expression of the cathepsin-B inhibitor cystatin-C reduces in vitro glioma invasion as well as in vivo tumor formation (Konduri et al. 2002). Tissue factor pathway inhibitor-2 (TFPI-2) is a Kunitz-type serine protease inhibitor that inhibits a variety of serine proteases and is a potential tumor suppressor in several malignancies (Sierko et al. 2007). In gliomas, TFPI-2 is probably silenced by promoter hypermethylation (Konduri et al. 2003) and its expression is inversely correlated with tumor grade. Moreover, the protein was demonstrated to inhibit glioma cell invasion in vitro suggesting that its loss may be directly linked to glioma aggressiveness (Rao et al. 2001).

An opposite role is evident for the serpin plasminogen activator inhibitor 1 (PAI-1), the major inhibitor of the fibrinolytic system. Paradoxically, PAI-1 expression is associated with worse prognosis in several tumors (Van De Craen et al. 2012). In gliomas, a grade-dependent upregulation of PAI-1 is consistently reported with the most intense expression in the areas of vascular proliferation and perinecrotic areas (Rao et al. 1993a; Kono et al. 1994; Landau et al. 1994; Arai et al. 1998; Muracciole et al. 2002; Colin et al. 2009); in addition, high PAI-1 expression (Muracciole et al. 2002) and serum levels (Iwadate et al. 2008) are negative prognostic factors in glioma patients. This seeming paradox likely reflects the non-protease-mediated functions of PAI-1 (Van De Craen et al. 2012) that include its effects on cell adhesion and migration (Bryan et al. 2008; Paugh et al. 2008) and promotion of angiogenesis (Hjortland et al. 2004). The data for

other endogenous protease inhibitors are equivocal. Changes in the expression of TIMPs were reported in gliomas by several groups. The most consistent data exist for the extracellular matrix-associated TIMP3, which is regarded as a tumor suppressor. TIMP3 promoter is hypermethylated in gliomas (Liu et al. 2010) and the hypermethylation correlates with the loss of TIMP3 expression in secondary glioblastomas; in addition, the region on chromosome 22 containing the TIMP3 gene is frequently deleted in a large proportion of secondary and some primary glioblastomas (Nakamura et al. 2005). Other mechanisms that may lead to TIMP3 downregulation involve its targeting by miR21 (Gabriely et al. 2008) and the frequent loss of the cell cycle regulator P14ARF encoded by the CDKN2A locus. P14ARF acts as a tumor suppressor via p53 stabilization but was recently shown to inhibit human glioblastoma-induced angiogenesis by upregulating the expression of TIMP3 (Zerrouqi et al. 2012). TIMP3 inhibits invasion and promotes apoptosis in several tumor cells (Baker et al. 1999). However in a glioma model, the presence of TIMP3 did not significantly affect the antitumor efficacy of an oncolytic adenovirus (Lamfers et al. 2005). For TIMP1, 2, and 4 some studies indicate decreased expression in glioblastomas compared to normal brain (Nakagawa et al. 1994; Mohanam et al. 1995; Aaberg-Jessen et al. 2009) and inhibitory effects on glioma cells (Merzak et al. 1994; Nakano et al. 1995; Matsuzawa et al. 1996; Hoshi et al. 2000; Groft et al. 2001; Nakada et al. 2001; Takahashi et al. 2002; LuW et al. 2004), whereas others suggest that these TIMPs are produced in excess and may participate on the tumor progression (Nakagawa et al. 1995; Lampert et al. 1998; Kachra et al. 1999; Saxena et al. 1999; Pagenstecher et al. 2001; Lu et al. 2004; Blazquez et al. 2008a; Rorive et al. 2010; Crocker et al. 2011). These conflicting results may reflect not only the different methodologies and the heterogeneity of the studied tumors but also the ambiguous role of TIMPs in tumor pathogenesis. This is best illustrated by TIMP2 that promotes the activation of MMP2 [see Sect. 12.1 and Strongin et al. (1995)], may activate the promigratory signaling pathways by binding to MMP14 on the cell membrane (Sounni et al. 2010), and has anti-angiogenic effects independent of MMPs (see Stetler-Stevenson and Seo (2005) for review).

The production of the membrane-bound and secreted proteases in stromal cells, such as reactive astrocytes, microglia, endothelial, and infiltrating immune cells, is an additional factor, which increases the complexity of their biological impact in gliomas (Fig. 12.4) (Rivera et al. 2010). Because of their localization in the extracellular space, these stromal proteases may augment the proteolytic systems deployed by the glioma cells. Examples of this cooperation include the activation of glioma MMP2 by microglial MMP14, which promotes glioma growth (Markovic et al. 2009) or activation of MMP2 in reactive astrocytes by glioma cell-derived plasmin (Le et al. 2003). Interestingly, forced expression of MMP14 directly in glioma cells induced their death (Markovic et al. 2009) further strengthening the ordered and highly context-dependent role of proteases.

With the exception of the activation of the caspase cascade, the reports on the mechanisms regulating the expression and activity of intracellular proteases implicated in glioma pathogenesis are scarce. Hypermethylation of the caspase-

Cathepsin-B, L MMP14 Cathepsin-D MMP11 MMP2 MMP2 Immune cells, Glioma cells MMP9 MMP9 microglia MMP14 Elastase ADAM10 tPA ADAMTS5 Cathepsin-D ECE-1 uPA, plasmin Local and bone Glioma cancer ADAM10 MMP9 marrow derived stem-like cells ADAM17 ? progenitor cells ? Cathepsin-B MMP9 MMP2 ECE-1 Reactive MT MMPs Neovasculature astrocytes GCP-II uPA UPA Cathepsin-D

Fig. 12.4 Examples of the extracellular proteases expressed by individual constituents of the glioma microenvironment. It is important to note that the list is non-exhaustive as the expression of several proteases was not yet analyzed in all cell types and the expression in individual cell types may dynamically change in response to microenvironmental stimuli. Cysteine proteases in *black*, metalloproteases in *red*, serine proteases in *green*, aspartate proteases in *blue. MMP* matrix metalloproteinase, *uPA* urokinase-type plasminogen activator, *tPA* tissue-type plasminogen activator, *ECE* endothelin converting enzyme, *MT MMPs* membrane type MMPs, *GCP-II* glutamate carboxypeptidase II

8 promoter, which leads to the block of the extrinsic apoptotic pathway, was observed in over 50 % of glioblastomas by Skiriute et al. (2012) and was associated with shorter patient survival. Several mechanisms were proposed to regulate the activity of the cysteine proteases calpains, although their in vivo relevance mostly remains to be determined (see Franco and Huttenlocher (2005) for review). Elevation of the intracellular concentration of Ca^{2+} , autocatalytic cleavage of the enzymes, and the interaction with phospholipids and the endogenous inhibitor calpastatin were demonstrated to influence the activity of calpains (Franco and Huttenlocher 2005). Interestingly, calpain-2 is phosphorylated by ERK after the activation of the EGFR signaling, which is essential for EGF-induced motility in fibroblasts (Glading et al. 2000, 2004), and may thus play an important role in the motility of glioma cells as well (see Sect. 12.4.1.5).

