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Type II transmembrane serine proteases as potential targets for cancer therapy

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Abstract

Carcinogenesis is accompanied by increased protein and activity levels of extracellular cell-surface proteases that are capable of modifying the tumor micro-environment by directly cleaving the extracellular matrix, as well as activating growth factors and proinflammatory mediators involved in proliferation and invasion of cancer cells, and recruitment of inflammatory cells. These complex processes ultimately potentiate neoplastic progression leading to local tumor cell invasion, entry into the vasculature, and metastasis to distal sites. Several members of the type II transmembrane serine protease (TTSP) family have been shown to play critical roles in cancer progression. In this review the knowledge collected over the past two decades about the molecular mechanisms underlying the pro-cancerous properties of selected TTSPs will be summarized. Furthermore, we will discuss how these insights may facilitate the translation into clinical settings in the future by specifically targeting TTSPs as part of novel cancer treatment regimens.

Keywords

cell surface proteolysis; protease inhibitors; type II transmembrane serine proteases

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Introduction

The first reviews on the type II transmembrane serine protease (TTSP) family were published at the turn of the millennium describing an emerging class of cell surface proteolytic enzymes (Hooper et al., 2001; Netzel-Arnett et al., 2003). At that time the knowledge about this family of proteases mainly comprised basic biochemical characteristics as well as expression data. Early on, it was evident that many TTSPs were differentially expressed in cancer. In the years following, the knowledge about the physiological and disease-related functions of TTSPs has rapidly accumulated. The generation of genetic loss-of-function and gain-of-function animal models and the characterization of human mutations have greatly enhanced our understanding of TTSP functions in a wide variety of organ systems under normal conditions and during disease initiation and progression, including cancer (Bugge et al., 2007, 2009; Szabo and Bugge, 2008; List, 2009; Antalis et al., 2010) (Table 1). Thus, it has been demonstrated that TTSPs play key roles in diverse processes including epithelial differentiation, homeostasis, iron metabolism, hearing, and blood pressure regulation (Szabo and Bugge, 2011). Furthermore, considerable headway has been made towards characterizing the regulation by cognate inhibitors, and identification of physiologically relevant pro-teolytic substrates (Table 1). Early studies demonstrated that dysregulated expression of TTSPs is associated with several cancers. In more recent studies, promotional or causal roles of TTSPs have been demonstrated in vivo using genetic engineering or administration of protease inhibitors to manipulate protease levels and activity. As evidence continues to accumulate about their functional roles in cancer development and progression, TTSPs represent exciting future therapeutic targets. This review will focus on four TTSPs (matriptase, hepsin, TMPRSS2 and TMPRSS4) that to date have been most extensively studied in cancer. We will evaluate studies describing their roles in solid tumor progression, and their potential for targeted therapy.

Matriptase

This protease is one of the most extensively studied TTSPs with more than 300 published articles characterizing expression profiles, gene-regulation, structural biology, regulation by endogenous inhibitors, identification of critical substrates, determination of physiological and pathophysiological functions, and development of synthetic inhibitors and imaging tools. Approximately one third of the studies describe proposed roles of matriptase in cancer by employing cell culture models, *in vivo* studies using tumor grafting, or genetically engineered mouse models. Matriptase is upregulated in breast, cervical, colorectal prostate, endometrial, esophageal squamous cell carcinoma, gastric, head and neck, and pancreatic carcinoma; and in tumors of the lung, liver, and kidney among others (Cheng et al., 2006; Bugge et al., 2007; List, 2009; Webb et al., 2011). Increased matriptase expression correlates with advanced clinicopathological stages in many of these cancers, and *de novo* expression is found in ovarian and cervical carcinoma where expression levels also correlate with histopathological grade (Tanimoto et al., 2001, 2005; Lee et al., 2005). Matriptase activity is mainly regulated by the transmembrane serine protease inhibitors, hepatocyte growth factor activator inhibitor-1 and -2 (HAI-1 and HAI-2) in vivo (Szabo et al., 2007, 2008, 2009a,b). In expression studies, an imbalance between matriptase, HAI-1 and HAI-2 exists in several

