PTPL1/PTPN13 Regulates Breast Cancer Cell Aggressiveness through Direct Inactivation of Src Kinase

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Abstract

The protein tyrosine phosphatase PTPL1/PTPN13, the activity of which is decreased through allelic loss, promoter methylation, or somatic mutations in some tumors, has been proposed as a tumor suppressor gene. Moreover, our recent clinical study identified PTPL1 expression level as an independent prognostic indicator of a favorable outcome for patients with breast cancer. However, how PTPL1 can affect tumor aggressiveness has not been characterized. Here, we first show that PTPL1 expression, assessed by immunohistochemistry, is decreased in breast cancer and metastasis specimens compared with nonmalignant tissues. Second, to evaluate whether PTPL1 plays a critical role in breast cancer progression, RNA interference experiments were performed in poorly tumorigenic MCF-7 breast cancer cells. PTPL1 inhibition drastically increased tumor growth in athymic mice and also enhanced several parameters associated with tumor progression, including cell proliferation on extracellular matrix components and cell invasion. Furthermore, the inhibition of Src kinase expression drastically blocked the effects of PTPL1 silencing on cell growth. In PTPL1 knockdown cells, the phosphorylation of Src on tyrosine 419 is increased, leading to the activation of its downstream substrates Fak and p130cas. Finally, substrate-trapping experiments revealed that Src tyrosine 419 is a direct target of the phosphatase. Thus, by identification of PTPL1 as the first phosphatase able to inhibit Src through direct dephosphorylation in intact cells, we presently describe a new mechanism by which PTPL1 inhibits breast tumor aggressiveness. Cancer Res; 70(12); OF1–11. ©2010 AACR.

Introduction

PTPL1 (also called PTPN13, FAP-1, PTP-BAS, and PTP1E), the nonreceptor-type protein tyrosine phosphatase (PTP) with the highest molecular weight (270 kDa), contains multiple interactive domains (1, 2). Its physiologic functions are poorly documented. PTP-BL (mouse homologue of PTPL1) KO mice present abnormal regulation of signal transducer and activator of transcription signaling in T cells (3); mice that lack the PTP-BL PTP activity show mild impairment of motor nerve repair (4), and we recently described the role of this phosphatase in adipocyte differentiation (5).

We reported the first evidence of the negative action of PTPL1 on cancer growth through our work on the anti–growth factor effect of antiestrogens in breast cancer (6–9). Other groups have confirmed that the PTPL1/PTPN13 gene presents the characteristics of a tumor suppressor gene (10, 11). Its expression is frequently downregulated or silenced through promoter hypermethylation within several tumor types (12, 13). A mutational analysis of colorectal cancers identified different somatic mutations in PTPL1 (14). Additionally, the PTPL1/PTPN13 gene is located on chromosome 4q21, a region frequently deleted in ovarian and liver cancers (15). In agreement with these data, we recently showed that PTPL1 expression is an independent prognostic marker for increased overall survival in breast cancer, indicating that PTPL1 is an important regulatory element of human breast tumor aggressiveness (16).

A number of potential PTPL1-interacting partners point to a role for PTPL1 in several steps of tumor progression, such as modification of cell shape and motility, and indicate its potential role in cancer metastasis. These potential partners include PIP2 (1), TAPP1/2 (17), EphrinB1 (18), TRIP6/ZRP1 (19), and PARG1 (20), all of which are involved in the maintenance of the cytoskeleton.

In this study, we show that PTPL1 plays a critical role in breast cancer progression by acting on pathways dependent on cell-matrix interactions. We also delineate the underlying molecular mechanism of this effect, which involves a decrease of Src phosphorylation and the activation of Src substrates, FAK and p130cas. Using complementary substrate trapping, colocalization, and in cellulo dephosphorylation methods, we show that PTPL1 directly and specifically dephosphorylates Src on the activating tyrosine 419 (Y419). Our findings therefore...
provide a novel mechanism through direct Src dephosphorylation by which PTPL1 regulates breast cancer aggressiveness.