In conclusion, multiple proteases show differential expression in glioma tissue as a result of a number of different pathogenetic mechanisms eventually leading to the dysregulation of the proteolytic homeostasis in gliomas. In addition, the dysregulation of the proteolytic activity in the extracellular space can be triggered by various mechanisms originating from changes in the stromal as well as the malignant cells. The relative importance of the various mechanisms may change during glioma progression and in some cases the proteolytic homeostasis can be impaired even without an overt overexpression of the protease(s). Conversely, the overexpression of a protease by itself need not be sufficient to change the proteolytic balance in the presence of counteracting compensatory mechanisms in the tumor microenvironment or in tumor cells.

12.4 Protease-Mediated Protein Processing in Gliomas and Participation of Proteases on the Biological Hallmarks of Gliomas

Extracellularly localized and plasma membrane-bound proteases are important tools used both by glioma cells as well as by the stromal cells to shape the glioma microenvironment. Their substrates include structural protein components of the extracellular matrix (ECM), zymogens of other proteases, and regulatory molecules such as chemokines, cytokines, and cell surface receptors or plasma membranebound proteins that may be released into the extracellular space (Fig. 12.5). These proteases therefore frequently serve as direct (e.g., via protease-activated receptors) or indirect (e.g., by modifying or releasing signaling molecules) mediators of intercellular communication. The biological effects of their proteolytic activities are manifold; proteases contribute to the profound remodeling of the unique ECM of human brain observed in glioblastoma (Bellail et al. 2004) and promote glioma cell dissemination. Cleavage of the ECM not only removes the physical barriers to glioma dissemination but also releases growth factors sequestered in the ECM (e.g., VEFG, TGF- β) and produces fragments of ECM proteins with new biological activities (e.g., anti-angiogenic peptides) that influence glioma cell proliferation,



Fig. 12.5 Proteins regulated by plasma membrane-bound and extracellular proteases in the glioma microenvironment. *CAR* Coxsackievirus and Adenovirus Receptor, *ECM* extracellular matrix, *HB-EGF* heparin-binding EGF-like growth factor, *HGF* hepatocyte growth factor, *PAR* protease-activated receptors



Fig. 12.6 Proteins regulated by intracellular proteases contributing to glioma pathogenesis. *CAR* Coxsackievirus and Adenovirus Receptor, *CDK* cyclin dependent kinases, *FASN* fatty acid synthase, *IkB* inhibitors of NF κ B, *p75NTR* p75 neurotrophin receptor, *DUBs* deubiquitinating enzymes

resistance to apoptosis, and neovascularization. Finally, by shedding cell surface molecules responsible for the activation of the immune system such as NKG2D ligands (Eisele et al. 2006; Wolpert et al. 2014) and activating latent TGF- β (Huber et al. 1992; Leitlein et al. 2001), proteases aid glioma cells to escape from the immune surveillance.

In contrast with the extracellularly localized proteases, the role of the intracellular proteases is largely restricted to the expressing cells, possibly with the exception of some proteases present in the secretory pathway and exosomes or released into the extracellular space due to apoptotic or necrotic disintegration of the cells. The substrates of these proteases relevant for the progression of glioblastomas are less explored, but include the cytoskeletal and organellar proteins, components of the signal transduction pathways, proteins regulating and executing vesicular transport, gene expression and replication, autophagy, and apoptosis. Importantly, the proteasome together with the deubiquitinating enzymes (DUBs) are critical regulators of many cellular proteins implicated in glioma pathogenesis (Fig. 12.6).

12.4.1 Proteases and Glioma Invasion

The widespread infiltration of the surrounding brain tissue by glioma cells is a long recognized hallmark of gliomas (Bramwell 1888) and in gliomas with IDH mutation, individual invading glioma cells were demonstrated to be dispersed

throughout the brain (Sahm et al. 2012). The locoregional treatments (i.e., surgical removal of the tumor with subsequent radiation therapy) therefore almost invariably fail and the tumor recurs usually within 2-3 cm of the original location.

Several reports establish a critical role of the extracellular and membrane-bound metalloproteases (especially MMP2, MMP9, MMP14, ADAMTS), the serine protease u-PA, and secreted lysosomal cysteine proteases including cathepsin-B in glioma invasiveness (reviewed in Binder and Berger 2002; Levicar et al. 2003b; Rao 2003; Mentlein et al. 2012). Indeed, MMP2 and MMP9 (Kim et al. 2011), ADAM17 (Chen et al. 2013a), as well as uPA and its receptor uPAR (Yamamoto et al. 1994a; Zhang et al. 2000; Colin et al. 2009) are abundantly expressed at the invasive edge. In addition, the urokinase-type plasminogen activator receptor (uPAR) and cathepsin-B are expressed by glioma cells infiltrating the surrounding brain tissue (Mikkelsen et al. 1995).

The activation of proteolytic systems seems to be sufficient as well as necessary for glioma cell invasiveness and involves proteases expressed by the malignant as well as stromal cells (Le et al. 2003). MMP14 is a key enzyme endowing glioma cells with the ability to spread and migrate on myelin (Paganetti et al. 1988; Amberger et al. 1994). Interestingly, even non-glioma cells such as fibroblasts could gain the capacity to migrate on an otherwise unpermissive myelin substrate as well as to invade the myelinated optic nerve fibers after the introduction of MMP14 (Belien et al. 1999). Similarly, introduction of ADAM17 into an astrocytic cell line caused upregulation of several invasion and angiogenesis-promoting genes and resulted in increased invasiveness and formation of high grade brain tumors upon intracranial implantation (Katakowski et al. 2009). MMP2 (gelatinase-A) is overexpressed in the majority of glioblastomas (Yamamoto et al. 1996; Kunishio et al. 2003; Hagemann et al. 2012) and a number of studies demonstrated that MMP2 may be one of the shared downstream components critical for the execution of the cell invasion program. MMP2 is produced as an inactive zymogen that is activated in the extracellular space by a complex mechanism that involves MMP14 and TIMP2 (see Kessenbrock et al. (2010) and references therein). Blocking MMP2 by RNAi (Kargiotis et al. 2008; Badiga et al. 2011), inhibitors (Noha et al. 2000; Nuti et al. 2011), or interference with the pathways that drive its expression (e.g., by modulating miRNA (Nan et al. 2010; Pan et al. 2012), the PI3K-Akt (Koul et al. 2001; Kubiatowski et al. 2001; Kwiatkowska et al. 2011; Jung et al. 2013) and other signaling pathways (Blazquez et al. 2008b; Kamino et al. 2011; Guan et al. 2012) decrease the invasiveness of glioma cells. Similar indispensable proinvasive role was demonstrated by targeting uPA and its receptors uPAR, MMP9, cathepsin-B (Kondraganti et al. 2000; Gondi et al. 2004a, b; Lakka et al. 2004) and cathepsin-L (Levicar et al. 2003b) with an additive effect when multiple proteases were targeted.

Recently, a number of other proteases including the ones localized predominantly intracellularly were also shown to contribute to glioma invasiveness. These include the metallo- [MMP1 (Gessler et al. 2011), MMP3 (Mercapide et al. 2003), MMP13 (Inoue et al. 2010), MMP15 (Zhang et al. 2005), MMP16 (Li et al. 2013a), MMP19 (Lettau et al. 2010), MMP26 (Deng et al. 2010), ADAMs 8 and 19 (Wildeboer et al. 2006), ADAMTS 4 and 5 (Held-Feindt et al. 2006)] as well as serine [(Miyata et al. 2007), FAP (Mentlein et al. 2011), PCSK6 (Delic et al. 2012), PCSK5A (Maret et al. 2012), furin (Mercapide et al. 2002; Wick et al. 2004), HGFA (Uchinokura et al. 2006)], and cysteine proteases [cathepsin-H (Sivaparvathi et al. 1996a), cathepsin-L (Sivaparvathi et al. 1996c; Levicar et al. 2003a), calpain-2 (Jang et al. 2010)].