cancer types including ovarian and colorectal cancer where the matriptase/ HAI-1 ratio is increased and in prostate and endometrial carcinoma where matriptase/HAI-2 ratios are increased (Oberst et al., 2002; Saleem et al., 2006; Vogel et al., 2006; Bergum and List, 2010; Nakamura et al., 2011). A causal effect of matriptase expression was demonstrated in mice with transgenic expression of matriptase in the epidermis. These transgenic mice develop spontaneous squamous cell carcinoma, dermal inflammation and increased susceptibility to carcinogen-induced tumorigenesis (List et al., 2005). A follow-up study identified the preform of hepatocyte growth factor (pro-HGF) as a critical proteolytic target for matriptase in epidermal carcinogenesis using mouse genetic analysis (Szabo et al., 2011). When matriptase transgenic mice are crossed to mice with conditional epidermal deletion of the membrane receptor for pro-HGF/ HGF, c-Met, the matriptase-mediated malignancy is prevented, demonstrating that the oncogenic potential of matriptase in mouse epidermis is dependent on the HGF/ c-Met signaling pathway (Szabo et al., 2011) (Figure 1). Importantly, from a matriptase inhibitor perspective, the oncogenic properties of matriptase are completely abolished in double transgenic mice that also express transgenic epidermal HAI-1, which demonstrates that restoring the matriptase/HAI-1 balance in the epidermis rescues the skin from undergoing carcinogenesis (List et al., 2005). In this study, transgenic HAI-1 was expressed constitutively before the onset of transgenic matriptase-mediated tumor formation, thus representing a preventative study. Recently, it was shown that inducible matriptase inhibition initiated after the establishment of carcinomas is also efficient for cancer intervention (Sales et al., 2015). Induction of transgenic HAI-2 impaired malignant progression and caused regression of established individual tumors. Tumor regression correlated with reduced accumulation of tumor-associated inflammatory cells, likely caused by diminished expression of pro-tumorigenic inflammatory cytokines (Sales et al., 2015). These data suggest that matriptase may be a therapeutic target for both squamous cell carcinoma chemoprevention and for the treatment of established tumors.

Other studies that have assessed the consequence of matriptase/inhibitor imbalance include orthotopic xenografting of prostate cancer cells which showed that HAI-2 overexpression or matriptase silencing in N2 cells significantly decreased tumorigenicity and metastatic capability in mice (Tsai et al., 2014). In a pancreatic cancer model using orthotopic transplantation it was demonstrated that transgenic expression of HAI-1 in S2-CP8 cells, which display low levels of endogenous HAI-1, significantly decreased the development of distant metastasis in mice (Ye et al., 2014). The role of matriptase *in vivo* has also been studied in detail in breast cancer. In an oncogene-induced mouse mammary carcinoma model, hypomorphic matriptase mice with reduced levels of matriptase displayed a significant delay in tumor formation and blunted tumor growth (Zoratti et al., 2015). The reduced tumor growth was associated with a profound decrease in cancer cell proliferation. Mechanistic studies demonstrated that the proliferation deficiency was caused by the impairment of carcinoma cells, in cell lines and in vivo, to initiate the activation of the c-Met signaling pathway in response to fibroblast-secreted pro-hepatocyte growth factor (pro-HGF) (Figure 1). In primary mammary carcinoma cells and human breast cancer cell lines, addition of HAI-1 and HAI-2 inhibited pro-HGF mediated c-Met signaling and cell proliferation (Zoratti et al., 2015). Importantly, inhibition of matriptase catalytic activity using a selective small-molecule inhibitor efficiently abrogates the activation of c-Met, Gab1

and AKT, in response to pro-HGF, which functionally leads to attenuated cancer cell proliferation and invasion. The selective inhibitor of matriptase, IN-1 used in the study contains a ketobenzothiazole serine trap and was designed based on the auto-catalytic domain (RQAR) of matriptase (Colombo et al., 2012). It still remains to be tested whether IN-1 is suitable as an anti-tumor drug *in vivo*. Other inhibitors have been developed including MCoTI-II (based on cyclic microproteins of the squash *Momordica cochinchinensis* trypsin-inhibitor family) which inhibits the proteolytic activation of pro-HGF by matriptase but not by hepsin, in both purified and cell-based system (Gray et al., 2014).