Materials and Methods

Immunohistochemistry

The tissue array containing selected areas of paraffin-embedded sections from primary breast cancers, benign breast tissues, and lymph node metastases was obtained from SuperBioChips Laboratories. It was analyzed with anti-PTPL1 (AC21 from Abcam) as previously described (21). Staining was revealed using a standard avidin-biotin enhanced immunoperoxidase technique (R.T.U. Vectastain Kit, Vector Laboratories). PTPL1 immunostaining was cytoplasmic. Tissue microarray was scanned with a Slide Scanner (Hamamatsu NANO-ZOOMER), and cytoplasmic staining was evaluated with the Definiens developer (7.0) program (MRI, Montpellier).

Cell culture, plasmids, and antibodies

HEK293, MDA-MB-231, and MDA-MB-436 cells were cultured in DMEM; MCF-7 and BT 549 cells in Dulbecco’s modified Eagle’s medium Ham’s F12/DMEM (50%/50%); T47D and ZR 75.1 cells in RPMI medium (Invitrogen), all supplemented with 10% FCS. The expression construct PTPL1 wild-type (wt) was described previously as pHM6-PTPL1 (1). Mutants PTPL1-YF/D and PTPL1-CS were obtained as described (8). All glutathione S-transferase (GST) fusion proteins were constructed in pGEX-4T1 (Pharmacia Biotech; ref. 8). Ssrc and SrcY530F expression vectors were a gift of Dr. S. Roche (CRBM, Montpellier, France). The following monoclonal and polyclonal antibodies were used: anti-HA (12CA5, Roche); anti-p130cas (BD Biosciences); anti-phosphotyrosine (4G10 and PY20) and anti-actin (Sigma); anti-PTPL1 (H300, Santa Cruz Biotechnology); anti-phospho Fak (Y397 and Y576/577; Cell Signaling Technology).

Transfection and establishment of stable cell lines

Transient transfections were carried out using the jet PEI Cationic Polymer Transfection Reagent method (Qbiogene) with a ratio 1:10 of Src/PTPL1 wt or mutant or empty pHM6 vector.

siRNA transfections were carried out using the Oligofectamine reagent method (Invitrogen). The two PTPL1-specific siRNAs (Sis3:7313-GGAAAGAAGAGUUCGUUA-7331 and Sis4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNAs (Si3:7313-GGAAAGAAGAGUUCGUUA-7331 and Si4:1028-CAGAUCAGCUUUCCGUA-1046), the Src-specific siRNas were produced in Escherichia coli BL21 as previously described (8). After one wash with the substrate-trapping buffer [20 mmol/L Tris (pH 7.5), 100 mmol/L NaCl, 1 mmol/L EDTA, 1% Triton X-100, 10% glycerol] containing 10 mmol/L DTT, expression level and integrity of GST fusion proteins were verified by SDS-PAGE and Coomassie blue staining (data not shown).

Substrate trapping in vitro

Substrate trapping experiments were performed on cells treated with 10^{-4} mol/L pervanadate for 30 minutes (8). Briefly, cell lysates were incubated on ice for 30 minutes in the presence of 5 mmol/L iodoacetic acid to irreversibly inactivate endogenous PTPs. After incubation, DTT was added for 10 minutes at 4°C to a final concentration of 10 mmol/L, to inactivate iodoacetic acid. Lysates were then incubated overnight at 4°C with 20 μL GST fusion protein–coupled beads (10 μg/μL). After seven washes, affinity complexes were analyzed by immunoblotting.

Growth assays

For Matrigel outgrowth assays, 20,000 cells were resuspended in culture medium containing 10% FCS (0.5 mL) and added to 24-well plates that had been precoated with Matrigel (0.2 mL, 9.6 mg/mL; BD Biosciences). Phase-contrast optical photomicrographs were taken after 5 days. Alternatively, 20,000 cells were plated in triplicate in 24-well dishes that had been coated with 10 μg/cm² fibronectin (Becton Dickinson) in medium containing 10% FCS. Cells were fixed at various times with methanol, and their DNA content was determined by the diaminobenzoic acid fluorescence assay (22).

Cell attachment assay

For cell attachment assays, 96-well dishes were coated with fibronectin, Matrigel, or collagen 4 (Sigma) overnight (10 μg/cm²) and then blocked for 30 minutes with 0.5% bovine serum albumin (BSA) in PBS. Cells were trypsinized and resuspended at a final concentration of 10^6/mL in culture medium containing 10% FCS. Two hundred microliters of the cell suspension were added to the wells, and the plates were incubated at 37°C for 30 minutes. The medium was then carefully suctioned out, and the wells were washed three times with
culture medium. The colorimetric MTT assay was used to determine the number of remaining cells (adherent cells).