The pathways and mechanisms by which proteases contribute to glioma invasion are diverse, strongly context-dependent, and in several cases highly redundant and overlapping.

12.4.1.1 Extracellular Matrix Cleavage

By cleaving the ECM, proteases remove the physical barriers hindering glioma invasion. Hyaluronic acid, tenascins, and the proteoglycans lecticans are major components of the brain ECM (Bellail et al. 2004). The fibrillar proteins typical for the ECM in other organs were previously thought to be largely restricted to the vicinity of blood vessels (collagen IV, fibronectin, laminin) or completely absent (collagen I), but there is increasing evidence that they are produced by glioma cells in situ (Paulus et al. 1994; Senner et al. 2008; Huijbers et al. 2010; Payne and Huang 2013; Serres et al. 2013). The brain-specific components and mesenchymal fibrillar proteins are subject to proteolytic degradation by several proteases. For example, the lecticans are cleaved by numerous ADAMTS, in particular the aggrecanases ADAMTS4 and ADAMTS5 (Held-Feindt et al. 2006) that are typically elevated in brain tumors, but contribution of several other MMPs including MMP19 is likely (Lettau et al. 2010). The broad range of extracellular components cleaved by MMPs (Yong et al. 2001; Hagemann et al. 2012) and aspartate and cysteine cathepsins, together with the profound dysregulation of their activities in brain tumors, makes these proteases most likely candidates involved in the degradation of ECM.

12.4.1.2 Modification of the Function of Cell Adhesion Molecules

CD44 is a major hyaluronic acid cell receptor on glioma cells and promotes their migration and invasion upon proteolytic cleavage. MMP9 binds to and cleaves CD44 (Chetty et al. 2012); in addition, CD44 can be cleaved by ADAM10 in response to CD44 ligation (Murai et al. 2004). The released extracellular fragment of CD44 was shown to directly promote glioma migration and invasion (Chetty et al. 2012), whereas the cell membrane-bound CD44 fragment is cleaved by γ -secretase. The liberated intracellular domain translocates to the cell nucleus where it acts as a transcription factor (Murakami et al. 2003) and may play a role in glioma cell adhesion (Chetty et al. 2012). Other examples of proteolytically processed cell adhesion molecules implicated in glioma migration are the ADAM 10 substrates N-cadherin (Kohutek et al. 2009) and L1CAM (CD171) (Yang et al. 2011).

12.4.1.3 Direct or Indirect Activation of the Migration-Promoting Signaling Pathways

Protease expression is associated with the activation of motility-promoting signaling cascades. Motility is decreased in glioma cells after the downregulation of uPA by RNAi in parallel with the disorganization of the cytoskeleton, downregulation of the small GTPase of the Rho-subfamily Cdc42, and decreased PI3K/Akt phosphorylation (Chandrasekar et al. 2003). The underlying mechanisms may include binding of uPA to uPAR, which converts the latter into a membrane-bound chemokine and triggers intracellular signaling (Eden et al. 2011). In addition, uPA may proteolytically activate HGF (Naldini et al. 1992), a cell motility enhancing growth factor (Moriyama et al. 1996). The tissue factor (TF) is robustly upregulated in glioma cells in response to hypoxia (Rong et al. 2009) and may trigger the local activation of the coagulation cascade proteases such as fVIIa or thrombin that subsequently initiate the promigratory signaling through the protease-activated receptors (PARs) (Gessler et al. 2010). Similarly to uPA, thrombin facilitates the maturation of HGF by activating the protease HGF activator (Uchinokura et al. 2006). Metalloproteases such as MMP14 were also demonstrated to promote promigratory MAPK signaling possibly through EGFR transactivation as well as by EGFRindependent mechanisms (Gingras et al. 2001; Langlois et al. 2007).

Zheng et al. (2007) further showed that ADAM17, a sheddase involved in the release of membrane-bound growth factors and cytokines, is implicated in the hypoxia-mediated increase in glioma invasiveness by activating the EGFR signaling pathway. Proteases such as MMP9 are also able to promote glioma cell migration by cleaving the IGFII-IGFBP complexes thereby releasing the cell motility enhancing IGF-II (Insulin-like growth factor-II, Rorive et al. (2008) and references therein). The cytokine TGF- β released from the extracellular matrix or from infiltrating microglia is another mediator that strongly promotes glioma invasiveness (Wesolowska et al. 2008; Ye et al. 2012). TGF- β is produced in a latent form and several proteases including plasmin, MMP2, thrombin, MMP14, and furin-like proteases are involved in its maturation (Leitlein et al. 2001; Jenkins 2008).

12.4.1.4 Removal of Migration Inhibitors and Proteolytic Modification of Extracellular Matrix-Promoting Glioma Migration

The brain ECM and myelin in particular are inhibitory to cellular migration (Caroni and Schwab 1988; Schwab and Caroni 1988). bNI-220, one of the most potent CNS myelin inhibitory proteins, was shown to be cleaved and inactivated by MMP14 (Belien et al. 1999), which promoted glioma cell invasiveness. Another inhibitory molecule is brevican (Yamada et al. 1997), a CNS-specific proteoglycan of the lectican family, that is upregulated in gliomas (Gary et al. 1998; Viapiano et al. 2005; Viapiano and Matthews 2006) and requires proteolysis for the promotion of glioma invasion. The studies by Viapiano et al. (2008) and Hu et al. (2008) demonstrate that the transfection of full length brevican that is resistant to the ADAMTS-mediated cleavage does not promote the malignant phenotype of glioma cells, whereas proteolytic cleavage or an N-terminal fragment of the brevican

molecule promotes glioma cell adhesion, migration, and invasiveness as well as in vivo tumor growth (Hu et al. 2008; Viapiano et al. 2008). Although the downstream mechanisms remain to be established, the resulting N-terminal fragment of brevican seems to promote EGFR activation and expression of cell adhesion molecules and fibronectin (Hu et al. 2008). The EGFR activation may further promote glioma invasiveness by increasing protease expression (see Sect. 12.3). Yet another example of a secreted ECM molecule modified by proteolysis is the TGF- β -induced protein (betaig-h3). This protein has pleiotropic effects on cell–cell and cell–extracellular matrix interactions (Thapa et al. 2007) and influences adhesion and migration. In a study by Kim et al. (2012), betaig-h3 inhibited glioma cell invasion in vitro and its MMP9-mediated cleavage was suggested to be in part responsible for the proinvasive effects of MMP9 (Kim et al. 2012).

