The plasminogen activation system in tumor growth, invasion, and metastasis

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Abstract. Generation of the serine proteinase plasmin cell-directed tissue remodeling. Moreover, the system from the extracellular zymogen plasminogen can be also supports cell migration and invasion by plasmin-incatalyzed by either of two other serine proteinases, the dependent mechanisms, including multiple interactions urokinase- and tissue-type plasminogen activators (uPA between uPA, uPAR, PAI-1, extracellular matrix and tPA). The plasminogen activation system also in- proteins, integrins, endocytosis receptors, and growth cludes the serpins PAI-1 and PAI-2, and the uPA receptor factors. These interactions seem to allow temporal and (uPAR). Many findings, gathered over several decades, spatial reorganizations of the system during cell migrastrongly suggest an important and causal role for uPA- tion and a selective degradation of extracellular matrix catalyzed plasmin generation in cancer cell invasion proteins during invasion. The increased knowledge about through the extracellular matrix. Recent evidence sug- the plasminogen activation system may allow utilization gests that the uPA system is also involved in cancer of its components as targets for anti-invasive therapy.

Key words. Serine proteinases; serpins; integrins; cell migration; anti-invasive therapy.

Introduction

For several decades, it has been assumed that plasminogen activation plays an important role in tumor invasion and metastasis. The basic idea was that plasminogen activators released from cancer cells catalyze the proteolytic conversion of the inactive zymogen plasminogen to the active proteinase plasmin, which in turn catalyzes degradation of proteins in basement membranes and extracellular matrix (ECM) and thus facilitates cancer cell invasion into the surrounding tissue [for reviews see refs $1-3$]. There are two types of plasminogen activators, the urokinase-type (uPA) and the tissue-type (tPA). uPA is generally agreed to be the enzyme of most relevance to tumor biology, while the primary role of tPA is generation of plasmin for fibrinolysis in blood vessels. There are two main plasminogen activator inhibitors, PAI-1 and PAI-2. The uPA receptor (uPAR) is a cell membrane-anchored uPAbinding protein, concentrating plasminogen activation activity at the cell surfaces [for a review see ref. 2].

Based on evidence from experimental invasion and metastasis models and on expression patterns for components of the uPA system in tumors and normal tissues, it now seems beyond reasonable doubt that this enzyme system plays a central role in tumor biology. The system appears to be involved not only in cancer cell migration and invasion, but also in other processes in tumors which may collectively be called cancer celldirected tissue remodeling. Examples of such processes are angiogenesis [for reviews see refs 4, 5] and desmoplasia, i.e., stimulation of fibroblast proliferation and ECM protein synthesis [for reviews see refs 6, 7]. Such processes, although involving migration and invasion by noncancer cells, may strongly influence tumor growth, invasion, and metastasis. It has also been realized that the system has plasmin-independent functions, related to signal transduction and interactions of PAI-1 and uPAR with integrins and the ECM protein vitronectin and of plasminogen activator-inhibitor complexes with endocytosis receptors of the low-density lipoprotein receptor (LDLR) family. This evidence was * Corresponding author. to a large extent obtained with noncancer cells, but no

qualitative differences exist between cancer cells and normal cells such as endothelial cells with respect to the basic processes of migration and invasion [for reviews see refs 1, 3].

In this review, we will describe the recent rapid increase in knowledge about the biochemistry, molecular biology, and cell biology of plasminogen activation in relation to tumor growth, invasion, and metastasis. Rather than being comprehensive, our review will cover specific areas undergoing rapid development. For other and earlier developments in the field, the reader is referred to other reviews $[1-3, 8-16]$.

Biochemical properties of plasmin, uPA, and tPA

The serine proteinase plasmin (M_r) approximately 90,000) consists of two disulfide bond-linked polypeptide chains. The N-terminal A chain contains five socalled kringle domains. The C-terminal B chain contains a typical serine proteinase domain, which is responsible for catalytic activity (fig. 1). Plasmin catalyzes the hydrolysis of peptide bonds on the C-terminal side of Lys and Arg residues. Plasminogen is the onechain zymogen counterpart of plasmin, with an activity 104 - to 106 -fold lower than that of plasmin. Conversion of plasminogen to plasmin, comprising proteolytic cleavage of a single peptide bond (Arg561-Val562 in human plasminogen), can be catalyzed by either uPA or tPA. The concentration of plasminogen in blood plasma is approximately $2 \mu M$, but there is also a large pool of extravascular plasminogen [for reviews see refs 1, 2, 17].

Angiostatin, reportedly an inhibitor of angiogenesis (see below), is a plasmin fragment consisting of kringles $1-3$ or kringles 1–4 [18]. It can be generated from plasminogen and plasmin in vitro by pancreatic elastase, a variety of metalloproteinases, and by plasmin autoproteolysis [18–24]. Angiostatin has been reported to contain at least one free sulfhydryl group [22].

The serine proteinase uPA $(M_r$ approximately 55,000) consists of two disulfide bridge-linked polypeptide chains, a C-terminal B chain, containing a serine proteinase domain, and an N-terminal A chain (amino acids 159–411 and 1–158, respectively, in human uPA). The A chain contains a growth factor domain (amino acids $1-49$), a kringle domain (amino acids $50-131$), and an interdomain linker region (amino acids 132– 158) (fig. 1). The one-chain zymogen form of uPA, pro-uPA, has an activity about 250-fold less than that of two-chain uPA [25]. Conversion of pro-uPA to twochain uPA occurs by proteolytic cleavage of a single peptide bond (Lys158-Ile159 in human uPA). The con-

