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Gene Expression of the Lysophosphatidic Acid Receptor 1 Is a Target of Transforming Growth Factor Beta

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Abstract

The lysophosphatidic acid (LPA) receptor LPA₁/Edg2 is the first identified LPA receptor. Although its wide tissue distribution and biological functions have been well studied, little is known about how LPA_1 is transcriptionally regulated. In the current study, we showed that LPA_1 is a physiological target of transforming growth factor beta (TGF β)-mediated repression. In both normal and neoplastic cells, TGF β inhibits LPA₁ promoter activity, LPA₁ mRNA expression, and LPA1-dependent chemotaxis and tumor cell invasion. Knockdown of the TGF^β intracellular effector Smad3 or Smad4 with lentivirally transduced shRNA relieved these inhibitory effects of TGF β . Interestingly, the LPA₁ promoter contains two potential TGF β inhibitory elements (TIEs), each consisting of a Smad binding site and an adjacent E2F4/5 element, structurally similar to the TIE found on the promoter of the well-defined TGF β target gene *c-myc*. Deletion and point mutation analyses indicate that the distal TIE located at 401 bp from the transcription initiation site, is required for TGF β repression of the LPA₁ promoter. A DNA pull-down assay showed that the -401 TIE was capable of binding Samd3 and E2F4 in TGFβ-treated cells. TGFβ-induced binding of the Smad complex to the native -401 TIE sequence of the LPA₁ gene promoter was further verified by chromatin immunoprecipitation assays. We therefore identified a novel role of TGF β in the control of LPA₁ expression and LPA₁-coupled biological functions, adding LPA₁ to the list of TGFβ-repressed target genes.

Keywords

cancer; LPA; TGFβ; LPA₁; migration; invasion

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The authors declare no conflict of interest.

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INTRODUCTION

Lysophosphatidic acid (1-acyl-*sn*-glycerol-3-phosphate) is a naturally occurring intercellular mediator of diverse biological processes including neurogenesis, angiogenesis, wound healing, immunity, and carcinogenesis (1). LPA is produced by activated platelets during coagulation and thus is a normal constituent of serum (2). LPA is a ligand of multiple G protein-coupled receptors (GPCRs) (3). The LPA₁/Edg2, LPA₂/Edg4 and LPA₃/Edg7 receptors are members of the endothelial differentiation gene (Edg) family, sharing 50-57% homology in their amino acid sequences (3). In addition to the Edg LPA₁₋₃ receptors, GPR23/P2Y9/LPA₄ of the purinergic receptor family, and the related GPR92/LPA₅ and P2Y5/LPA₆ have been reported to be additional LPA receptors (4-6).

LPA₁ is expressed in most adult tissues and in embryonic cells (3). Only minor abnormalities such as craniofacial dysmorphism and defective sucking behavior were found in *lpa*₁-deficient mice (7). However, more recent studies of *lpa* -/-₁ mice subjected to various pathophysiological conditions revealed that LPA₁ is involved in initiation of neuropathic pain (8), embryonic and adult neurogenesis, and promotion of pulmonary and renal fibrosis (9, 10). Some of these biological functions of LPA₁ are attributed to the motility-stimulating activity of LPA in mammalian cells. Substantial evidence indicates that LPA₁ is the primary LPA receptor subtype to mediate LPA-dependent chemotaxis and tumor cell invasion (11). In contrast to the LPA₂ receptor that is commonly overexpressed in various cancers (12-14), gene expression profiling studies failed to show any consensus increase in LPA₁ expression between normal and malignant cells (15-19). Instead, some expression profiling or array analyses suggest decreases in LPA₁ mRNA expression in various malignancies (15, 17-19).