**Xenograft studies**

In vivo experiments were performed in compliance with the French guidelines for experimental animal studies (Direction des Services Vétérinaires, Ministère de l’Agriculture, agreement no. B 34-45). Before cell implantation, a 1-cm-long silastic tube (silicone tube inside diameter 0.062 in. and outside diameter 0.095 in.) filled with a solid mixture of estradiol and cholesterol as a carrier (1:10) was implanted subcutaneously in the interscapular region of Swiss nu/nu (nude) mice (Charles River Laboratories International). Two days later, $10^7$ cells were injected orthotopically into the thoracic mammary gland of athymic nude mice. Injected mice were examined every 3 or 4 days for tumor appearance. Tumor size was measured by a digital caliper, and tumor volumes were estimated according to the formula for an ellipse: $(\text{short dimension})^2 \times (\text{long dimension}) / 2$.

**Immunoprecipitation and immunoblot analysis**

Forty-eight hours after transient transfection, cells were washed twice in ice-cold PBS and lysed in lysis buffer [40 mmol/L Tris (pH 8), 5 mmol/L MgCl$_2$, 40 mmol/L Na$_3$P$_2$O$_7$, 1% Triton X-100, 10 mmol/L EDTA, 50 mmol/L NaF, 100 μmol/L Na$_4$P$_2$O$_7$, 1% TritonX-100, 10mmol/L AEBSF]. Equal amounts of each cell lysate were immunoprecipitated with 2 μg antibodies overnight at 4°C and then incubated for 2 hours with 40 μL protein A–Sepharose (6%) blocked in PBS, 4% BSA. Immune complexes were washed five times in lysis buffer before immunoblotting. Immune complexes or 100 μg of total proteins were separated on 7.5% or 10% SDS/polyacrylamide gels before immunoblotting, as described (8), with the indicated antibody.

**Immunofluorescence microscopy**

Forty-eight hours after transient transfection, HEK293 cells that had been plated on coverslips were fixed with 3.7% formaldehyde in PBS for 15 minutes and permeabilized with 0.5% Triton X-100 in PBS for 10 minutes. Immunolabeling was performed as described (8) with FITC or Texas red–conjugated secondary antibodies (Jackson ImmunoResearch Laboratories). Coverslips were mounted with mounting medium and visualized with a Bio-Rad 1024 CLSM system using a 60× (1.4 numerical aperature) planapochromatic objective (Nikon). A series of optical sections were collected and projected onto a single image plane using the laser sharp 1024 software and processing system.

**Statistical analysis**

The results of the cell proliferation, migration, adhesion, and tumor growth assays were assessed with the Student’s $t$ test. For immunohistochemistry study, the statistical significance of differences between groups was evaluated by the Mann-Whitney test or the Wilcoxon rank sum test. All statistical tests were two sided, and $P$ values <0.05 were considered to be statistically significant.

**Results**

**PTPL1 regulates breast cancer cell aggressiveness in vitro and in vivo**

We have previously shown that the PTPL1 mRNA expression level is negatively correlated with breast tumor aggressiveness (16). In this study, we compared PTPL1 expression at the protein level by immunohistochemical analysis of tissue microarray that contained five benign breast tissues adjacent to breast cancer, 34 primary infiltrating ductal carcinomas, and 10 matched pairs of primary tumors and lymph node metastases. Although the specimens were heterogeneous, PTPL1 expression in cancers was significantly lower than in benign tissues (Fig. 1A and B). Furthermore, lymph node metastases showed significantly lower levels of PTPL1 expression than paired primary tumors (Fig. 1A and C). In agreement with this result, highly invasive breast cancer cell lines (MDA MB 231, MDA MB 436, and BT 474) expressed lower PTPL1 levels than poorly invasive breast cancer cell lines (MCF7, T47D, ZR 75.1; Supplementary Fig. S1).