Figure 1. Schematic presentation of uPA and some of its pericellular interacting partners. uPA consists of a serine proteinase domain (SPD), a linker, a kringle (K), and a uPAR-binding epidermal growth factor-like domain (E). uPAR has three domains and is anchored to the membrane by a GPI anchor. Domains 1 and 3 make contact with uPA. Plasmin has a serine proteinase domain (SPD) and five kringles (K) and binds to pericellular proteins with C-terminal lysines. The RCL of PAI-1 is able to bind to the active site of uPA. Vitronectin, in the substratum, has an N-terminal PAI-1- and uPAR-binding somatomedin B domain (SomB) next to an integrin-binding RGD sequence. The α and β integrin subunits have transmembrane helices (TM) and are anchored to the cytoskeleton. Integrins can interact with uPAR. As a representative of the uPA-PAI-1 complex-binding endocytosis receptors of the LDLR family, VLDLR is indicated with a transmembrane domain (TM), an O-linked sugar domain, two epidermal growth factor-like domains (E) which are separated from a third one by a YWTD spacer region, and a ligand-binding cluster of eight complement-type repeats (C).

version can be catalyzed by plasmin or several other proteinases [for reviews see refs 1, 13]. Proteolytic cleavage of uPA in the linker region gives rise to the aminoterminal fragment (ATF), i.e., the growth factor domain and the kringle, and low molecular-weight uPA forms (LMW-uPA), i.e., the serine proteinase domain and part of the linker. uPA has a restricted substrate specificity. Besides the conversion of plasminogen to plasmin, uPA catalyzes conversion of the inactive onechain proforms of hepatocyte growth factor/scatter factor (HGF/SF) and macrophage-stimulating protein (MSP) to their active two-chain forms. HGF/SF and MSP have sequence similarity to plasmin, but are devoid of proteolytic activity and act by binding to receptor tyrosine kinases [for a review see ref. 26]. uPA also catalyzes intradomain cleavage of uPAR (see below).

The serine proteinase tPA $(M_r$ approximately 70,000) is also synthesized and released from cells in a single-chain form, which can be proteolytically converted to a twochain form by cleavage of a single polypeptide bond (Arg275-Ile276 in human tPA). The two chains are held together by a disulfide bond. The N-terminal A chain contains, starting from the N terminus, a fibronectin type II domain, a growth factor domain, and two kringle domains, while the C-terminal B chain contains the serine proteinase domain. The plasminogen activation activity of single-chain tPA is 10- to 50-fold lower than that of the two-chain form. The activity of both single-chain and two-chain tPA is stimulated considerably by fibrin, in agreement with the role of tPA as a fibrinolytic enzyme [for reviews see refs 9, 12, 17].

Biochemical properties of uPAR

The amino acid sequence of uPAR [27–31] exhibits three repeats, each of approximately 90 amino acids, suggesting the existence of three homologous, independently folded domains (domains 1, 2, and 3, as numbered from the N terminus) (fig. 1). Accordingly, stable receptor fragments with internal disulfide bridges can be produced by limited proteolysis [32–35]. Based on the similarity of the disulfide pattern of domain 1 to that of snake venom α neurotoxins [33, 34], a model for the unknown three-dimensional structure of the uPAR domains was proposed [36]. uPAR is bound to cell membranes by a glycosyl phosphatidyl inositol (GPI) anchor [37]. Anchorless, soluble uPAR variants have also been identified in conditioned medium from various cell lines [38] and in body fluids from cancer patients [39–42] and may arise by differential splicing [28, 30, 43], by proteolysis, or by phospholipase C cleavage of the GPI anchor.

Pro-uPA and active uPA bind to uPAR with the same affinity, with a K_d in the subnanomolar range [44].

uPAR binds the growth factor domain of uPA [45], the uPAR-binding residues being localized at one side of a seven residue-long Ω loop [46–49]. uPA binds to a site composed of amino acids from both domain 1 and domain 3 of uPAR [32, 35, 48, 50–52] (fig. 1). Based on site-directed mutagenesis, two subregions within domain 1 of human uPAR, spanning residues 2–10 and 47–53, seemed critical for uPA binding [53]. By chemical modification and photoaffinity labeling of human uPA and human uPAR, Arg53, Tyr57, and Leu66 in uPAR domain 1, and His251 in uPAR domain 3 appeared to come in close contact with the above-mentioned Ω loop in uPA [46, 52]. In vitro, uPA is able to cleave the Arg83-Ala84 and Arg89-Ser90 bonds between domains 1 and 2 of human uPAR. The cleavage abolishes uPA binding [54, 55]. N-terminally truncated variants of uPAR, consisting of domains 2 and 3, have also been demonstrated in vivo [42, 56].

uPAR also binds vitronectin, with a K_d in the subnanomolar range. The binding is stimulated by pro-PA, uPA, ATF, and the uPA-PAI-1 complex, but is inhibited by PAI-1 [57–60]. Interdomain proteolytic cleavage of uPAR prevented its binding to vitronectin [61].

uPAR binds β 2 integrins in a purified system [62] and may also be able to associate with β 1 and β 3 integrins (see below).

Serpin inhibitors in the plasminogen activation system

PAI-1 and PAI-2 belong to the serpin (serine proteinase) inhibitor) family. Of decisive importance for the inhibitory mechanism of serpins is the surface-exposed, approximately 20 amino-acid-long reactive center loop (RCL) (fig. 2). The reactive center peptide bond (the P_1 - P_1' bond) in the RCL interacts with the active site of the proteinase, resulting in a stable complex of 1:1 stoichiometry [for reviews see refs 63, 64]. The three-dimensional structure of serine proteinase-serpin complexes has not been determined. Nevertheless, complex formation seems to comprise $P_1 - P'_1$ bond cleavage and coupling of the P_1 residue to the active-site serine of the proteinase by an ester bond [65], the N-terminal part of the RCL becoming inserted as strand 4 in β -sheet A, translocation of the proteinase across the plane of β sheet A towards the other pole of the molecule [66, 67], and conformational changes occurring in the so-called flexible-joints region, i.e., the region around α -helices D and E [68, 69] (fig. 2).