Several groups recently reported that LPA_I expression is repressed by Nm23 (20, 21). Nm23 is the first identified metastasis suppressor gene that, by definition, inhibits the process of metastasis but not growth of primary tumors (20). In human breast carcinomas, LPA₁ expression inversely correlated with that of Nm23 (21). However, little is known about how Nm23 represses LPA₁. Furthermore, there is no evidence that LPA₁ expression is elevated in metastatic cancer compared to primary tumors. Thus, LPA₁ expression is apparently controlled by complex regulatory mechanisms involving other unrecognized activators or repressors. In the present study, we showed for the first time that that transforming growth factor beta (TGF β), a platelet-derived cytokine co-present with LPA in the circulation and tumor microenvironments, represses *LPA₁* gene transcription and LPA₁-dependent motility-stimulating activity via a TGF β inhibitory element (TIE) containing both Smad and E2F4/5 binding sites on the *LPA₁* gene promoter. These results represent a novel form of crosstalk between TGF β and LPA signaling.

RESULTS

TGFβ inhibits expression of LPA₁

Previous studies showed that LPA stimulates production and release of TGF β (22, 23), trans-activates the intracellular effectors of TGF β (24) or cooperates with TGF β to regulate gene expression (25). However, little is known about whether TGF β communicates with LPA signal transduction to modify cellular responses to the multi-functional LPA. To

explore this possibility, we treated the MDA-MB-231 breast carcinoma and the SKOV-3 ovarian carcinoma cell lines with TGF β for 3 or 6 hours, and monitored changes in mRNA expression of LPA signaling molecules including various LPA receptors. MDA-MB-231 and SKOV-3 cells expressed LPA1, LPA2, LPA3, LPA4 and LPA6 mRNAs as shown by quantitative PCR (qPCR) (Fig. S1A). The treatment with TGF β for 6 hours resulted in 62% and 37% decreases in LPA1 mRNA levels in MDA-MB-231 and SKOV-3, respectively (Fig. 1A). TGF β did not downregulate mRNA levels of other LPA receptors present in these cells (Fig. S2). To generalize the observation of the specific inhibitory effect of TGF β on LPA₁, we examined a panel of breast, ovarian and other cancer cell lines, including BT-549, Caov-3 and DOV-13. Treatment with TGF\beta induced 30-67% decreases in LPA1 mRNA levels in these cell lines (Fig. 1B). Most of the cancer cell lines such as BT-549, SKOV-3 and DOV-13 were resistant to the growth inhibitory effect of TGF β as we reported recently (25). Thus, the inhibition of LPA₁ expression by TGF β was independent of the cytostatic program of TGF β . In addition, TGF β also downregulated expression of LPA₁ in normal primary and immortalized epithelial cells such as primary mammary epithelial cells (1001-8), primary ovarian epithelial cells (NOE-71), immortalized breast epithelial cell line MCF-10A, and immortalized ovarian surface epithelial cell line IOSE-29 (Fig. 1B). In an independent project to profile transcriptional effects of TGF β in the OE33 esophageal cancer cell line, we also observed TGFB-induced decrease in LPA1 mRNA by 45% (data not shown). The only exception to the negative regulation by TGF β was the DLD1 colon cancer cell line. DLD1 was deficient in T β RII as reported previously (26) and as evidenced by the inability of TGF β to induce Smad3 phosphorylation in this particular line (Fig. 1C). It is also worth noting that LPA₁ was highly expressed in DLD1 cells (27, 28), likely as a result of the absence of TGF β -mediated repression.