To directly address the role of PTPL1 in tumor aggressiveness, we engineered, from the noninvasive and poorly tumorigenic MCF-7 breast cancer cells, stable clones expressing a shRNA directed against PTPL1. PTPL1 expression was inhibited by ~95% in two different shRNA-PTPL1 clones (Fig. 2A). We investigated the effect of PTPL1 extinction on xenograft growth in nude mouse mammary fat pads. Tumor growth from the MCF-7 shRNA-PTPL1 clones was markedly higher than that of tumors from control clones (Fig. 2B), suggesting that PTPL1 actively contributes to a less aggressive phenotype.

**PTPL1 affects cell growth on extracellular matrix components, cell invasiveness, and adhesion**

To test biological parameters associated with tumor cell aggressiveness, which were quantifiable in rapid in vitro assays, we chose to downregulate PTPL1 expression by siRNA to avoid clone divergence. Five days after transfection in MCF-7 cells, PTPL1-siRNAs efficiently decreased PTPL1 expression by ~80% (Fig. 3A). We first studied the growth of cells as cell monolayers on plastic, and no differences were observed between cells transfected with PTPL1-siRNAs and control cells (data not shown). Considering that PTPL1 extinction is effective in vivo, we tested its effect on MCF-7 cells grown under more physiologic conditions. Inhibition of PTPL1 expression increased the size of the round colonies formed by MCF-7 cells seeded on Matrigel (a reconstituted basement membrane; Fig. 3B). Indeed, quantification of the large colonies showed comparable increases, 2.5-fold and 3-fold, by PTPL1-siRNA3 and PTPL1-siRNA4, respectively (Fig. 3C). Furthermore, time course experiments on cells plated on fibronectin, a basement membrane component, revealed that cells expressing PTPL1-siRNA grew exponentially with a doubling time of 28 hours, which was significantly lower than that of control cells (41 hours; Fig. 3D). Similar results were obtained with two other poorly tumorigenic breast cancer cell lines (Supplementary Fig. S2). These growth effects require coating with extracellular matrix components, suggesting that PTPL1 could play a role
in the signaling pathways initiated by cell-matrix interactions. We then analyzed cell adhesion and invasion, which are closely related to cell-matrix interactions. The invasive activity of MCF-7 cells was significantly increased in cells transfected with PTPL1 siRNA compared with control cells (Fig. 4A, left bars), suggesting an inhibitory role of PTPL1 on cell invasion. Because basal MCF-7 cell invasiveness is very low, we confirmed the inhibitory role of PTPL1 on another breast cancer cell line, T47D. PTPL1 extinction increased the invasiveness of these cells by ∼40%, depending on the substrate (Fig. 4B). Furthermore, immunofluorescence experiments on MCF-7 cells plated on fibronectin showed a drastic decrease in the number of focal adhesions after PTPL1 extinction, corroborating the influence of PTPL1 on the cell adhesion process (Fig. 4C).

**Src kinase is essential for PTPL1 biological activity, and knockdown of PTPL1 stimulates the Src kinase pathway**

Next, we sought to determine the mechanism of these effects. Some experiments have suggested that PTPL1 might inactivate Src kinase activity *in vitro* (18, 23). Moreover, the Src kinase family plays a major role in the regulation of focal adhesion and cell growth induced by cell-matrix interactions in normal and malignant cells (24, 25). Thus, we hypothesized that PTPL1 regulates breast cancer cell aggressiveness through inactivation of the Src kinase pathway. To test this hypothesis, we downregulated Src expression in PTPL1-siRNA MCF-7 cells (Fig. 5A) and analyzed their capacity to grow on Matrigel and fibronectin. Although the silencing of Src protein did not affect cell growth, it strongly inhibited the positive effect of PTPL1 knockdown (Fig. 5B and C), suggesting that PTPL1 expression inhibits Src signaling in basal conditions.