PAI-1 (M_r approximately 50,000) reacts quickly with both uPA and tPA [for a review see ref. 13]. PAI-1 binds to vitronectin with high affinity, while plasminogen activator-complexed PAI-1 does not [for a review see ref. 70]. Vitronectin-binding residues were localized to α -helix E, β -stand 1A and α -helix F of PAI-1,

Figure 2. A model of the three-dimensional structure of PAI-1. The RCL is shown in orange. The P_1 and the P'_1 residues are indicated by orange spheres. The large central β -sheet A is shown in blue, except β -strand 1A. The regions implicated in binding to vitronectin are shown in green $(\alpha$ -helix F) or red $(\alpha$ -helix E, β -strand 1A) [71–73]. Activity-neutralizing antibodies bind to α -helix F and the flanking sequences [189]. The black spheres indicate basic residues, which were implicated in binding of anthranilic acid derivatives to PAI-1 [191]. The figure is a Molscript display of the model of Aertgeerts et al. [197].

overlapping with the flexible-joints region $[71-73]$ (fig. 2). PAI-2 (M_r approximately 50,000) is also able to inhibit both uPA and tPA, although it reacts more slowly than PAI-1 with both proteinases [for reviews see refs 8, 12, 16].

The serpin α 2-antiplasmin is the primary inhibitor of plasmin and ensures a short half-life of plasmin in blood and tissues [for a review see ref. 17].

Biochemical properties of vitronectin

Vitronectin is a M_r 78,000 glycoprotein, present in blood plasma and extravascularly in many forms of ECM [for reviews see refs 74, 75]. The N-terminal somatomedin B domain (amino acids 1–44) of vitronectin binds both PAI-1 [for a review see ref. 70] and uPAR [58] (fig. 1), which, accordingly, compete for binding [58, 59]. Amino acids 45–47 constitute an RGD sequence (fig. 1), binding the integrins $\alpha V\beta$ 1, $\alpha V\beta$ 3, $\alpha V\beta$ 5, α IIb β 3, and α 8 β 1 [74, 75]. PAI-1 and integrins compete for binding to vitronectin [76, 77].

Pericellular localization of components of the uPA system in cell cultures

Binding to uPAR causes accumulation of pro-uPA and uPA on cell surfaces. Immunocytochemical studies with cell cultures showed that uPAR and its complexes with pro-uPA and uPA often accumulate at specific sites at cell-substratum contact areas. In several cell types, mostly of fibroblastic origin, the accumulation sites had the characteristics of focal contacts, where integrins cluster and interact with actin filaments [for a review see ref. 13]. uPAR-integrin and/or uPAR-vitronectin interactions seemed to contribute to the accumulation at these sites. Thus, uPAR coimmunoprecipitated with β 1 integrins from human 293 embryonic kidney cells [62]. In human HT-1080 fibrosarcoma cells, uPAR-bound uPA was localized to focal contacts in cultures with a vitronectin substratum, but not with a fibronectin substratum [78]. In the same cells, uPAR consistently colocalized with the β 1 integrin subunit, but displayed varying colocalization with β 3, α 3, α 5, α 6, and α V integrin subunits, depending on whether the cells were cultured on vitronectin, fibronectin, or laminin substrata [79]. Given the affinity of uPAR to vitronectin, but not to other ECM proteins, and the differential binding specificity of different combinations of integrin subunits, this observation suggests very specific uPARintegrin interactions, which are regulated by binding of uPAR to vitronectin and by ligation of the integrins. In addition, uPAR and β 2 integrins colocalized on human neutrophils and monocytes [80–82]. With reference to the biochemical evidence for uPAR- β 2 integrin binding (see above), the colocalization may be caused by direct binding of the extracellular domains of the two proteins.

During cell migration, uPAR usually becomes concentrated at the leading cell edge [for a review see ref. 13]. Evidence obtained with monoclonal antibodies with differential affinity to free and uPA-ligated uPAR suggested that the ligation contributes to the accumulation of uPAR at specific sites [83]. Antibody-induced polarization of human neutrophils led to reversible dissociation of uPAR and $\alpha M\beta$ 2, uPAR becoming accumulated in lamellipodia [84]. Thus, the pericellular localization of uPAR seems to be dynamic in nature.

Many GPI-linked proteins, integrins, and signal transmitters are accumulated in so-called rafts, which are specific membrane subdomains with a high content of cholesterol and glycosphingolipids, resistant to extraction with Triton $X-100$ at 4 °C, and often forming membrane invaginations, so-called caveolae, together with membrane-embedded proteins of the caveolin family [for reviews see refs 85, 86]. Accordingly, uPAR is found in caveolae in several cell types [62, 87–89], together with β 1 integrins [62].

In cell cultures, PAI-1 is bound to vitronectin at the substratum [for a review see ref. 13], while plasminogen seems to be localized at the ventral cell surface [10].

Pericellular plasminogen activation and plasmin activity in cell cultures

Activation of pro-uPA bound to uPAR at cell surfaces proceeds much faster than activation of fluid-phase pro-uPA. Active uPA bound to uPAR at the cell surface catalyzes plasminogen activation much more efficiently than fluid-phase uPA. The enhancement of pro-uPA activation and of uPA-catalyzed plasminogen activation seems to be due to cell surface coaccumulation with plasminogen. Plasminogen presumably binds to pericellular proteins with C-terminal lysines [for reviews see refs 13, 90].