In prostate cancer, several matriptase inhibitors have been tested in xenograft models. In an ectopic subcutaneous model, a small molecule inhibitor of matriptase, CVS-3983, significantly suppressed the growth of human prostate cancer cell lines in nude mice (Galkin et al., 2004). The authors propose that the effect was mainly cause by the abrogation of invasion since tumors remained localized to the site of injection in treated mice and failed to invade the subscapular area as compared to tumors in vehicle treated mice. Similarly, using matriptase inhibitors based on bis-basic secondary amides of sulfonylated 3-amidinophenylalanine in an orthotopic xenograft mouse model of prostate cancer resulted in reduced tumor growth, and tumor dissemination (Steinmetzer et al., 2006). Together, these findings demonstrate that matriptase is critically involved in cancer progression and lay the groundwork for future studies developing and testing small-molecule matriptase inhibitors and their potential as novel targeted therapeutic drugs in cancer.

Hepsin

Hepsin/TMPRSS1 was the first serine protease characterized to contain a transmembrane domain, and was named based on its original identification in hepatocytes (Leytus et al., 1988). Hepsin is also expressed in kidney, pancreas, stomach, prostate and thyroid (Tsuji et al., 1991a,b). Studies of knockout mouse models of hepsin have demonstrated that this protease plays an important role in cochlear development, is involved in regulating levels of the thyroid secreted hormone, thyroxine, and is responsible for pro-HGF activation in the liver (Guipponi et al., 2007; Hanifa et al., 2010; Hsu et al., 2012).

Many cancers display increased expression levels of hepsin including cancer of the prostate, breast (Xing et al., 2011), ovary (Tanimoto et al., 1997), kidney (Betsunoh et al., 2007), and endometrium (Matsuo et al., 2008). Several studies have revealed that hepsin is critically involved in prostate cancer progression. Klezovitch and colleagues used transgenic mice to show that the overexpression of hepsin, under the control of the probasin (PB) promotor, leads to a disorganized basement membrane and promotes prostate cancer metastasis to the liver, bone and lungs when crossed to the LPB-Tag prostate cancer model (Klezovitch et al., 2004).

The Wnt/ β -Catenin signaling pathway has been shown to play an important role in prostate cancer progression. Dysregulation of this pathway by prostate-specific deletion of the adenomatous polyposis coli (*Apc*) gene results in high-grade prostatic intraepithelial neoplasia (PIN) lesions with rare occurrences of microinvasive characteristics in mice

(Bruxvoort et al., 2007; Valkenburg et al., 2014). Crossing PB-Hepsin mice to the prostatespecific *Apc*-deletion model (*APC*^{PBKO}) to generate PB-Hepsin/*APC*^{PBKO} mice results in progression from high-grade PIN lesions to large invasive adenocarcinomas (Valkenburg et al., 2015). Prostate tumors from PB-Hepsin/*APC*^{PBKO} mice are hyperproliferative, and contained significant numbers of apoptotic cells (Valkenburg et al., 2015).

A separate transgenic mouse model of prostate cancer has been developed by the overexpression of the human *c-Myc* proto-oncogene in the prostate epithelium. These transgenic mice develop PIN lesions that progress to invasive adenocarcinomas at approximately 6 months of age and show common molecular features with human prostate tumors (Ellwood-Yen et al., 2003). When PB-hepsin mice are crossed into this model of prostate cancer, bitransgenic mice develop adenocarcinomas earlier than PB-Myc mice and histological analysis detected higher grade adenocarcinoma indicating that hepsin cooperates with c-Myc to promote tumor progression in this model (Nandana et al., 2010).

PB-Hepsin/LPB-Tag bitransgenic mice were subsequently used to assess whether targeted inhibition of hepsin attenuates prostate cancer progression *in vivo*. Tang et al. identified a small molecule inhibitor of hepsin, hepIn-13, and treated PB-hepsin/LPB-Tag mice with oral doses of the inhibitor 13-weeks after mice had initially developed low-grade prostate tumors. Tumor metastasis was observed in the non-treated control group whereas HepIn-13 blocked metastasis to bone, liver, and lung in a dose-dependent manner (Tang et al., 2014).