12.4.1.5 Cytoskeleton and Membrane Protrusion Remodeling

The dynamics of the actin fibers and the remodeling of the focal adhesions are critical determinants of cellular motility. Intracellular proteases such as the cysteine proteases of the calpain family importantly contribute to this process by the cleavage of the adhesion complex proteins (e.g., tallin, FAK, and paxillin) and of the actin regulators (e.g., cortactin and the small GTPase RhoA) (Carragher and Frame 2002; Franco and Huttenlocher 2005). In neuronal cells, EGF and brainderived neurotrophic factor (BDNF) lead to calpain-2 phosphorylation via MAPK signaling (Zadran et al. 2010) and this posttranslational modification is necessary for the promigratory effects of EGF signaling (Glading et al. 2000, 2004; Cuevas et al. 2003). In gliomas, calpain-2 promotes cell migration after the binding of betaig-h3 (TGF- β -induced protein) to the α -5- β -1 integrin on the surface of glioma cells (Ma et al. 2012) and was shown to be required for glioma invasiveness by regulating the invadopodia dynamics and MMP2 secretion (Jang et al. 2010; Lal et al. 2012).

Somewhat surprisingly, low levels of active caspase-3 likewise promote glioma migration and invasion probably by the processing of gelsolin (Gdynia et al. 2007), a protein involved in actin remodeling (Silacci et al. 2004).

12.4.2 Proteases and Glioma Cell Proliferation and Apoptosis

Results of recent studies provide evidence that multiple different proteolytic mechanisms contribute to the cell cycle deregulation in glioma cells. They include the proliferative signaling mediated by the presenilin-generated carboxyterminal fragment of the overexpressed Notch receptor (Stockhausen et al. 2010; Capaccione and Pine 2013), by increased activation or activity of the protease-activated receptors (Hayakawa et al. 2007; Gessler et al. 2010), by the upregulation of some ADAM family members possibly activating the EGFR-PI3K-AKT signaling pathway (Bulstrode et al. 2012; Zheng et al. 2012; Chen et al. 2013b), and by the reduced degradation of the overexpressed or mutated tyrosine kinase receptors such as EGFR and MET by the ubiquitin-proteasome system (Hede et al. 2013). The

protein components of the cell cycle machinery as well as their regulators are targeted for degradation by the ubiquitin-proteasome system (Vlachostergios et al. 2012; Hede et al. 2013). However, several specific cysteine isopeptidases called deubiquitinating enzymes (DUBs), which remove the ubiquitin chains from the ubiquitinated proteins, reverse the function of ubiquitination as an integral component of the core cell cycle machinery and of the cell cycle check points (Clague et al. 2012; Fraile et al. 2012; Cox et al. 2013; Li et al. 2013a). Besides their involvement in the control of cell cycle progression, DUBs participate also in the regulation of the signaling pathways, DNA damage repair, and apoptosis (Panner et al. 2010; Ramakrishna et al. 2011; Clague et al. 2012; Eichhorn et al. 2012; Fraile et al. 2013; Li et al. 2012; Fraile et al. 2012; Fraile et al. 2012; Eichhorn et al. 2012; Fraile et al. 2013; Li et al. 2012; Eichhorn et al. 2012; Fraile et al. 2011; Clague et al. 2012; Eichhorn et al. 2012; Fraile et al. 2011; Clague et al. 2012; Eichhorn et al. 2012; Fraile et al. 2012; Li et al. 2012; Fraile et al. 2011; Clague et al. 2012; Eichhorn et al. 2012; Fraile et al. 2012; Fraile et al. 2013; Li et al. 2012; Fraile et al. 2012; Fraile et al. 2012; Eichhorn et al. 2012; Fraile et al. 2012; Fraile et al. 2012; Eichhorn et al. 2012; Fraile et al. 2012; Fraile et al. 2012; Fraile et al. 2013; Lee et al. 2013) and thus their functions may be influenced by the inherent redox disturbances in cancer.

Defects in the initiation and execution of apoptosis represent a hallmark of malignant cells including transformed astrocytes and proteolytic enzymes are indispensable players in the apoptotic pathways. Although some glioma cell lines are sensitive to apoptosis induction by TRAIL (tumor necrosis factor- α -related apoptosis-inducing ligand) and anti-Fas agonistic antibodies, many others including those with the stem cell features show resistance against the extrinsic death receptor (DR)-mediated apoptosis (Xiao et al. 2002; Yang et al. 2007; Capper et al. 2009; Bellail et al. 2010; Tao et al. 2012). Despite the high frequency of CASP8 gene promoter, hypermethylation together with the absence of procaspase-8 protein expression in gliomas (Ashley et al. 2005; Martinez et al. 2007; Skiriute et al. 2012), reexpression of procaspase-8 in response to the DNA methyltransferase inhibitor 5-aza-2'-deoxycytidine treatment was not sufficient to restore TRAIL sensitivity in glioma cells. These results suggest the participation of additional factors responsible for the resistance to TRAIL (Capper et al. 2009). Indeed, other studies showed that the resistance of glioma cells against apoptosis induction by activated DRs is often caused by the combination of several factors including the downregulation of procaspase-8 and -10 expression and the inhibition of their activation at the death-inducing signaling complex (DISC) by c-FLIP₁ and c-FLIP₅, RIP, and PED/PEA-15 proteins (Xiao et al. 2002; Yang et al. 2007; Bellail et al. 2010; Panner et al. 2010). There is evidence that glioma cells can be killed by the granzyme-B (GrB)/perforin apoptosis pathway triggered by tumor-infiltrating lymphocytes which establish immunological synapses with tumorigenic cells (Hishii et al. 1999; Barcia et al. 2009). The synapsing CD8⁺GrB⁺ T cells showed GrB polarization towards tumor cells, which displayed a pycnotic or fragmented nucleus and a high positivity of the cleaved caspase-3, together indicating induced entry of the tumor cells into the execution phase of apoptosis (Barcia et al. 2009). Despite the very low percentage of synapsing cytotoxic T lymphocytes in all examined glioma cases, suggesting a deficient immune response (Barcia et al. 2009), a recent immunohistochemical study revealed that the higher expression of cleaved caspase-3 in gliomas was associated with longer survival of surgically treated glioma patients (Kobayashi et al. 2007). Tumor microenvironment of gliomas frequently contains hypoxic and acidic regions. Since hypoxia and

acidic stress induce overexpression of serpinB9 in glioma stem cells (Li et al. 2009; Hielmeland et al. 2011), this serpin, being a physiological irreversible inhibitor of GrB (Rousalova and Krepela 2010), may protect them from the GrB/perforinmediated immune killing. Compared to the normal brain cortex tissue and primary neurons, glioma cells and tumors are hypersensitive to the (cytochrome-c + dATP)mediated induction of the apoptosome-driven activation of procaspase-9 and -3 (Johnson et al. 2007). The authors attributed the differential sensitivity of the apoptosome apparatus activation to high Apaf-1 mRNA and protein levels in the tumor tissue compared with low Apaf-1 levels in the normal adjacent brain tissue. These differences in Apaf-1 levels correlated with differences in the levels of the transcription factor E2F1, an activator of Apaf-1 transcription, which was overexpressed in gliomas and bound to Apaf-1 promoter specifically in the tumor tissue (Johnson et al. 2007). A systems medicine model was recently suggested to predict the susceptibility of gliomas to apoptosis execution via the apoptosomedependent procaspase activation. Based on the Apaf-1, procaspase-9, procaspase-3, Smac, and XIAP protein expression levels, the mathematical model predicted the sensitivity of glioma cell lines to temozolomide in vitro. Even more importantly, higher sensitivity to apoptosis induction was predicted by the model for the patients with longer progression free survival (Murphy et al. 2013).