The most obvious consequence of pericellular plasmin generation is degradation of fibrin and other ECM proteins [for a review see ref. 13]. It should be noted, however, that native collagens are resistant to plasmin [for reviews see refs 1, 2]. The pericellular localization of PAI-1 on vitronectin may selectively protect vitronectin against uPA-mediated degradation [78]. Plasmin also catalyzes activation of latent transforming growth factor- β and release of basic fibroblast growth factor from its ECM-binding sites [for a review see ref. 2]. In addition, plasmin may contribute to activation of zymogens of matrix metalloproteinases (MMPs) [for a review see ref. 91]. Experiments with mice with disruptions of the genes for plasminogen, uPA, and tPA (*plasminogen*−/−, *uPA*^{−/−}, and *tPA*^{−/−} mice, respectively) confirmed the physiological importance of the plasminogen activation system in activation of MMP-3, MMP-9, and MMP-13 [92–94], but suggested additional activation mechanisms for MMP-2 [93, 94]. Coaccumulation with uPA on cell surfaces accelerates activation of MMP-2 and MMP-9 [95].

Pericellular plasminogen activation in cell cultures can be followed by plasmin autoproteolysis and generation of angiostatin, through the concomitant action of a reductase catalyzing formation of one or more free sulfhydryl groups [20, 22, 96].

Activation of intracellular signal transduction cascades through uPAR

Much attention has been focused on the possibility that uPA-uPAR binding activates intracellular signal transduction cascades without plasmin generation and proteolytic activation of growth factor precursors. This is most simply demonstrated by showing activation of signaling cascades by proteolytically inactive uPA variants, also excluding effects of minor contaminations of proteolytically active uPA. The possibility of uPAR becoming occupied by the added inactive variant, leading to an increase in fluid-phase uPA activity due to endogenous uPA, should also be excluded [11]. The most easily interpretable results will therefore be obtained with cells with low endogenous uPA production, which are also expected to have a low background in uPA-stimulated signal transduction pathways.

Despite the technical difficulties, evidence is increasing for uPA-initiated signaling through uPAR. In a variety of cell lines, uPAR coimmunoprecipitated and/or colocalized with tyrosine kinases, including hck, fyn, lck, lyn, fgr, Jak1, and Tyk2 [81, 89, 97–99]. In some cases, the colocalization depended on uPA ligation of uPAR [89, 97]. Moreover, varying between cell lines, uPA ligation of uPAR stimulated tyrosine phosphorylation of hck, focal adhesion kinase, paxillin, p130CAS, mitogen-activated protein kinase (MAPK), and several unidentified proteins, and activated the kinase activity of hck and MAPK and the DNA-binding ability of Stat1 [97–102]. Signaling via G protein-regulated enzymes, i.e., protein kinase $C\varepsilon$ [103], and G protein-regulated second messengers, i.e., cAMP [104] and diacylglycerol [105–107], have also been implicated in uPAR-activated signaling cascades. The relative order of the different molecules in uPAR-stimulated signaling cascades and the possibility of cell type specificities in the activated pathways have not yet been clarified.

Initiation of intracellular signals from the GPI-anchored uPAR would be expected to require extracellular interaction with membrane-spanning proteins but until now, putative signal transducers remain unidentified. It is interesting, however, that ATF-induced signaling in THP-1 cells was mimicked by addition of soluble uPAR, provided that it was proteolytically cleaved between domains 1 and 2 [97], by uPAR fragments harboring residues 88–92 of the domain 1-domain 2 linker, and by peptides covering this region [108]. On this basis, uPA was proposed to activate signaling cascades by cleaving the interdomain linker [108]. The apparent discrepancy between this hypothesis and the fact that signaling can be initiated with proteolytically inactive uPA variants was resolved by suggesting that uPA can also activate uPAR by inducing a conformational change in uPAR, exposing proteolytic cleavage sites to endogenous proteinases [108].

Pericellular reaction of uPA with inhibitors and endocytosis of uPA-inhibitor complexes

uPAR-bound uPA reacts with PAI-1 at approximately the same rate as fluid-phase uPA [109, 110]. The uPARbound uPA-PAI-1 complex is endocytosed and degraded much faster than PAI-1 and uPAR-bound pro-uPA and uPA. The endocytosis occurs by binding of the complex to clathrin-coated pit-localized endocytosis receptors of the LDLR family, either α_2MR/LRP , gp330/megalin, or VLDLR [for reviews see refs 13, 111–113]. uPAR is, as a consequence of its binding to the uPA moiety of the complex, coendocytosed [114], but later recirculated to the cell surface [115]. Ligand binding by receptors of the LDLR family is critically dependent on clusters of complement-type repeats. The receptors also contain epidermal growth factor precursor homology domains (fig. 1). Each receptor binds several structurally unrelated ligands, including lipoproteins and proteinase-inhibitor complexes [for reviews see refs 112, 113]. The receptor-associated protein (RAP) functions as a chaperone for folding of the endocytosis receptors in endoplasmatic reticulum [for a review see ref. 116]. RAP is an invaluable tool for studying ligand-endocytosis receptor binding, since it inhibits the binding of all known ligands to the recep-

tors [for a review see ref. 112].

The plasminogen activation system in adhesion in cell cultures

The classical role of plasminogen activation is one of counteracting cell-substratum and cell-cell adhesion, as pericellular plasmin generation leads to degradation of adhesion receptors and their ECM ligands [for reviews see refs 1, 2].

Under some conditions, however, binding of uPA to uPAR promotes cell-substratum adhesion. Thus, integrin-independent adhesion of several human cell lines to vitronectin was stimulated by binding of uPA or uPA fragments to uPAR [60, 62, 117–123]. PAI-1 inhibited uPAR-dependent adhesion to vitronectin [76, 122]. These findings are consistent with the biochemical evidence for uPA-stimulated uPAR-vitronectin binding (see above) and show that uPAR can act as an adhesion receptor. Conceivably, initiation of signaling cascades by uPA-uPAR binding may also contribute to regulation of cell adhesion.