TGFβ attenuates LPA₁-dependent cell migration and invasion

Since TGF β represses LPA₁ mRNA expression, we anticipated that TGF β would attenuate LPA₁-dependent actions of LPA. Although each of the Edg-family LPA receptors may contribute to cell motility in certain cellular contexts, substantial evidence supports an essential and probably sufficient role for LPA₁ in driving random migration, chemotaxis and tumor cell invasion (27, 29, 30). In breast and ovarian cancer cell lines we examined, LPA stimulated robust chemotactic responses as analyzed by the transwell assay (Fig. 2A upper). LPA also drastically promoted invasion of these cells through Matrigel (Fig. 2A lower). In agreement with the crucial role of LPA1 in stimulation of cell motility, shRNA knockdown of LPA1 expression (Fig. S3) or pharmacological inhibition of LPA1 with Ki16425 decreased LPA-induced chemotaxis (Fig. 2C & 2D). On the other hand, TGF β only weakly increased migration of MDAMB-231, SKOV-3 and DOV-13 cells (Fig. 2A upper). This trend of increase in chemotactic migration towards TGF β was not statistically significant. Nevertheless, TGF β was capable of stimulating modest but significant increases in invasion of SKOV-3 and DOV-13 cells (Fig. 2A *lower*). However, the ability of TGF β to stimulate invasion of breast and ovarian cancer cell lines was much weaker than that of the potent motogen LPA. Levels of TGF β receptors did not seem to correlate with the responsiveness of these cells to TGF β (Fig. S1B.)

When MDA-MB-231, SKOV-3 and Dov-13 cells were co-stimulated with both LPA and TGF β , TGF β significantly inhibited LPA stimulation of migration and invasion. We observed 30-50% decreases in migration and 60-80% decreases in invasion in the presence of LPA and TGF β compared to the effects of LPA alone (Fig. 2A). Similarly, pretreatment of MDA-MB-231 and SKOV-3 cells with TGF β also significantly inhibited LPA-mediated cell migration and invasion (Fig. 2B). In all cell lines we examined, the TGF β mediated inhibition of invasion was more prominent than the effect of TGF β on migration. This was likely due to the longer incubation of the cells with TGF β during the invasion experiments. These data demonstrated that TGF β repression of LPA₁ expression was sufficient to impair LPA₁-dependent cell migration and invasion.

TGF β represses LPA₁ expression and LPA₁-dependent cell migration and invasion in a Smad-dependent manner

Upon binding of TGF β to its receptors, both Smad-dependent and Smad-independent pathways are activated by the kinase activity of TGF β receptors (T β Rs) (31). Regulatory Smads (R-Smads), such as Smad2 and Smad3, are phosphorylated by TBRs, and form heterodimer with Smad4 to translocate to the nucleus where the Smad complex regulates transcription of target genes (32). In addition, TGF\beta activates TβR-associated proteins and other intracellular signaling pathways such as MAPK, PP2A/p70S6K, RhoA and TAK1/ MEKK1 to elicit Smad-independent responses to TGF β (33). To elucidate the mechanism underlying TGF β repression of LPA₁, we examined the possibility for the participation of the Smad-dependent pathways in the process. Smad3, but not Smad2, was reported to be the R-Smad involved in binding to TIE to downregulate TGF β target genes, most notably *c-myc* (34). We therefore knocked-down Smad3 expression in MDA-MB-231 and SKOV-3 cells using lentivirally transduced shRNA. Expression of Smad3 protein was efficiently silenced by Smad3 shRNA (Fig. 3A). The silencing of Smad3 reduced the inhibitory effect of TGF β on expression of LPA₁ (Fig. 3B). Furthermore, in Smad3 knockdown cells, TGF^β no longer inhibited LPA-driven cell migration (Fig. 3C upper) and invasion (Fig. 3C lower). These results suggest a Smad3-dependent mechanism to repress LPA1 expression and LPA1-linked migration and invasion by TGFβ. In further support of this, Smad3 knockdown was accompanied by considerable increases in basal and LPA-induced cell migration and invasion (Fig. 3C). Likewise, shRNA knockdown of Smad4, the co-Smad in these cells, also inhibited the effects of TGF β on LPA₁ expression and LPA₁-dependent cell migration (Fig. 3D, 3E & 3F).