Taken together, the proteolytic balance represents a prominent homeostatic regulator affecting both the proliferation and apoptosis of glioma cells.

12.4.3 Proteases and Glioma Neovascularization, Formation of Necrotic Areas and Pseudopalisades

Glioblastomas rank among the most vascularized neoplasms and typically contain areas of microvascular proliferation and a large number of dysplastic vessels. In fact, endothelial cells in glioblastomas are responsible for a substantial proportion of the extracellular matrix degrading proteolytic activity within the glioma microenvironment. Using CNS-1 cells in a rat glioma model, Regina et al. demonstrated that endothelial cells were the dominant source of the MMP9 activity in the tumors (Regina et al. 2003). MMP2, MMP9 (Rao et al. 1996; Vince et al. 1999; Raithatha et al. 2000), cathepsin-B (Mikkelsen et al. 1995; Sivaparvathi et al. 1995; Wang et al. 2005), and uPA (Yamamoto et al. 1994a) are expressed by vascular structures in gliomas. Interestingly, whereas endothelial cells in the intracranial rat glioma tumors strongly upregulated MMP9, this upregulation was absent in the subcutaneous tumors, suggesting that complex microenvironmental signals are important for the induction of proteases in endothelial cells (Regina et al. 2003).

Mechanistically, membrane-bound and extracellular proteases are well-known regulators as well as executors of the process of glioma neovascularization (Lakka et al. 2005). The vascular structures are generated with the participation of local as well as bone marrow-derived cells by several mutually nonexclusive mechanisms including angiogenesis, vasculogenesis, vascular cooption, vascular mimicry, and transdifferentiation of glioma stem cells into vascular cell types (Weis and Cheresh
2011). During angiogenesis, the endothelial cell-produced matrix metalloproteinases, cysteine proteases such as cathepsin-B, and serine proteases such as uPA and plasmin mediate the degradation of the basal membrane, thus permitting the invasion of endothelial cells and sprouting of new vessels (Lakka et al. 2005). The proteolytic remodeling of extracellular matrix also leads to the release of proangiogenic growth factors. By releasing sequestered VEGF, MMP9 was shown to participate on the angiogenic switch in pancreatic cancer (Bergers et al. 2000) and a similar mechanism seems to operate in glioblastomas (Du et al. 2008). In an animal model, ablation of tumor cell derived and stromal MMP9 impeded vascular remodeling and recruitment of endothelial and pericyte progenitors (i.e., vasculogenesis) (Du et al. 2008). Interestingly, MMP9 on bone marrow-derived CD45⁺ tumor infiltrating cells was sufficient to induce angiogenesis by increasing the bioavailability of VEGF in this model (Du et al. 2008). The expression of MMP9 was also able to reverse the anti-angiogenic and growth inhibitory effect of SPARC overexpression in meduloblastoma cells (Bhoopathi et al. 2010). Thus the presence of a supercritical amount of MMP9 in the glioma microenvironment, most likely irrespective of its cellular source, seems to be necessary and sufficient to induce vascular remodeling and angiogenesis.

Another mode of glioma neovascularization involves the accumulation of glioma cells along preexisting vessels (vascular cooption) with an ensuing intravascular thrombosis, which leads to necrosis and hypoxia-induced angiogenesis (Rong et al. 2009). Proteases play various roles during this process. The enzymatic activity of matrix metalloproteinases contributes to the disruption of the endothelial cell barrier function (Ishihara et al. 2008; Rivera et al. 2010) and vessel destabilization. The serine proteases of the blood coagulation cascade thus gain access to the increased levels of tissue factor (TF) expressed by glioma cells, which initiates blood clotting and occlusion of the vessel (reviewed in Rong et al. 2009). Angiogenesis is activated by the resulting tissue hypoxia. In addition thrombin generated by the coagulation cascade stimulates endothelial cells by upregulating the α -v- β -3 integrin (Tsopanoglou et al. 2002), promotes the production of VEGF in glioma cells through PAR-2 signaling (Yamahata et al. 2002; Dutra-Oliveira et al. 2012), and leads to the activation of the proangiogenic HGF (Abounader and Laterra 2005; Uchinokura et al. 2006). The pathologic activation of the proteolytic coagulation cascade was also suggested to foster glioma stem cells in the perivascular niche (Garnier et al. 2010; Magnus et al. 2010).

Other proteases may be involved in glioma neovascularization by mechanisms not directly involving the degradation of the ECM. Endothelin converting enzyme (ECE) is expressed by glioma cells and glioma vasculature together with other components of the endothelin system (Egidy et al. 2000; Naidoo et al. 2005). ECE proteolytically converts a precursor protein into endothelin-1, which promotes vascularization due to its proproliferative and promigratory effects on endothelial cells (reviewed in Kaur et al. 2005). Clinical studies targeting ET-1 in glioblastoma are underway (Phuphanich et al. 2008) and an alternative approach could involve ECE inhibition (Berger et al. 2005). Glutamate carboxypeptidase II (prostate-specific membrane antigen, PSMA) is expressed in the neovasculature of several

malignancies (Chang et al. 1999) including glioblastoma (Wernicke et al. 2011). In addition to being a maker of tumor neovascularization (Chang et al. 1999), PSMA seems to be functionally important as its absence or inhibition was demonstrated to prevent angiogenesis through the modification of integrin signaling in endothelial cells (Conway et al. 2006; Grant et al. 2012).

Proteases are driving the formation of the pseudopalisades, a typical morphological feature of glioblastomas. These highly cellular regions typically surround necrotic areas, are hypoxic, exhibit significant gelatinolytic activity (Brat et al. 2004), and abundant expression of cathepsin-B and PAI-1 (Colin et al. 2009). The increased cellularity of these structures is not due to the increased cell proliferation but rather reflects an increased migratory capacity of the glioma cells (Brat et al. 2004), which is promoted by proteases. Hypoxia, EGFR activation, and PTEN loss increase the expression of tissue factor in glioma cells (Rong et al. 2009) and the interaction of this protease cofactor with the coagulation fVIIa together with the activation (reviewed in Dutzmann et al. 2010).

Noteworthy, proteases also exert anti-angiogenic effects (Rege et al. 2005; Lopez-Otin and Matrisian 2007; Ribatti 2009). ADAMTS1 and 8 were identified based on their sequence homology with the angioinhibitory thrombospondin-1 and similarly to thrombospondin-1 inhibit endothelial cell proliferation and angiogenesis (Vazquez et al. 1999), possibly by the sequestration of VEGF (Luque et al. 2003) or via the release of anti-angiogenic peptides from thrombospondin-1 and 2 (Lee et al. 2006). Interestingly, ADAMTS8 is downregulated in the majority of gliomas by a so far unknown mechanism (Dunn et al. 2006) and may therefore contribute to the excessive neovascularization of these tumors. A cell surface protease neprilysin (neutral endopeptidase 24.11, CD10) likewise inhibits angiogenesis by cleaving and inactivating the basic fibroblast growth factor (Goodman et al. 2006). Somewhat unexpectedly, anti-angiogenic effects are also observed in the case of proteases traditionally viewed as promoters of tumor progression. Several endogenous angiogenesis inhibitors such as endostatin, tumstatin, and angiostatin are proteolytic fragments produced from the ECM or plasminogen (Rege et al. 2005; Ribatti 2009). Indeed, MMP9 is crucial for the liberation of the C-terminal domain from collagen-IV producing tumstatin (Hamano et al. 2003) and the furin-mediated activation of MMP14 is crucial for the generation of vasculostatin from the membrane-bound brain-specific angiogenesis inhibitor 1 (BAI1) (Cork et al. 2012). Supporting the functional importance of these processes, the absence of MMP9 in mice leads to decreased levels of circulating tumstatin and increased growth of experimental tumors (Hamano et al. 2003). Similarly, the absence of MMP12 and MMP19 is associated with enhanced tumor growth owing to the promotion of angiogenesis (Houghton et al. 2006; Jost et al. 2006). Even more surprisingly, a proteolytically produced fragment of MMP2 corresponding to its hemopexin domain blocks glioma growth by inhibiting angiogenesis as well as proliferation and migration of glioma cells (Bello et al. 2001). This might explain the bewildering results of a recent study that showed a reduced in vivo growth of glioma cells overexpressing MMP2 and a more pronounced destabilization of the tumor vasculature together with higher tumor proliferation in its absence (Tremblay et al. 2011).