 β 1-integrin-dependent adhesion of 293 cells to fibronectin was inhibited by transfection with uPAR cDNA or by addition of soluble uPAR [62]. Anti-uPAR antibodies and uPAR antisense oligonucleotides reduced adhesion of monocytes to ligands for $\alpha M\beta 2$, while activation or ligation of $\alpha M\beta$ 2 promoted uPARmediated adhesion of monocytes to vitronectin [82, 124]. Addition of soluble uPAR restored adhesion of uPAR-depleted human HL-60 monocytic cells to endothelial cells, the adhesion being mediated by binding of β 2 integrins ($\alpha M\beta$ 2 and $\alpha L\beta$ 2) on the HL-60 cells to intercellular adhesion molecule-1 (ICAM-1) on the endothelial cells [125]. Interestingly, binding of uPA to uPAR counteracted $\alpha M\beta$ 2-dependent adhesion [82, 124, 125]. Together with the findings concerning uPARintegrin colocalizations (see above), these observations show that uPAR and uPA may also affect cell adhesion by regulating the functions of integrins, in an integrin-, ECM-, and cell type-specific manner, probably depending on direct extracellular uPAR-integrin contacts.

The plasminogen activation system in cell migration in cell cultures

Cell migration, defined as locomotion of a cell over an ECM substratum, involves extension and binding of integrins and other adhesion receptors to their ECM ligands at the leading cell edge. The cell-ECM adhesions at the leading edge provide guidance and traction for pulling the cell forward, mechanical force being generated by contraction of the actin cytoskeleton. Dissociation of integrin/ligand complexes allows retraction of the trailing edge [for a review see ref. 126]. Cell migration may also involve transport of membrane proteins from the trailing to the leading edge through a polarized endocytic cycle [for a review see ref. 127].

There are many reports of uPA stimulating cell migration by catalyzing plasmin generation [for a review see ref. 13], in good agreement with the expectation that plasmin-catalyzed degradation of ECM proteins and adhesion receptors helps release the trailing cell edge. In endothelial cells, generation of the plasmin fragment angiostatin by plasmin autoproteolysis could provide a negative feedback on plasmin-dependent cell migration, as an antimigratory effect, specific for endothelial cells, was ascribed to angiostatin [128, 129]. Limited proteolysis of uPAR, followed by activation of signaling cascades, is another conceivable proteolytic mechanism allowing uPA to stimulate cell migration. Thus, soluble uPAR with a proteolytic cleavage between domains 1 and 2 mimicked uPA in stimulating chemotaxis of THP-1 cells in parallel with tyrosine kinase hck activation [108].

There is also evidence for nonproteolytic stimulatory effects of uPA-uPAR binding on cell migration. Thus, enzymatically inactive, but uPAR-binding uPA variants stimulated migration of a variety of cell types [62, 97, 101, 103, 105, 106, 117, 118, 130–137]. These promigratory effects of uPA may depend on enhancement of adhesion of the leading edge by stimulation of uPARvitronectin binding. Accordingly, transfection of 293 cells with uPAR cDNA conferred on them uPAR-dependent migration towards vitronectin [62]. uPA may also act by activating intracellular signal transduction cascades at the leading edge. Thus, pro-uPA or ATF stimulation of migration of MCF-7 cells was inhibited by a synthetic inhibitor of MAPK [101]. In addition, nonproteolytic uPA and uPAR effects on cell migration may depend on regulation of integrin-binding activity at both the leading and the trailing edge. Thus, transfection of 293 cells with uPAR cDNA inhibited their integrin-dependent migration towards fibronectin, in parallel with uPAR and β 1 integrin colocalization [62].

PAI-1 inhibited integrin-dependent migration of rabbit vascular smooth muscle cells and of two human epithelial cell lines [76, 77], stimulated integrin-dependent migration of a melanoma cell line [122], inhibited migration of bovine aortic endothelial cells, and stimulated migration of bovine aortic smooth muscle cells [138]. Both inhibitory and stimulatory effects may be related to PAI-1 inhibition of integrin binding to vitronectin (see above), the net effect of PAI-1 depending on the relative importance of integrin-vitronectin binding at the leading and the trailing cell edges. In this scenario, uPA may regulate cell migration by complexing PAI-1, thereby removing it from vitronectin and relieving integrin-vitronectin binding from PAI-1 inhibition [76]. PAI-1 is also expected to inhibit stimulation of cell migration by uPA-catalyzed plasmin generation (see above).

Mutually conflicting results were reported concerning the possible role in cell migration of endocytosis of plasminogen activator-inhibitor complexes by receptors of the LDLR family. Plasmin-dependent migration of human umbilical vein smooth muscle cells was inhibited by RAP [136, 139], in agreement with the expectation that maintenance of a high cell surface plasminogen activation activity in the presence of PAI-1 must require constant endocytosis of uPAR-bound uPA-PAI-1 complexes and recirculation of uPAR to the cell surface. Conceivably, endocytosis could also be necessary for uPA stimulation of migration by nonproteolytic mechanisms, by participating in a polarized endocytic cycle [127], thereby removing uPAR-mediated adhesion at the trailing edge and allowing uPAR to enhance new rounds of adhesion at the leading edge. On the other hand, migration of murine embryonic fibroblasts on vitronectin was accelerated by genetic deficiency of α_2MR/LRP , in parallel with increased cell surface plasminogen activation activity but, paradoxically, was not affected by RAP [140]. However, since the endocytosis receptors have many ligands, effects of RAP and endocytosis receptor deficiency may be caused by inhibition of the binding of ligands other than plasminogen activator-inhibitor complexes.

It seems possible to arrive at a model unifying the many observations by assuming that proteolytic and nonproteolytic mechanisms of uPA action on cell migration are operating simultaneously in individual migrating cells. If pro-uPA is converted to active uPA at the ventral surface of the cells, nonproteolytic mechanisms could dominate at the leading edge, and proteolytic mechanisms at the trailing edge. The relative importance of the proteolytic and the nonproteolytic elements and the net effect of (pro-)uPA and PAI-1 would be expected to depend on the level of expression by the migrating cells of uPAR, endocytosis receptors, and integrins, of the composition of the ECM, of the pericellular localization of (pro-)uPA and PAI-1, of mechanisms for pro-uPA activation, and of the stimuli that induce cell motility.