In an orthotopic xenograft model of prostate cancer, LnCaP cells were stably transfected to overexpress hepsin (LnCaP-34) and injected into the anterior lobe of the prostate. Increased final tumor weights were observed in mice injected with LnCaP-34 cells compared to LnCaP cells expressing endogenous levels of hepsin (LnCaP-17 cells) (Li et al., 2009). Additionally, metastatic lesions to the periaortic lymph nodes were observed in mice injected with LnCaP-17 cells (Li et al., 2009). To determine whether inhibition of hepsin decreases the tumor growth *in vivo*, mice injected with LnCaP-34 cells were treated with a PEGylated form of Kunitz domain-1, a potent hepsin active site inhibitor derived from HAI-1. Treatment of established orthotopic LnCaP-34 xenografts tumors with PEGylated Kunitz domain-1 significantly decreased contralateral prostate invasion and lymph node metastasis (Li et al. 2009).

In addition to prostate cancer, hepsin has been shown to have increased expression in breast cancer (Xing et al., 2011). To determine whether hepsin promotes tumor progression in breast cancer, Tervonen et al. performed grafting studies using primary mouse mammary epithelial cells from transgenic mice harboring a Whey acidic protein (*Wap*) promoter-controlled *c-Myc* transgene. The primary cells, that also expressed doxycyclin-inducible hepsin, were transplanted into cleared fat pads of syngeneic wild-type virgin hosts. Chronic doxycyclin-induced expression of hepsin resulted in decreased tumor latency in these mice, thus indicating a promotional role for hepsin in breast cancer progression (Tervonen et al., 2016). Interestingly, hepsin acutely downregulated its cognate inhibitor, HAI-1, in human MCF10A immortalized mammary epithelial cells, thereby further increasing the hepsin/HAI-1 ratio. Furthermore, hepsin induced cellular changes in MCF10A cells commonly

associated with invasive phenotypes and endowed cells with a strong capacity to proteolytically activate pro-HGF, leading to activation of the c-Met receptor (Figure 1).

Hepsin is also frequently overexpressed in ovarian cancer, where 80% of ovarian carcinomas express hepsin mRNA whereas normal ovaries do not express hepsin mRNA (Tanimoto et al., 1997). In a subcutaneous transplantation study designed to determine whether hepsin expression promotes tumor growth, the parental SKOV3 human ovarian carcinoma, SKOV3 cells expressing WT-hepsin, or SKOV3 cells expressing a catalytically dead (CD) mutant form of hepsin were subcutaneously implanted into nude mice. SKOV3 cells expressing WT-hepsin displayed increased tumor volume compared to both the CD-hepsin and parental control cells, indicating that over-expression of active hepsin in ovarian cancer promotes ovarian tumor growth (Miao et al., 2008)

TMPRSS2 and TMPRSS4

TMPRSS2 and TMPRSS4 are two other members of the TMPRSS/Hepsin subfamily of TTSPs and remain relatively uncharacterized. Like many other TTSPs, expression of TMPRSS2 is localized to several types of epithelial tissues, including in the colon, small intestine, lung, kidney, pancreas, and most notably in the prostate (Jacquinet et al., 2001), where expression is highest. Both the physiological function and substrates of TMPRSS2 have yet to be identified; therefore much of what is known about TMPRSS2 originates from its association with cancer. TMPRSS2 has long been associated with prostate cancer following the identification of the oncogenic gene fusion product with erythroblast transformation specific (ETS) transcription factors, such as ETS-related gene (ERG) (Clark and Cooper, 2009; Shah and Small, 2010). Despite this, the role of the native TMPRSS2 protein and its proteolytic activity in cancer is vastly understudied. In normal prostate epithelia, TMPRSS2 expression is localized to the cell membrane, however, mislocalization to the cytoplasm in prostate cancer has been observed (Lucas et al., 2008). In addition, both primary and metastatic prostate tumors from patients display increases in TMPRSS2 levels, with increasing expression correlating with elevated Gleason score, suggesting that TMPRSS2 may play a pro-oncogenic and pro-metastatic role (Lucas et al., 2008). Knockdown studies in human LNCaP prostate cancer cells demonstrated that reduction of TMPRSS2 expression in cancer cells decreased cellular invasion, tumor size, and incidence of metastases following xenografting in mice (Ko et al., 2015). Interestingly, loss of TMPRSS2 expression does not impact cellular proliferation of LnCaP cells in culture (Ko et al., 2015). However, a role of the tumor micro-environment is not taken into consideration in mono-culture, therefore, a role for TMPRSS2 for cancer cell proliferation cannot conclusively be excluded. It is worth noting that in a similar study, shRNA-mediated silencing of TMPRSS2 in LNCaP-derived, bone metastatic castration-resistant (LNCaP C4-2B) cells led to a significant reduction in cell proliferation and cell invasion compared with scrambled shRNA controls (Lucas et al., 2014).