TGF β represses the transcriptional activity of the LPA₁ gene promoter which contains two potential TIEs

The TGF β -Smad pathway both activates and represses gene transcription. There is a long list of TGF β activated targets such as *type I collagen* and cyclin-dependent kinase inhibitors $p21^{Cip1}$ and $p15^{Ink4b}$. Conversely, only a few TGF β -repressed genes have been well defined with the *c-myc* and *Id1* being the best characterized. Downregulation of *c-myc* by TGF β is mediated by the Smad3-Smad4-E2F4/5-p107 complex that binds to the consensus TGF β inhibitory element (TIE, GGCTTGGCGGGAAA) which consists of a repressive Smad binding element (RSBE) (35) and an E2F binding site on the *c-myc* gene promoter. Different from *cmyc*, *Id1* is inhibited by TGF β through combined effects of a Smad binding element

(SBE) and a separate CREB binding site that recruits the ATF3 repressor to the *Id1* gene promoter (36). Interestingly, analysis of the human LPA_1 gene promoter sequences revealed the presence of two potential TIEs, one located at -401 (designated -401 TIE) and the other at -40 (designated -40 TIE) from the transcription initiation site (Fig. 4A). The composite TIE consisting of the Smad and E2F4/5 binding sites is present only in the LPA_1 gene promoter but not in the promoters of other LPA receptors (LPA_{2-6}) (Fig. S4). Between these two TIEs, there is also an SBE (-324 GTCT -321) and a probable ATF site (-348 TGACGCTC -341) with 5 out of 8 nucleotides matching with the ATF consensus sequence (TGACGTCA).

We therefore cloned a 1242-bp fragment of the LPA_I gene promoter (-1156 to +86) into the pGL2-Basic-Luc vector to construct pGL2-LPA₁-Luc. MDA-MB-231 and SKOV-3 cells were transfected with pGL2-LPA₁-Luc and cultured with TGF β or vehicle for 16 hours before measurement of luciferase activity in cell lysates. TGF β treatment resulted in modest but consistent decrease in luciferase activity (Fig. 4B). Deletion of the proximal -401 TIE (named del in Fig. 4) at -366 abolished the negative effect of TGF β on the LPA_I promoter-driven luciferase activity (Fig. 4B), suggesting that the deleted sequence containing the -401 TIE, rather than the potential SBE-ATF3 or the further downstream -40 TIE, is the major site for TGF β repression of LPA_I transcription. Indeed, similar to the deletion mutant, point mutation of the -401 TIE (GGC<u>TTTGG</u>CGCG to GGCT<u>AATT</u>CGCGC) also eliminated the repressive effect of TGF β on the LPA_I promoter activity. However, mutation of the -401 TIE (GGC<u>TTTCG</u>CGCC) only slightly reduced the effect of TGF β , which was statistically insignificant. Taken together, these experiments indicate that the -401 TIE site is required for TGF β -Smad mediated repression of the LPA_I gene.

Smad complex binds to the -401 TIE of the LPA₁ promoter

To gain evidence that the Smad complex binds to the LPA_1 promoter at the -401 TIE, we performed DNA pull-down assay using biotinylated double-stranded oligonucleotides corresponding to the sequences between -413 and -378 that included the -401 TIE of the LPA_1 promoter. MDA-MB-231 and SKOV-3 cells were treated for 1 hour with TGF β or vehicle. The 36-bp DNA fragment was incubated with cell lysates to allow binding and precipitating Smad3 and E2F4 as detailed in Materials and Methods. As demonstrated in Fig. 5A, co-precipitated Smad3 and E2F4 were detected from TGF β -treated cells but not from vehicle-treated control cells, suggesting that the 36-bp DNA fragment is capable of binding active Smad3 and E2F4.

To determine if TGF β induces Smad3 and E2F4 binding to the native -401 TIE region of the *LPA*₁ promoter, we performed chromatin immunoprecipitation (ChIP) assays in MDA-MB-231 and SKOV-3 cells. The qPCR analysis of Smad3 immunoprecipitates from MDA-MB-231 and SKOV-3 cells showed 3.8- and 3.7-fold induction of Smad3 binding to the -401 TIE (Fig. 5B). We also observed 2.0- and 1.8-fold increases in Smad3 binding to the -401 TIE in MDA-MB-231 and SKOV-3, respectively. Thus TGF β induced physical binding of activated Smad3 to the -401 TIE and to a lesser extent, to the -40 TIE of the *LPA*₁ promoter. The binding of E2F4, another partner of the Smad complex, to the -401 TIE also increased by 2.5 and 2.7 fold following TGF β treatment of MDA-MB-231 and SKOV-3