The plasminogen activation system in cell invasion in cell culture model systems

When progressing from migration to invasion, an additional complexity is added, as invasion comprises not only cell locomotion, but also the active penetration of cells into ECM. A variety of cell culture invasion assays are available, including assays with invasion into isolated human amniotic membrane, into fibrin and collagen gels, and into other types of reconstituted ECM, so-called Matrigel. Experiments with such assays have shown that plasmin generation, as catalyzed by uPARbound uPA on the surface of the invading cells, is a rate-limiting factor for invasion by many cell types [for a review see ref. 13].

PAI-2 was consistently found to inhibit invasion [for a review see ref. 13]. The findings with PAI-1 were more variable. PAI-1 inhibited uPA- and uPAR-dependent invasiveness of human A549 and Calu-1 lung carcinoma cells [141], while coexpression of uPA, uPAR, and PAI-1 correlated with optimal invasiveness of human lung cancer cells [142], and transfection of human PC-3 prostate carcinoma cells with PAI-1 cDNA did not change their invasiveness [143]. The variability of the observed effects of PAI-1 may be due to an inhibitory effect on invasion of excessive plasminogen activation. Although high levels of PAI-1 may protect ECM against plasminogen activation-mediated proteolysis so that invasion becomes inhibited, low levels of PAI-1 may be needed to protect ECM proteins for traction. The divergent possibilities for the role of PAI-1 in cell migration (see above) may also contribute to the variable observations concerning the role of PAI-1 in invasion. All in all, the effect of PAI-1 on invasion is expected to depend on expression by the invading cell of the other components of the uPA system, of endocytosis receptors, of integrins, and on the composition of the ECM.

The endocytosis receptors may or may not play a role in cell invasion. Thus, RAP was reported to inhibit invasion of human umbilical vein smooth muscle cells into Matrigel [139], but to be without effect on invasion of the same cells into a collagen gel [136].

The plasminogen activation system in some physiological and nonneoplastic pathophysiological processes—evidence from mice with specific gene deficiencies

Mice with targeted disruption of the genes for uPA and tPA [144], PAI-1 [145], uPAR [146], plasminogen [147], and vitronectin [148] develop to term, grow to adulthood, and are fertile. A variety of studies with these mice resulted in findings of high significance for understanding the basic functions of the system, and therefore also of its role in cancer.

plasminogen−/− mice and *uPA*−/−-*tPA*−/− mice developed disseminated intra- and extravascular fibrin deposits, resulting in widespread organ damage, a low body weight, and a short life span [147]. These defects were corrected by concomitant *fibrinogen* gene deficiency [149]. Therefore, fibrinolysis was suggested to be the critical and perhaps only essential physiological role of plasminogen activation [149]. It should be noted, nevertheless, that laminin is also an in vivo plasmin substrate [150]. There was much less abnormal fibrin deposition in $tPA^{-/-}$ mice and $uPA^{-/-}$ mice than in *plasminogen*−/− mice and *uPA*−/−-*tPA*−/− mice, implying that uPA can substitute for tPA in fibrinolysis [144]. There was also much less disseminated fibrin deposition in *uPAR*−/−-*tPA*−/− mice than in *plasminogen*−/− and *uPA*−/−-*tPA*−/− mice, suggesting that binding of uPA to uPAR is less important for uPA-mediated fibrinolysis [151]. *PAI*-1−/− mice had a mild hyperfibrinolytic state and a greater resistance to venous thrombosis [145] and displayed decreased fibrin deposition after lung injury [152–154].

 $uPA^{-/-}$ mice had increased susceptibility to lung infection with *Cryptococcus neoformans* and a reduced recruitment of leukocytes to the infection sites [155] and increased susceptibility to staphylococcal botryomycosis [156]. *plasminogen*−/− mice had impaired recruitment of leukocytes to inflammatory sites [157]. The accumulation of leukocytes, mainly neutrophils and eosinophils, in peritoneum during thioglycollate-induced peritonitis was significantly reduced in *uPAR*−/− mice compared to wild-type mice [125].

The fact that *plasminogen*−/−, *uPA*−/−, *uPAR*−/−, *PAI*-1^{-/-}, and *vitronectin*^{-/-} mice develop to term shows that the uPA system is not essential in development, in apparent contradiction to predictions from cell culture experiments of a general regulatory role of the system in cell migration and invasion (see above) and from studies of the expression of the components of the system [for reviews see refs 1, 2, 13]. It is unknown whether this is due to functional overlap with and compensatorily increased expression of other enzyme systems, and/or to the essential functions of the system being restricted to specific processes like fibrinolysis and cell migration and invasion in inflammation.

Levels of plasminogen activation system components in tumors and patient prognosis

The levels of uPA, PAI-1, and uPAR in human malignant tumors are significantly higher than in the corresponding normal tissues [for reviews see ref. 13, 158], but their levels in a given tumor type vary considerably between individual patients. In a variety of malignancies, patients with high tumor uPA levels have a shorter disease-free interval and a shorter overall survival than patients with a low level [for reviews see refs 13, 14]. In contrast, tPA levels are correlated with a good prognosis [for a review see ref. 158]. The finding that high tumor levels of PAI-1 also predict a poor prognosis [for reviews see refs 13, 14] first came as a surprise, since it is in apparent contradiction to the original idea of cancer cell dissemination being promoted by pericellular uPA-catalyzed plasmin generation, and it has been an important motive for searching for functions of PAI-1 other than inhibition of uPA. High levels of uPAR in tumors are also correlated with a poor prognosis [for reviews see refs 13, 14].