Proteases probably participate in the anti-angiogenic treatment-induced changes of the tumor vessels towards a more mature morphology and function. This vascular "normalization" (Goel et al. 2011) improves the perfusion and oxygenation of the tumors and is an important mechanism supporting the effectiveness of radiotherapy and cytotoxic therapies (Jain 2005; Sato 2011). In a mouse glioma model, VEGFR2 blockade promoted pericyte recruitment and a temporary restoration of the vascular morphology accompanied by the remodeling of the abnormally thick basal membrane. Collagenase IV enzymatic activity in the perivascular areas was significantly increased by the anti-VEGFR2 treatment, and the thinning of the basal membrane was prevented by a coadministration of a matrix metalloprotease inhibitor, further confirming the important role of the proteases in the process (Winkler et al. 2004).

In conclusion, the effects of proteases on angiogenesis are diverse as proteases may promote or inhibit the formation of new vessels depending on the stage of tumor development and the presence of their substrates in the tumor microenvironment.

12.5 Exploitation of Glioma-Associated Proteases as Possible Markers and Therapeutic Targets: Failures and Promises

Numerous studies examined the association between the expression of proteases and clinicopathologic data and expression of several proteases was even suggested to predict patient survival.

Patients with anaplastic astrocytomas with positive immunoreactivity for the cleaved caspase-3 in more than 10 % tumor cells had better survival rate in a study by Kobayashi et al. (2007). Similarly, higher immunohistochemical staining for carboxypeptidase-E was associated with longer survival (Horing et al. 2012). On the contrary, higher expression of ADAM8 (He et al. 2012a), CSN5 (Jab1) (He et al. 2012b), MMP13 (Wang et al. 2012), kallikrein 6 (Drucker et al. 2013), uPA (Bindal et al. 1994; Hsu et al. 1995), MMP1 (Zhang et al. 2011; Xu et al. 2013), and cathepsin-B (Colin et al. 2009) are negative prognostic factors in gliomas. However, these potentially clinically applicable results are mostly based on small scale studies or explorative microarray analyses and thus will require validation in larger patient cohorts before these candidate proteases can be accepted as reliable molecular markers in neurooncology (Jansen et al. 2010; Weller et al. 2013). Analysis of the TCGA data shows a possible prognostic significance of the proteases USP15 (Eichhorn et al. 2012) and YME1-like-1 (Bredel et al. 2009). These promising microarray-based results will need to be converted into standardized clinically applicable assays enabling the risk assessment for the individual glioma patient.

According to some authors, proteases may also be exploited for the visualization of the tumor tissue. Complete surgical resection of the tumor is an important factor influencing the prognosis of glioma patients and several methods such as microscopic surgery, intraoperative MRI, or 5-ALA fluorescence-guided resection are currently used to improve the identification and surgical removal of the tumor tissue (Black et al. 1997; Stummer et al. 2006). A recent work by Cutter et al. (2012) provides evidence that the differential expression of proteases such as cysteine cathepsins in the tumor tissue compared to normal brain may be utilized to differentiate tumor borders. The authors used fluorescently quenched activity-based probes that were constructed from suicide protease inhibitors. Proteolytic cleavage of such probes leads to the liberation of the quencher and the covalent attachment of the fluorochrome to the protease active site. Topical application of such probes rapidly visualized tumors in a preclinical glioma model as well as in the resected human glioma tissue (Cutter et al. 2012) suggesting its possible utility in guiding glioma resection.

Dysregulated proteolytic activity and often a direct role in glioma progression make proteases promising therapeutic targets. Several concepts may be envisioned for the therapeutic exploitation of glioma-associated proteases.

In addition to directly targeting the "prooncogenic" functions of gliomaassociated proteases, the enzymatic activity of certain proteases may be used for the selective activation of a prodrug in the tumor tissue (tumor-activated prodrugs) (Atkinson et al. 2008). This approach relies on the highly elevated expression of the target protease in the tumor and its ability to efficiently convert the prodrug into a highly cytotoxic compound. The serine protease prostate-specific antigen (PSA) and the MMPs were studied in this context in several tumor types (Atkinson et al. 2008), but to the best of our knowledge, this approach has not been tested in gliomas. Similarly, the expression of proteases restricted to or highly upregulated in gliomas may be utilized as a means of targeted delivery of conventional chemoor radiotherapy. GCP-II (PSMA, prostate-specific membrane antigen) is being tested as a therapeutic target in prostate cancer (Mullard 2013), but its expression in the vasculature of several tumors including gliomas make it a possible target in gliomas as well (Wernicke et al. 2011). Recently, the pronounced expression of uPA in gliomas was suggested for the selective targeting of the tumors by a recombinant uPA-directed oncolytic virus that markedly improved survival in a rodent glioma model (Hasegawa et al. 2010).

Downregulation of the target protease by RNA interference or the inhibition of the upstream signaling cascades driving protease expression are potential therapeutic approaches, the latter possibly being a contributing factor to the effects of therapies targeting receptor tyrosine kinases and the downstream signaling pathways (Lakka et al. 2000; Mao et al. 2012). Indeed, data from preclinical glioma models suggest that inhibition or genetic ablation of proteases or their respective critical activators in glioma cells leads to the induction of apoptosis (Gondi et al. 2009; Chetty et al. 2010), suppression of cell proliferation, invasiveness and inhibition of tumor-induced angiogenesis, as well as tumorigenicity in experimental animals (Rao 2003; Lakka et al. 2005; Badiga et al. 2011; Veeravalli et al. 2012; Kesanakurti et al. 2013).

Low-molecular-weight protease inhibitors have become an effective strategy in the treatment of cardiovascular and infectious diseases (reviewed in Turk 2006) and the hope is that they could also improve the outcomes in cancer patients.

Given the important role of MMPs in glioma invasiveness, MMP inhibitors were among the first protease inhibitors tested in glioblastomas. Four clinical trials testing the broad spectrum MMP inhibitor marimastat in combination with temozolomide or radiotherapy in patients with grade III and IV tumors were published. Overall, the therapeutic effects were small and the treatment was accompanied by musculoskeletal toxicity in a large proportion of patients (Groves et al. 2002, 2006; Larson et al. 2002; Levin et al. 2006). Possibly, more specific MMP inhibitors and/or optimized dosing and timing of administration may prove more efficacious in future studies, in particular considering the potential of MMP inhibitors to block the proinvasive effects of radiotherapy and anti-angiogenic treatments (Lucio-Eterovic et al. (2009) and Sect. 12.3.1).