We therefore determined whether Src expression or activity was regulated by PTPL1 silencing. Src expression and Src Y530 phosphorylation, which locks human Src in an inactive conformation, were detectable and unaffected by PTPL1 silencing in native MCF-7 cells. SrcY419 phosphorylation, which is necessary for full Src catalytic activity, was low and only detectable after important protein loading and long enhanced chemiluminescence exposure. In these conditions, SrcY419 phosphorylation was increased in the presence of PTPL1 siRNA (Fig. 5D, first panel), indicating that PTPL1 inhibits Src activation. Then, we used MCF-7 cells transfected with a low amount of
Src expression vector (Fig. 5D) for further experiments on Src phosphorylation and signaling. The effect of PTPL1 extinction on cell growth on Matrigel was comparable in cells overexpressing Src and in native MCF-7 cells (Supplementary Fig. S3; Fig. 3C). Whereas SrcY530 was unaffected, SrcY419 phosphorylation was strongly increased in the presence of PTPL1 siRNA (Fig. 5D), corroborating the finding that the phosphatase counteracts Src-induced effects by inhibiting Src activation. We next analyzed whether PTPL1 also affected the activation of downstream Src substrates. Upon integrin stimulation, Fak is phosphorylated on tyrosine 397 (Y397), generating a high-affinity binding site for Src (25). Then, Src phosphorylates Fak on tyrosine residues, which are required for the full activation of Fak. Two of these residues are Y576/577. As expected, Fak-Y576/577 phosphorylation was increased when PTPL1 was silenced (Fig. 5D), although no changes were observed on Y397. The activated Fak/Src complex recruits proteins involved in cell adhesion, actin dynamics, proliferation, and survival, such as p130cas.

The proportion of p130cas coprecipitating with FAK was clearly increased in PTPL1 silenced cells (Fig. 5D). These results suggest that, through Src activation, PTPL1 silencing increases the tyrosine phosphorylation of critical proteins involved in integrin signaling.

**Src is a direct target of PTPL1**

Up to now, the effect of PTPL1 on Src phosphorylation has only been described *in vitro* (18, 23). Next, we tested whether PTPL1 overexpression was sufficient to change Src phosphorylation *in cellulo*. As Src kinase is mainly expressed as an inactive form in cells, we assessed PTPL1-induced phosphorylation changes in HEK293 cells overexpressing Src (to increase the amount of Src phosphorylated at Y419). Cells were cotransfected by expression vectors coding for wt PTPL1 or PTPL1-YF/DA, a catalytically inactive mutant of PTPL1. In the absence of PTPL1, Src was highly phosphorylated at Y419. This phosphorylation was abolished by the overexpression of wt PTPL1, whereas it was unaffected when the catalytically inactive PTPL1-YF/DA mutant was introduced in the cells (Fig. 6A). This result suggests that PTPL1 phosphatase activity is essential for Src hypophosphorylation.

Today, substrate trapping is currently used to identify PTP substrates (26). The *in vitro* assay was therefore performed on pervanadate-treated HEK293 cell lysates overexpressing a constitutively active form of Src, SrcY530F. Lysates were incubated with either GST alone, a recombinant PTPL1 catalytic domain fused to GST (GST-wt), or the substrate-trapping fusion protein GST-DA, which forms stable complexes with substrates. Whereas no protein retained by GST or GST-wt was detectable (Fig. 6B, lanes 2 and 3), the GST-DA trapping fusion protein specifically bound Y419-phosphorylated Src (Fig. 6B, lane 4). We next analyzed whether PTPL1 forms a complex with Src in cells. *In cellulo* substrate trapping was done in HEK293 cells expressing the constitutively active form of Src. Src was readily coimmunoprecipitated with the substrate-trapping mutant PTPL1-YF/DA (Fig. 6C, left panel, lane 3). However, no complex formation was detected with wt PTPL1 or control transfectants lacking PTPL1 (Fig. 6C, left panel, lanes 1 and 2). This specific interaction between the PTPL1 substrate-trapping mutant and Src was then confirmed in the reverse experiment in which the same lysates were immunoprecipitated with an anti-Src antibody. The substrate-trapping mutant complexed with Src, whereas wt phosphatase did not coprecipitate (Fig. 6C, right panel). Finally, we also studied the localization of PTPL1 and Src by confocal microscopy in HEK293 cells overexpressing Src and wt PTPL1 or PTPL1-YF/DA. PTPL1 and PTPL1-YF/DA both localized to the plasma membrane, as described previously (1). In cells overexpressing wt PTPL1, Src was detected in the cytoplasm and at the plasma membrane, leading to a partial colocalization with wt PTPL1 (Fig. 6D). In cells overexpressing PTPL1-YF/DA, Src was strongly delocalized to plasma membrane protrusions, and an intense colocalization with PTPL1 was observed (Fig. 6D, arrows). These data clearly show that PTPL1 directly regulates SrcY419 phosphorylation in intact cells.