Recently, interesting correlations between poor patient prognosis and high levels of soluble uPAR in blood plasma and other body fluids were reported [41, 42]. In addition, expression of uPAR and uPA in disseminated cancer cells in bone marrow of patients with gastric and breast cancers, respectively, predicted an early relapse [159, 160].

The plasminogen activation system in experimental metastasis in animals

Many experiments with animal model systems have shown convincingly that uPA-catalyzed plasmin generation is an important determinant of the rate of the overall process of tumor metastasis [for reviews see refs

1, 2, 13]. Recently, mice with specific gene disruptions were used for evaluating the role of the uPA system in tumor biology. The induction of blue nevi by 7,12 dimethylbenz(a)anthracene/croton oil occurred with equal efficiency in control and *uPA*−/− mice, but there was less local invasion in *uPA*−/− mice than in control mice, and *uPA*−/− mice had a drastically reduced progression to malignant melanomas [161]. Formation of vascular tumors after injection of polyoma middle Ttransformed endothelial cells was reported to be highly dependent on the expression of uPA by the injected cells as well as by the host [162]. *plasminogen*−/− mice displayed a slower growth of transplanted Lewis lung carcinoma and fewer regional lymph node metastases and lived longer after the transplantation than control mice, but did not have fewer metastatic foci in the lungs [163]. The incidence of lung metastases from mammary tumors induced by mouse mammary tumor virus and polyoma middle T antigen was up to ten-fold lower in *plasminogen*−/− mice than in control mice, while tumorigenesis and primary tumor progression were unaffected [164]. These results are also in agreement with the idea that uPA-catalyzed plasminogen activation is rate limiting for tumor growth, local tumor invasion, and formation of distant metastases.

Most experiments with animal model systems showed that to support tumor metastasis, uPA must be bound to uPAR [for reviews see refs 1, 2, 13]. Exceptionally, transfection of *murine* B16 melanoma cells with *human* uPA cDNA was reported to increase the ability of these cells to metastasize [165]. Since human uPA binds with only low affinity to murine uPAR, this report suggests that unbound uPA is active in metastasis. Metastasis studies with $uPAR^{-/-}$ mice should be able to throw more light on this issue, but remain to be reported.

Experiments with two animal model systems both gave results showing that PAI-2 expression by cancer cells suppress metastasis [166, 167]. In contrast, no consistent picture has emerged concerning PAI-1. Transfection of PC-3 cells with PAI-1 cDNA impaired their ability to metastasize in nude mice [143]. Transduction with adenovirus vector carrying PAI-1 cDNA of uveal melanoma cells, transplanted into the eyes of nude mice, resulted in a reduction both in the number of animals developing liver metastasis and in the metastatic burden in animals with metastasis [168]. Intravenous injection of PAI-1 inhibited the growth of xenografts of human DU145 and LNCaP prostate carcinoma cells in *scid*/ *scid* mice [169]. Metastasis of murine B16 melanoma was indistingushable in control mice and in mice overexpressing PAI-1 [170]. Expression of PAI-1 by human melanomas implanted onto nude mice correlated with metastatic behavior [171]. Bajou et al. [172] transplanted malignant keratinocytes onto a collagen I gel in the skin of control and *PAI*-1−/− mice. Upward migration of host-derived endothelial cells and stromal cells and downward migration of malignant cells were severely impaired in *PAI*-1−/− mice, but could be brought back to control levels by injection of adenovirus carrying PAI-1 cDNA. The latter results provide convincing evidence for a causal involvement of host PAI-1 in cancer cell invasion and angiogenesis.

Angiostatin has been reported to inhibit primary tumor growth and metastasis in animals by inhibition of tumor angiogenesis [18, 173–176].

Processes in tumors involving the plasminogen activation system

Most of the experiments described in the previous section gave little information about the actions of the plasminogen activation system at individual steps in tumor growth, invasion, and metastasis, and the situation in tumors in vivo is far more complex than in the cell cultures used to provide evidence for important roles of the system in cell migration and invasion. In tumors, not only cancer cells, but also nonmalignant cells are migratory and invasive, during processes of cancer cell-directed tissue remodeling. The system may contribute to tumor growth, invasion, and metastasis by being involved in such processes. Most information is available about the early steps in the metastatic process, e.g., invasion and intravasation, and the later steps, e.g., extravasation and colonization, will not be dealt with here.

A strategy widely used in attempts to identify tumor processes involving the uPA system has been determination of cells expressing its components by immunohistochemistry and in situ hydridization. There are limitations to this approach, however. An inherent difficulty is that there is not necessarily a correlation between the amount of a certain protein in a certain localization and its functional importance there. Moreover, there are discrepancies between the results reported by different groups [for a review see ref. 13]. Nevertheless, the localization studies published so far do demonstrate some important points. It was a general finding that each of the components is expressed not only by a single cell type, and that the expression pattern varies between different types of tumors [for a review see ref. 13]. The localization of the components may also vary between different tumors in the same tissue, depending on their degree of differentiation [177–179]. Some studies suggested collaboration between different cell types, each producing different components of the system [180]. The localization of the components in multiple cell types points to the system having multiple functions contributing to tumor growth, invasion, and metastasis. Thus, the presence of the components of the system on cancer cells suggests a function in cancer cell migration and invasion, their presence on stromal fibroblasts suggests a role in desmoplasia and stroma remodeling, and their presence on endothelial cells suggests a role in angiogenesis. Differential expression of PAI-1 by different cell types and in different tissue areas may contribute to cancer cell-directed tissue remodeling by allowing deposition of new ECM, e.g., during angiogenesis, in tissue areas with a high uPA activity.