More recently, proteasome inhibition was suggested as a potential therapeutic modality in gliomas. Proteasome is responsible for the proteolytic removal of regulatory proteins with growth inhibitory activity such as the CDK inhibitor p27 (Piva et al. 1999), the inhibitors of NFkB (IkB), and proteins p53, BID (Unterkircher et al. 2011), NOXA (Ohshima-Hosoyama et al. 2011), or activated caspases-8 and -3 (Kim et al. 2004) (see also Fig. 12.6). Proteasomal inhibition therefore induces the accumulation of these proteins; in addition, it enhances the expression of the apoptosis-inducing receptors such as Fas (Tani et al. 2001) or the TRAIL receptor DR5 (Hetschko et al. 2008) and triggers the endoplasmic reticulum stress (Kardosh et al. 2008). By these complex mechanisms proteasome inhibitors cause growth arrest and sensitization to proapoptotic stimuli as demonstrated in glioma cell lines (Kitagawa et al. 1999; Wagenknecht et al. 1999, 2000; Tani et al. 2001; Yin et al. 2005; Pedeboscq et al. 2008; Zanotto-Filho et al. 2012) and in patient-derived primary cells (Koschny et al. 2007). Proteasome inhibitors also enhanced the effectiveness of other chemotherapeutics (Ceruti et al. 2006), radiation (Ng et al. 2009), and TRAIL (La Ferla-Bruhl et al. 2007; Hetschko et al. 2008; Balyasnikova et al. 2011; Jane et al. 2011; Kahana et al. 2011; Seol 2011; Unterkircher et al. 2011) and had synergistic inhibitory effects on glioma stemlike cells in combination with the histonedeacetylase inhibitors (Asklund et al. 2012). In preclinical animal models, the antitumor activity was observed for lactacystin (Legnani et al. 2006; Wang et al. 2013a). However, studies using the new proteasome inhibitor salinosporamide A (Vlashi et al. 2010) or the most frequently utilized proteasome inhibitor approved for clinical application in other cancers bortezomib (Labussiere et al. 2008) failed at reducing the tumor growth in a xenotransplantation glioma model. Phase I clinical trials demonstrated safety of bortezomib in glioma patients (Kubicek et al. 2009; Phuphanich et al. 2010), but a phase II trial in patients with recurrent glioblastoma failed to show its efficacy in combination with vorinostat (Friday et al. 2012). Several other phase I and II studies of bortezomib in combination with other therapeutic modalities (Table 12.3) as well as testing of new proteasome inhibitors with improved in vivo efficacy (Roth et al. 2009) are underway (Vlachostergios et al. 2013). Another possibility to target the ubiquitin-proteosome system lies in the modulation of the deubiquinating enzymes (DUBs, reviewed in Hussain et al. (2009), Fraile et al. (2012)]. By cleaving the isopeptide bonds joining ubiquitin to other proteins, DUBs stabilize

Target	Agent	Phase and trial identifier	Remarks, reference
MMPs	Marimastat	II, III	Limited efficacy, musculoskeletal side effects (Groves et al. 2002, 2006; Larson et al. 2002; Levin et al. 2006)
Coagulation cascade	Low molecular weight heparin (LMWH)	II, NCT00028678, III, NCT00135876	Similar 12 month mortality rate in patients receiving a preventive dose of dalteparin compared to placebo (Perry et al. 2010), similar survival in patients using dalteparin compared to historical controls (Robins et al. 2008), trend for improved progression free survival and 1 year overall survival with concomitant chemoradiotherapy with LMWH (Zincircioglu et al. 2012)
Proteasome (presumably)	Nelfinavir	I, NCT01020292, NCT00915694, I/II NCT00694837	Mechanism probably involves proteasome inhibition (Pyrko et al. 2007).
Proteasome	Ritonavir/ lopinavir	II, NCT01095094	Minimal activity at the dose tested, did not prolong progression free survival at 6 months as a single agent in heavily pretreated patients (Ahluwalia et al. 2011)
Proteasome	Bortezomib	I, NCT00006773, NCT00994500, NCT00544284, NCT01435395	Ongoing
Proteasome	Bortezomib	II, NCT00108069, NCT00611325, NCT00990652, NCT00641706, NCT00998010	Ongoing
γ-Secretase	RO4929097	I//II, NCT01088763	Ongoing

Table 12.3 Clinical trials targeting proteases in gliomas

http://clinicaltrials.gov/

a number of proteins essential for the cell cycle regulation, chromatin remodeling, DNA damage repair, and signaling pathways including the membrane-bound receptors such as EGFR (Fraile et al. 2012; Liu et al. 2014). In the case of DUBs associated with the proteasome (i.e., UCHL5, USP14, and POH1), however, the inhibition leads to the block of proteasomal degradation of polyubiquitinated proteins. b-AP15, an inhibitor of the proteasome-associated DUBs, was recently demonstrated to have antitumor activity against a range of cancer cells with glioma cell lines of the NCI60 panel being particularly sensitive (D'Arcy et al. 2011). With few exceptions (see Table 12.1), the role of DUBs in glioma pathogenesis is nevertheless largely unknown and more research is needed before using DUB

inhibitors or approaches aiming at restoring the activities of tumor-suppressor DUBs (Fraile et al. 2012) in glioma therapy.

Some protease inhibitors were found to have novel, unexpected antitumor activities. The aspartate protease inhibitors widely used in the treatment of HIV infection such as nelfinavir and ritonavir were demonstrated to inhibit glioma growth. The mechanisms are currently not fully elucidated but presumably involve the induction of endoplasmic reticulum stress, interference with the activity of Hsp90, and reduction of MMP expression (Laurent et al. 2004; Liuzzi et al. 2004; Pyrko et al. 2007) (see Kast et al. (2013) for review). Clinical studies in glioma patients were rapidly initiated (Table 12.3) as these drugs have a favorable safety profile and have already been in clinical use.

Inhibitors of the γ -secretase (GSIs) seem to be another promising class of drugs (see Golde et al. (2013) for review). Originally designed for the treatment of Alzheimer's disease, GSIs are currently tested in several cancers including gliomas because of their inhibitory effect on the Notch signaling (Golde et al. 2013; Takebe et al. 2014). This pathway typically promotes the self-renewal and inhibits the differentiation of stem cells including glioma stem cells (Chen et al. 2010; Hu et al. 2011; Kristoffersen et al. 2013). Gliomas of the proneural subtype may be in particular sensitive to the inhibition of γ -secretase, as the Notch pathway seems to be typically activated in this subtype (Saito et al. 2014, #2290). In addition, the GSIs may also block the neurotrophin-induced glioma invasion (Wang et al. 2008a). In line with these results, GSIs inhibited glioma growth in preclinical models and enhanced the effects of temozolomide (Gilbert et al. 2010). Despite these promising results, there are several important areas that remain to be explored, such as possible off-target effects of GSIs on signal peptidase and the effects of GSI on angiogenesis and immune functions (Golde et al. 2013). For example, a recent report concluded that GSIs reduced the growth of xenotransplanted gliomas, but somewhat surprisingly enhanced the proliferation of endothelial cells in response to VEGF and increased the vascular density in the tumors (Zou et al. 2013). The vasculature was dysfunctional as the perfusion and oxygenation of the treated tumors was decreased similarly to observations in other cancers (see Liu et al. (2013) for review). In addition, γ -secretase was suggested to function as a tumor suppressor in squamous cell carcinoma (Li et al. 2007). Indeed, a prematurely halted clinical trial in patients with Alzheimer's disease (Doody et al. 2013) reported increased incidence of skin cancer. Inhibition of γ -secretase may have negative effect on the proliferation and self-renewal of normal stem cells in several organs (van Es et al. 2005; Hu et al. 2011). Despite a phase I trial with a γ -secretase inhibitor MK-0752 in pediatric patients with recurrent CNS malignancies demonstrated good tolerability (Fouladi et al. 2011), the obvious complexity of the effects of GSIs on the tumor microenvironment still precludes the straightforward claim that γ -secretase represents a suitable target for antiglioma treatment and requires further studies with careful evaluation of its therapeutic efficacy and safety.