In a study employing mice with a targeted deletion of the *Tmprss2* gene, it was demonstrated that the protease regulates cancer cell invasion and metastasis to distant organs in the TRansgenic Adenocarcinoma Mouse Prostate (TRAMP) model of prostate carcinogenesis (Lucas et al., 2014). TRAMP tumors in *Tmprss2*^{-/-} mice were significantly

larger than those in control mice, however, the incidence of metastasis to distant solid organs was substantially lower in the TRAMP tumors arising in the *Tmprss2*^{-/-} background. It was demonstrated that TMPRSS2 activated signaling incompetent pro-HGF to active HGF *in vitro* and it is hypothesized that TMPRSS2-activated HGF consistently promotes invasion and metastasis, but differentially enhances or suppresses proliferation. Importantly, a TMPRSS2 chemical inhibitor (bromhexine hydrochloride) suppressed distant metastasis to lung and liver sites in TRAMP mice (Lucas et al., 2014).

These links to prostate malignancy makes TMPRSS2 a promising target for drug therapies. Of notable interest is that no phenotype affecting normal development or physiological function has been observed in TMPRSS2 deficient mice. This suggests that targeted ablation of TMPRSS2 in cancer may have minimal side effects (Kim et al., 2006). Upstream, TMPRSS2 expression in prostate has been shown to be driven by androgen receptor signaling; one notable consequence of this is the pro-oncogenic TMPRSS2-ERG fusion protein. This link between androgen receptor signaling and TMPRSS2 has further pushed interest in androgen receptor inhibitors as possible targets for inhibiting prostate cancer growth and metastasis. The pro-oncogenic potential of TMPRSS2 has, as mentioned above, been linked to its activity, specifically pertaining to its role in activating the HGF/cMET pathway (Lucas et al., 2014). More recently, work has uncovered matriptase as a possible substrate for TMPRSS2. A recent study found that levels of active matriptase are increased in prostate cancer without increases in matriptase transcript levels (Ko et al., 2015). Furthermore, orthotopic grafts of LNCaP cells over-expressing TMPRSS2 exhibited increased levels of active matriptase, as well as increased metastases, when compared to grafts expressing a control vector or catalytically dead TMPRSS2 (Ko et al., 2015). Proteolytic homeostasis is important for maintaining normal tissue function, and increases in TMPRSS2 expression may shift the balance between matriptase activity and cognate inhibitors. Additionally, beyond the HGF pathway, TMPRSS2 has been shown to activate protease-activated receptor 2 (PAR-2) in LNCaP cells (Wilson et al., 2005), inciting another pathway which may be involved in promoting metastasis (Wilson et al., 2004). In addition to the TMPRSS2 inhibitor bromhexine hydrochloride mentioned above, other synthetic inhibitors based on substrate analogs have been developed and demonstrated to inhibit TMPRSS2 activity, as measured by cleavage of influenza hemagglutinin (HA) (Meyer et al., 2013). TMPRSS2 in airway epithelia is important for influenza infection, and inhibition of TMPRSS2 with small molecule antagonists can prevent influenza infection (Garten et al., 2015). However, these small molecule inhibitors also have strong affinities for other proteases, such as matriptase, making the precise therapeutic mechanism by which these molecules function unclear.