The hypothesis of a role for the uPA system in angiogenesis is supported by findings with angiogenesis model systems [for a review see ref. 181], with observations of an antagonist of uPA-uPAR binding inhibiting neovascularization of the murine B16 melanoma [182], and with a correlation between microvessel density and uPA levels in breast carcinomas [183]. On the other hand, plasminogen and plasminogen activators were not essential for outgrowth of endothelial cells from murine tissue explants into a fibrin gel [184], and an indistinguishable vascularization of Lewis lung carcinomas in *plasminogen*−/− and control mice argued against a role of plasmin in angiogenesis in this tumor [163]. Angiostatin inhibits angiogenesis, in agreement with its ability to inhibit endothelial cell migration (see above) and to inhibit endothelial cell proliferation [18, 24, 128, 129, 174, 175, 185]. Since angiostatin is derived from plasminogen, the finding of indistinguishable vascularization of Lewis lung carcinomas in *plasminogen*−/− and control mice [163] argues against angiostatin as an essential, naturally occurring regulator of angiogenesis. The findings of Bajou et al. [172] (see above) provided strong evidence for PAI-1 being necessary for tumor angiogenesis.

In view of the finding that fibrinogen deficiency corrects many effects of plasminogen deficiency in mice [149] (see above), the importance of fibrin and fibrinolysis for the role of the uPA system in tumor biology must be considered. Cancer cell spread may require invasion into extravascular fibrin deposits, which occur in many tumors and which may also provide a matrix for desmoplasia and angiogenesis [4, 7]. From the evidence for uPAR-independent actions of uPA in fibrinolysis (see above), it may also be speculated that uPAR-independent uPA-mediated fibrinolysis contributes to tumor invasion. The apparant paradox that tumor levels of tPA, the classical fibrinolytic enzyme, are correlated with a good rather than a poor prognosis (see above) may be resolved by assuming that tPA is not produced by the right cell types. More conclusive information about the role of fibrinolysis in tumor growth, invasion, and metastasis may be obtained with *fibrinogen*−/− and *plasminogen*−/−-*fibrinogen*−/− mice.

The plasminogen activation system as a therapeutic target

The components of the uPA system are potential targets for anti-invasive and anti-metastatic therapy. The most obvious target is the enzyme activity of uPA. Most classical proteinase inhibitors inhibit both uPA and tPA and are therefore also expected to inhibit fibrinolysis, but peptide sequences have recently been identified which may form the basis for development of selective uPA inhibitors [186]. The binding of uPA to uPAR is another potential target [for a review see ref. 13]. The best-characterized antagonist is a peptide selected from a phage-displayed peptide library [187], binding to a site composed of regions in uPAR domains 1 and 3, and most likely competing directly with uPA for binding [48, 52].

Several compounds have been found to inhibit the reaction of PAI-1 with uPA and tPA. Some monoclonal anti-PAI-1 antibodies inhibit the reaction [188], many of these having epitopes near α -helix F [189]. PAI-1neutralizing derivatives of diketopiperazine also bind near α -helix F [190]. PAI-1-neutralizing derivatives of anthranilic acid are believed to insert in a hydrophobic pocket lined by α -helices D, E, and F and β -strand 2A and to form salt bridges to basic residues in α -helices D and E [191]. PAI-1-neutralizing peptides corresponding to portions of the RCL probably insert in the cleft between β -strands 3 and 5 [192]. These compounds may therefore act by changing the conformation of the flexible-joints region and/or by preventing the loop insertion associated with complex formation (fig. 2). Sodium dodecyl sulfate [193] and peptides selected from a phage-displayed peptide library [194] also neutralized PAI-1, but their binding sites are unknown. Importantly, in order to neutralize the functions of PAI-1 in tumor invasion, it may also be necessary to neutralize its ability to inhibit the binding of uPAR and integrins to vitronectin.

An alternative approach is inhibition of biosynthesis of the components of the uPA system by antisense oligonucleotide therapy [for a review see ref. 14]. The potential use of angiostatin as a generally applicable anticancer drug, based on its ability to inhibit angiogenesis, has recently attracted much interest [195, 196].

Conclusions and perspectives

The original idea of plasminogen activation as a ratelimiting factor in tumor invasion and metastasis has been supported by many results with in vitro and in vivo model systems and by demonstration of correlations between patient prognosis and tumor levels of components of the uPA system. Most recently, experiments with mice with targeted disruption of the genes for these components have given results supporting this idea. But the increased knowledge about the system has also led to the realization that the system works in a far more complex way than described by the original hypothesis. Much evidence suggests that the system also has plasmin-independent functions, consisting in intracellular signal transduction cascades being initiated by binding of uPA to uPAR, in uPAR acting as a vitronectin receptor and as a regulator of integrin function, in PAI-1 acting as a regulator of uPAR and integrin binding to vitronectin, in interactions with endocytosis receptors, and in an interplay with other proteolytic enzyme systems. The dynamic state of the system allows spatial and temporal rearrangements of its components at cell surfaces during cell migration and invasion. Moreover, it has become clear that the system has a multifunctional role in tumor biology. The system seems to function not only in cancer cell migration and invasion, but also in remodeling of the tissue surrounding the cancer cells, which may contribute decisively to the overall process of metastasis. As the biologies of individual tumors are different, different processes may be rate limiting for the endpoint of metastasis in different tumors, and the importance of the uPA system may therefore vary.

Special problems are associated with understanding the role of PAI-1 in tumor biology. The unexpected finding that PAI-1 is a marker for a poor prognosis has been the impetus for a variety of studies with in vitro and in vivo model systems, but they have not yet provided one unifying hypothesis for the role of PAI-1. Some observations suggest that PAI-1 may counteract migration and invasion by inhibiting uPA, while other observations support the hypothesis that PAI-1 is needed for the optimal function of the uPA system in these processes, by regulating cell adhesion and by restricting proteolysis in time and space. The recent results with *PAI*-1^{-/-} mice [172] strongly suggest that PAI-1 expressed by noncancer cells does play a causal role in tumor growth and spread by protecting new ECM in tissue remodeling events like angiogenesis.

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