**Discussion**

We have recently shown that PTPL1 expression level is an independent prognostic indicator of favorable outcome for patients with breast cancer (16). In this study, we show that PTPL1 expression is decreased in breast cancers and
metastases compared with benign breast tissues. Moreover, using in vitro and animal models, we evaluated the impact of PTPL1 in breast cancer cell aggressiveness and delineated the molecular mechanism responsible for this effect. We found that PTPL1 regulates the aggressiveness of a poorly tumorigenic mammary cell line because we observed that silencing of phosphatase led to increased tumor growth in athymic mice. In line with our findings, Spanos and collaborators (27) have recently shown that PTPL1 inhibition, induced either by the presence of human papilloma virus type 16 E6 or by a shRNA strategy, induces tumor growth of murine tonsil epithelial cells when it was associated with the oncogene Ras(V12) (27).

Here, we show that PTPL1 induces phenotypic changes of breast cancer cells that are dependent on the cell-matrix interactions, suggesting an involvement of the signaling pathways initiated by these interactions such as integrin/Fak/Src kinase signaling (25). Silencing of PTPL1 expression is associated with increased cell proliferation when the cells are coated on extracellular matrix components, although the increase is not observed when cells are plated on plastic. We also show enhanced invasiveness associated with decreased cell adhesion of PTPL1 knockdown cells. PTPL1 associates with a number of actin-associated molecules (2), and it may play a general role in modulating cell invasion through the binding and/or dephosphorylation of substrates involved in cell adhesion and migration. Indeed, PTPL1 has been implicated in the regulation of cell invasion in ovarian cancer cells. In these studies, PTPL1 regulates cell motility by negatively acting on the phosphorylation of either TRIP6, after lysophosphatidic acid stimulation (28), or human epidermal growth factor receptor 2 (HER-2) receptor in the

![Figure 3. Cell growth on extracellular matrices of siRNA-PTPL1 transfected cells. A, 5 days after siRNA transfection, MCF-7 cells were lysed and cell extracts were analyzed by immunoblotting with anti-PTPL1 and anti-actin antibodies. B and C, mock-transfected (control-siRNA) and PTPL1-siRNA (PTPL1-siRNA) cell lines were coated on Matrigel. B, phase-contrast optical photomicrographs after 5 days of culture, and photographs after p-iodonitrotetrazolium violet staining. C, colonies on Matrigel with a diameter of >40 μm were counted on four different fields per well. Data given are the mean ± SD of quadruplet samples. *, P = 0.003 and **, P < 0.001 versus control siRNA. One representative experiment of four is shown. D, 1 day after siRNA transfection, cells were plated on fibronectin-coated wells and the DNA was quantified at different days, as described in Materials and Methods. Cell growth was expressed relative to day 1 (mean ± SD of six wells from two independent experiments of four). **, P = 0.0001 versus control siRNA.](cancerres.aacrjournals.org/content/vol70/issue12/Figure3)