The physiological role of TMPRSS4 is currently not known, however, a mutation in this gene has been associated with autosomal recessive cerebral atrophy (ARCA) (Lahiry et al., 2013). TMPRSS4 has been demonstrated to be upregulated in pancreatic, colorectal, thyroid, lung, and several other cancers (Wallrapp et al., 2000; Kebebew et al., 2005; Kim et al., 2010; Larzabal et al., 2011). Because of this broad expression profile in cancer, TMPRSS4 has been a focal point of anti-cancer research in recent years. TMPRSS4 has been shown to promote proliferative processes in lung and thyroid cancer cells, while shRNA targeting of TMPRSS4 transcripts causes reductions in proliferation (Guan et al., 2015; Hamamoto et al.,

2015; de Aberasturi et al., 2016). Work using cultured lung cancer cells demonstrated that TMPRSS4 promotes a mesenchymal and invasive phenotype, suggesting a role for epithelial to mesenchymal transition (EMT) (de Aberasturi et al., 2016). Interestingly, increases in markers for cancer stem cells (CSCs) such as aldehyde dehydrogenase (ALDH) and octamer-binding transcription factor 4 (OCT-4) are strongly positively correlated with TMPRSS4 expression (de Aberasturi et al., 2016). Several reports have suggested that TMPRSS4 associates with poor prognosis and survival in a variety of different cancers (Cheng et al., 2013a,b; Wu et al., 2014; de Aberasturi and Calvo, 2015; Wang et al., 2015), which may be a result of an increase in the CSCs population, although the factors leading to TMPRSS4 upregulation are still not identified. One recent finding suggests that increased TMPRSS4 in cancer may result from gene-silencing of tissue factor pathway inhibitor 2 (TFPI-2), a consequence of improper methylation (Hamamoto et al., 2015). However, the mechanism which connects TFPI-2 and TMPRSS4 expression remains unknown.

While the physiological substrates for TMPRSS4 are not yet fully elucidated, targeting the activity of this protease may have benefits in the treatment of several types of cancer. With several studies reporting reduced invasive and proliferative potential in lung and thyroid cells following silencing of TMRSS4 expression (Larzabal et al., 2011; Guan et al., 2015) inhibitors of TMPRSS4 may provide an edge in cancer treatment. Also, overexpression of TMPRSS4 in cell culture causes cancer cells to be more resistant to several chemotherapeutics (de Aberasturi et al., 2016). A few small molecule inhibitors derived from 2-hydroxydairylamide have been developed with inhibitory effects on the proteolytic activity of TMPRSS4, with the consequence of impacting cancer cell invasiveness in colorectal SW480 cancer cells (Kang et al., 2013). Given that TMPRSS4 impacts signaling pathways such as cyclic AMP response element-binding protein (CREB)-cyclin D1 (Guan et al., 2015), inhibition of TMPRSS4 could impact many downstream processes important for a variety pro-oncogenic processes.

In conclusion, several TTSPs are candidate targets for therapy and combined basic and translational research is needed to further move the findings from cell and animal models into the clinic. Meanwhile, several groups continue to develop new TTSP inhibitors, including inhibitors of matriptase and hepsin, which may provide an alternative non-kinase strategy to the existing c-Met inhibitors that are already in clinical use, to block cell pro-oncogenic signaling in cancer (Figure 1) (Han et al., 2014).

Imaging TTSPs in cancer

Because many TTSPs are highly upregulated in cancer, they represent potential molecular imaging targets to be used, not only for basic research purposes, but also for diagnostic imaging of cancer in the clinic. Early detection of primary tumors is critical for successful cancer management and therapy. Molecular imaging differs from traditional diagnostic imaging techniques such as computed tomography (CT), and magnetic resonance imaging (MRI), by measurement of biologic processes at the cellular and molecular levels including proteolytic activity, that are involved in the disease progression.