Other proteases were also suggested as potential targets in glioma treatment mostly based on preclinical data. Inhibition of the sheddase ADAM10 was demonstrated to block glioma growth by interfering with the abovementioned Notch signaling pathway (Floyd et al. 2012). In addition, the inhibition of ADAM10 may improve the ability of the immune system to eradicate glioma stem cell (Wolpert et al. 2014) and also block glioma cell migration and adhesion (Table 12.1, see Moss et al. (2008) for general review). Targeting of the extracellularly localized cathepsin-B by cell impermeable inhibitors (Withana et al. 2012) or its elimination by RNAi were also proposed, although at least in gliomas, the effects of downregulating cathepsin-B were most pronounced when combined with the targeting of other extracellular proteolytic systems (Gondi and Rao 2013). The proteolytic activation of the immunosuppressive TGF- β in gliomas may represent another example of a potential functional target of protease inhibitors (Huber et al. 1992; Leitlein et al. 2001).

Given the known high risk of thromboembolic events in patients with high grade gliomas and preclinical studies suggesting possible anticancer effects of low-molecular-weight heparin and direct thrombin inhibitors, inhibition of the blood coagulation proteases may seem beneficial in glioma patients (Ornstein et al. 2002; Hua et al. 2005a, b). The results from the so far performed clinical trials with low-molecular-weight heparins are however ambiguous (Perry et al. 2010), although some hints of potential benefit can be found (Robins et al. 2008; Zincircioglu et al. 2012). Given the observed increased risk of bleeding associated with their use (Perry et al. 2010) and the limited data on their clinical efficacy, the role of anticoagulation as an adjuvant antitumor therapy remains to be established (Perry 2010).

Despite the wealth of encouraging data in the preclinical studies, protease inhibitors were so far largely ineffective in the majority of the clinical trials in cancer patients (Coussens et al. 2002), including patients with gliomas (Groves et al. 2002, 2006; Larson et al. 2002; Levin et al. 2006; Ahluwalia et al. 2011). There are a number of causes that may have contributed to these failures:

- 1. Malignancies frequently "hijack" physiologically occurring mechanisms including the deployment of proteases; many "on-target" side effects should therefore be anticipated due to the interference with their physiological functions (see Sect. 12.1). This risk is illustrated by the musculoskeletal side effects observed in the clinical studies using MMP inhibitors (Coussens et al. 2002). In addition, several proteases act as tumor suppressors or produce anti-angiogenic mediators (see Sect. 12.4.3, Bello et al. (2001), Rege et al. (2005), Lopez-Otin and Matrisian (2007), Cork et al. (2012)] and their inhibition may thus facilitate tumorigenesis.
- 2. The complexity, functional overlap, and redundancy of the proteolytic cascades in gliomas suggest that targeting of several different types of proteases may be necessary to achieve the desired biological effects. This not only complicates the design of low molecular weight inhibitors capable of targeting several biochemically distinct protease classes but also brings about an increased risk of "on-target" side effects.
- 3. Incomplete understanding of the role of proteases in tumor progression and spatiotemporal and interindividual differences in the dependence of the tumors

on the protease-mediated events. The variability of protease expression (Fig. 12.1, Jaworski et al. 2010) and their differing functional role at various stages of tumor progression requires careful characterization and selection of appropriate patients for clinical trials as well as for subsequent use in clinical practice.

- 4. Limitations of current preclinical glioma models in determining the clinical efficacy of anti-protease therapies. The in vitro systems and long term propagated glioma cell lines grown in serum-containing media have numerous limitations (Schulte et al. 2011) and may produce misleading results. For example, an adenoviral-mediated overexpression of PAI-1 in a glioma cell line reduced their invasiveness through Matrigel, but not in brain tissue (Hjortland et al. 2003). Similarly, several studies with the proteasome inhibitor bortezomib in glioma cell lines indicated its growth inhibitory effects, which was not recapitulated in more complex in vivo models or so far completed clinical studies (Friday et al. 2012; Vlachostergios et al. 2013). Reliable preclinical models recapitulating the heterogeneity of tumor cells (Snuderl et al. 2011), enabling the assessment of the effects of therapeutic interventions on the stromal cells (Jones and Holland 2012), as well as the complex host-tumor pro-tumorigenic and anti-tumorigenic interactions are needed.
- 5. Absence of appropriate biomarkers of achieving target protease inhibition in the clinical setting. Identification of the biologically active dose is necessary before performing large phase III trials. Furthermore, the design of clinical trials represents another challenge as the effect of agents that do not directly kill cancer cells cannot be measured by reduction of tumor size (Coussens et al. 2002).
- 6. Last but not least: some of the compounds targeting proteases were rushed into clinical trials at an unprecedented pace and in several cases in suboptimal settings. Enormous need to improve the outcome of otherwise untreatable diseases, but also patent issues and competition may have contributed to such decisions in the past, but these factors are unfortunately likely to play a role in the future trials as well (Coussens et al. 2002).

Conclusion

Proteases are important regulators of the biological functions of proteins under both physiological and pathological conditions. Their dysregulation in gliomas is a consequence of complex changes in the glioma microenvironment and involves transformed glioma cells as well as various cell types present in the tumor stroma. Despite some common patterns, glioblastomas are, similarly to other parameters, heterogeneous also in terms of protease expression and activity. Proteases participate on almost every aspect of gliomagenesis acting both as regulators and executors and may therefore represent promising therapeutic targets. However, the role of individual proteases at various stages of the disease progression is usually complex, highly context dependent, and redundant. This might have contributed to the failures of the initial attempts on therapeutic targeting of proteases in gliomas as well as in other cancers. Designing effective and safe anti-glioma strategies exploiting proteases will therefore require a more in-depth understanding of their physiological and pathophysiological roles. Equally important will be the identification of critical protease-mediated processes in individual glioma subtypes and careful selection of subgroups of glioma patients most likely to benefit from therapies interfering with the functions of proteases.

Acknowledgment This work was supported by grants IGA 12237-5/2011, PRVOUK-P27/LF1/1, UNCE 204013 and by the project "BIOCEV—Biotechnology and Biomedicine Centre of the Academy of Sciences and Charles University" (CZ.1.05/1.1.00/02.0109), from the European Regional Development Fund.

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