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HER-2–overexpressing SKOV3 cell line (29). On the other hand, the non–receptor tyrosine kinase Src alters the actin cytoskeleton and the adhesion networks that control cell migration and also transmits signals that regulate proliferation and cell survival (24, 25). Thus, in human cancers, elevated Src activity has been shown to increase growth rate (30) and migratory and metastatic potential (31) while inhibiting cell-cell adhesion (32). In human breast cancers, Src activity is reported to be elevated (33). The interaction of Src with numerous breast cancer–associated growth factors and signaling pathways, such as prolactin (34), epidermal growth factor receptor (35), extracellular signal-regulated kinase 1/2, phosphoinositide 3-kinase (36), and estrogen receptor (37), supports the notion that Src activity contributes to the growth and survival of breast cancer cells. Therefore, we investigated the implication of Src signaling in the PTPL1 biological effects. We showed that in MCF-7 cells, interruption of Src expression inhibited PTPL1 knockdown–dependent growth induction and Src activity was increased in PTPL1 knockdown cells. There are a number of candidate phosphatases for Src Y530 dephosphorylation, including cytoplasmic PTP1B (38), Shp1 (39), Shp2 (40), and transmembrane enzymes PTPα (41), PTPe (42), and PTPα (43). Conversely, no phosphatase was shown to dephosphorylate Src Y419 in intact cells, whereas some experiments have suggested that PTPL1 might inactivate Src kinase activity in vitro (18, 23). In this study, we use in cellulo dephosphorylation, colocalization, and substrate-trapping experiments both in vitro and in cellulo to identify the PTPL1 substrate in Src signaling. We showed that PTPL1 partially colocalizes with Src and specifically dephosphorylates Src on Y419. Recently, two studies have reported interacting proteins necessary for PTPL1 action on HER2 and Src signaling. Necl-2 forms a complex with PTPL1 and HER2, allowing silencing of HER-2/HER3 signaling by PTPL1 (44). RIL forms a complex with PTPL1 and...
Src, inducing a PTPL1-dependent Src dephosphorylation (45). In the latter case, experiments were performed in colon cancer cells in which inactivation of Src activity requires the presence of both PTPL1 and RIL (45). In agreement with Boumber and colleagues (46) who have shown that RIL transcription is suppressed in multiple types of human cancer cells, including breast cancer cells such as MCF-7 and T47D, no RIL expression was detected in the MCF-7 cells used in our experiments (data not shown), indicating that RIL was not implicated in PTPL1 action in our model. Moreover, the absence of interaction between Src and wt PTPL1 in substrate-trapping experiments indicated that PTPL1 and Src did not complex with any other partners, such as RIL or Necl-2, in our cell culture conditions.

In estrogen receptor–positive (ER-positive) breast cancer cells, acquisition of tamoxifen resistance is associated with increased levels of Src kinase activity and a more motile and invasive phenotype (47, 48). Pharmacologic inhibition of Src strongly enhances the inhibitory effects of tamoxifen on cell growth (49). Moreover, treating ER-positive breast cancer cells with a combination of a Src kinase inhibitor and tamoxifen suppresses growth and invasion and prevents the acquisition of tamoxifen-resistant growth (50). In ER-positive breast cancer cells, we have shown that PTPL1 is upregulated by antiestrogens and has a major role in the negative effect of tamoxifen on growth factor signaling (6). Our data link PTPL1 to Src in the regulation of breast cancer aggressiveness and corroborate the hypothesis that the metastatic spread and progression of

Figure 5. Implication of Src kinase activity for PTPL1 biological activity. A, 5 days after siRNA transfection, MCF-7 cells were lysed and cell extracts were analyzed by immunoblotting using anti-Src, anti-PTPL1, and anti-actin antibodies. One day after siRNA transfection, cells were plated on fibronectin (B) and Matrigel (C). Outgrowth of transfected cells was monitored as described in Fig. 2C and D. Data given are the mean ± SD of triplicate (B) and quadruplicate (C) samples. One representative experiment of three is shown. B, *, P ≤ 0.003. C, **, P ≤ 0.035. D, 1 day after siRNA transfection, MCF-7 cells were (second, third, and fourth panel) or were not (first panel) transiently transfected with the Src expression vector. The phosphorylation state of specific tyrosine residues in Src (top blot) or FAK (middle blot) was monitored by Western blotting using anti-pSrcY419 and anti-pSrcY530 or anti-pFakY397 and anti-pFak576/577 antibodies. Equivalent amounts of Src or FAK expression were confirmed by reprobing the blots with anti-Src and anti-FAK antibodies. For Fak/p130cas association (bottom blot), lysates were immunoprecipitated (IP) with anti-Fak antibody and immunoblotted with anti-p130cas. An equal immunoprecipitation level of FAK was confirmed by direct immunoblotting of the membrane after stripping with anti-Fak antibody.
this disease can be mitigated by blocking Src activation in tamoxifen-resistant breast cancer.

In summary, by identifying Src as the PTPL1 target in signaling pathways dependent on cell-matrix interactions, we presently describe a new mechanism by which PTPL1 inhibits tumor progression that may explain the increased aggressiveness of breast tumors expressing a low level of PTPL1 (Supplementary Fig. S2). This interplay between Src and PTPL1 points to the necessity for further studies on the mechanisms by which the catalytic activity of this phosphatase is regulated and reinforces the interest in new therapeutic routes combining antiestrogens and Src inhibitors.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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