The use of activity-based probes in mouse models has confirmed that proteolytic activity is a viable marker for cancer imaging in vivo for e.g. cysteine proteases (Sanman and Bogyo, 2014). Antibodies provide an alternate approach for targeting proteases and have the advantage of being very potent and specific (Figure 1). Antibodies that exclusively bind to the active form of matriptase with picomolar affinity were generated and validated in cell culture before evaluating their in vivo targeting capability (Darragh et al., 2010). Fluorescently labeled anti-matriptase IgG was administered to mice bearing xenografted tumors that were positive or negative for matriptase. Antibodies localized to matriptase expressing tumors, permitting visualization of matriptase activity, whereas tumors without matriptase expression were not visible (Darragh et al., 2010). In a follow-up study by the same group, it was demonstrated that the anti-matriptase IgG was capable of detecting matriptase in formalin-fixed paraffin-embedded tissue samples. Importantly, the significance of active matriptase at the protein level in colon cancer was further documented using immunofluorescence showing that active matriptase was undetectable in healthy colon whereas it was detected in adenocarcinomas of every stage (LeBeau et al., 2013). Furthermore, the preclinical utility of the antibody for the detection and quantitation of active matriptase in vivo was investigated using the nuclear imaging modality SPECT. The matriptase probe showed uptake in both xenografted cell lines and patient derived xenografts (PDX) using near infrared fluorescence imaging (NIR) optical imaging (LeBeau et al., 2013).

Using a different approach Napp et al. performed optical imaging in combination with a fluorescently labeled antibody directed against matriptase, and an activatable probe to determine expression and activity matriptase in orthotopic pancreatic (AsPC-1) xenografts *in vivo* (Napp et al., 2010). By applying NIR imaging in combination with a Cy5.5 labeled matriptase-specific antibody (recognizing both active and inactive matriptase), it was demonstrated that matriptase is expressed *in vivo* in primary tumors as well as in distant metastases. To study matriptase activity *in vivo*, an activatable probe, substrate S*DY-681, consisting of an eight amino acid peptide with a matriptase-preferred cleavage site and two fluorscent dyes quenching each other in the native state was utilized. Upon proteolytic cleavage, the fluorescence dyes separate, resulting in amplification of fluorescence. Matriptase activity was detected in tumors and this activity could be inhibited with synthetic active-site matriptase inhibitors (Napp et al., 2010).

Kelly and coworkers used phage display to isolate hepsin binding peptides with nanomolar affinity in monomeric form and high specificity. The identified peptides were able to detect human prostate cancer on tissue microarrays and in cell based assays. Imaging agents were synthesized by conjugating multiple peptides to fluorescent nanoparticles to further improve avidity through multivalency and pharmacokinetics. When hepsin targeted nanoparticles were injected into mouse xenograft models, they bound specifically to hepsin-expressing LNCaP xenografts compared to PC3 xenografts that did not express hepsin (Kelly et al., 2008).

The development of sensitive and selective imaging agents and inhibitors for TTSPs will provide a platform technology that can be used in diagnosis, treatment and evaluation of treatment efficacy.

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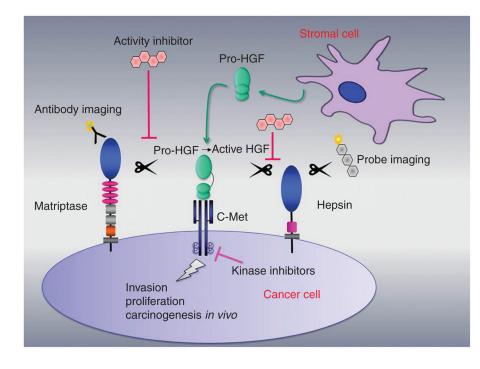


Figure 1. Simple schematic representation showing two TTSPs, matriptase and hepsin, that are localized on the cell surface of cancer cells

Proteolytic cleavage of stromal cell-secreted pro-HGF to signaling competent HGF elicits the HGF/c-Met pro-oncogenic signaling pathway in cancer. Matriptase activates pro-HGF in squamous cell carcinomas (Szabo et al., 2011) and in breast cancer *in vivo* (Zoratti et al., 2015). Hepsin has been reported to activate pro-HGF in immortalized mammary epithelial cells (Tervonen et al., 2016) and in prostate cancer cells (Owen et al., 2010). TMPRSS2 (not shown) has been proposed to activate pro-HGF in prostate cancer (Lucas et al., 2014). The development of inhibitors of matriptase, hepsin or TMPRSS2 may represent alternatives to existing receptor tyrosine kinase inhibitors to impair invasion, proliferation and metastasis. Diagnostic imaging of protease activity is also being explored using, e.g. specific antibodies and activity-based probes.

Table 1

Table depicting the associated cancers, known *in vivo* substrates, and mutant phenotypes for the reviewed TTSP family members.

Name	Associated cancer type	In vivo substra	In vivo substrates (tissue type)		Mutant phenotypes -physiological function	
Matriptase	• Breast ¹⁻³	•	Pro-prostasin (epi	idermis) ³⁰	Mouse loss-of-fur	ction models
	• Cervix ⁴ • Colon ⁵⁻⁷	•	Pro-filaggrin (epi –	ggrin (epidermis) Not processed in matriptase deficient mice	•	Impaired epidermal barrier functio (loss of tight junctions) -32-
	 Endometrium Esophogeal⁹ 	o		and humans, (direct cleavage not demonstrated) ³¹ ,		<i>34</i> Impaired intestinal
	Gastric ¹⁰ Head and neck ^{11–13}	•	Pro-HGF(breast c	39		barrier (loss o tight junctions 33,34
	• Kidney ¹⁴	•	PAR-2 (epidermis	_{S)} 27	•	Chronic inflammation the colon ^{5,35}
	• Leukemia ¹⁵ • Liver ¹⁶				•	Abnormal hai formation ^{32,3}
	 Lymphoma¹⁷ Mesothelioma 				•	Thymic hypoplasia ^{.32}
	 Pancreatic 19, Prostate 6, 21- 	20			•	Decreased saliva secretic and Sjögren's syndrome-like
	• Skin-squamou cell and basal cell carcinoma ²⁶⁻	IS			•	disease ^{34,37} Abnormal too enamel ³⁶ Human loss-o
						function mutations Reduced epidermal barrier function ^{31,38}
					•	Ichtyosis 31,38,40
					•	Hypotrichosis 31,38,40
					•	Abnormal permanent teeth ³⁸
					•	Follicular atrophoderma
TMPRSS2	• Prostate ^{41–42}	3 N.R.			•	No difference in weight or histopatholog of unchalleng TMPRSS2 knockout mic compared to

Name	Associated cancer type		In vivo substrates (tissue type)		Mutant phenoty function	Mutant phenotypes -physiological function	
						wildtype mice ⁴⁴	
TMPRSS4	•	Breast 45,46	N. R.		•	No differences	
	•	Cervix ⁴⁷				in weight or histopathology of unchallenge	
	•	Colon ^{48, 49}				TMPRSS4 knockout mice	
	•	Gall bladder ⁵⁰				compared to wildtype	
	•	Hepatocellular carcinoma ^{51, 52}				mice ⁵⁸	
	•	Lung 53–56				Human mutation	
	•	Pancreas ⁵³			•	autosomal recessive	
	•	Thyroid ⁵⁷				cerebral atroph (ARCA) ⁷¹	
Hepsin	•	Breast 59, 60	• Pro	o-HGF (Liver) ⁶⁹	•	Impaired	
	•	Ovarian ^{61, 62}				cochlear development ⁷⁰	
	•	Prostate 62–68			•	72 Impaired	
						hepatic structural homeostasis ⁶⁹	

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⁷ Vogel et al., 2006;
⁸ Nakamura et al., 2009;
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¹¹ Szabo et al., 2011;
¹² Cheng et al., 2014;
¹³ Baba et al., 2012;
¹⁴ Jin et al., 2006;
¹⁵ Gao et al., 2012;
¹⁶ Tsai et al., 2006;

¹⁷Chou et al., 2013;

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²⁰Uhland et al., 2009;

²¹Riddick et al., 2005;

²²Tsai et al., 2014;

²³Wu et al., 2010;

²⁴Tripathi et al., 2011;

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²⁶List et al., 2005;

²⁷Sales et al., 2014;

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³¹Alef et al., 2008;

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⁷²Hanifa et al., 2010.

N.R., Not reported.

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