cells. However, no significant increase in binding of E2F4 to the -40 TIE in TGF β -treated MDA-MB-231 cells was observed. In these ChIP experiments, we included the *c-myc* TIE as positive controls and confirmed the binding of Smad3 and E2F4 to the *c-myc* TIE in SKOV-3 cells treated with TGF β . In sum, these experiments provide mechanistic insight into the TGF β -mediated repression of *LPA*₁ transcription and LPA₁-linked biological activities.

DISCUSSION

In the present study, we showed that the LPA_I gene is a direct target of TGF β -mediated repression. This inhibitory effect of TGF β on LPA₁ expression is detected in both normal and neoplastic cells with intact T β R and Smad signaling. Importantly, the inhibition of LPA_I by TGF β is sufficient to suppress the LPA₁-dependent migratory responses to LPA. The detailed analysis of the underlying mechanism indicates that TGF β triggers downregulation of LPA_I through activation of Smad and binding of the Smad-E2F4 complex to the -401 TIE of the LPA_I gene promoter, a process analogous to the well-defined mode of repression of *c*-*myc* (34).

Among the multiple LPA receptors, LPA₁ is the only receptor subtype transcriptionally repressed by the TGF β -Smad signaling. In TGF β -challenged cells, Smad3 forms a large complex with E2F4/5-p107 and Smad4 in the cytoplasm, translocates to the nucleus and binds to the TIE motif where the complex recruits other co-repressors and silences gene expression (37). Hence both Smad binding site and the conjugated E2F4/5 element are instrumental to TGF β repression of target genes (34). Extensive analysis of the promoter sequences of other LPA receptors does not identify any TIE consensus sequence in the LPA₄, LPA₅ and LPA₆ promoters (Fig. S4). There are putative RSBE in the LPA₂, and LPA₃ promoter sequences. However, none of these RSBEs is closely linked to a nearby E2F4/5 binding site. It is intriguing that the two TIE sites of the LPA_{I} gene promoter do not function equally. The -401 TIE was identified to be the major one for Smad-mediated repression of LPA_1 while the contribution of the -40 TIE was negligible. This difference could be attributed to the fact that only 4 out of 11 nucleotides match with the consensus E2F4/5 sequence at the -40 TIE while the -401 TIE matches the consensus at 9 out of 11 nucleotides. Alternatively, the TIE location relative to the transcriptional initiation site or other regulatory sequences beyond the TIE sites could influence the interaction with the Smad complex and the transcriptional repression..

The biological function of LPA₁ has been a subject of extensive studies in both *in vitro* cell culture and genetic animal models (8-10, 27). Compared to other LPA receptors, LPA₁ is most widely expressed (3). The nearly ubiquitous distribution of LPA₁ has led to the assumption that LPA₁ is constitutively expressed. However, a few recent studies have hinted at the regulation of LPA₁ by intracellular and extracellular cues (38, 39). The most exciting observation is that LPA₁ is one of the target genes repressed by the metastatic tumor suppressor Nm23 (20). Another study showed that germline polymorphism of fibroblast growth factor receptor 4 (FGFR4) at residue 388 (G388R) correlates with enhancement of LPA₁ expression and more aggressive migratory and invasive responses to LPA in tumors carrying R388 FGFR4 (40). Although LPA₁ expression may be indeed regulated by Nm23

and FGFR4, it is not known whether or how these modulators affect transcription, stability or translation of LPA_1 . The results from the current study represent the first example that an endogenous factor could transcriptionally restrain expression of LPA_1 and LPA₁-dependent cellular effects.

The roles of LPA and LPA receptors in cancer have drawn considerable attention in recent years. The LPA₂ receptor is overexpressed in ovarian, breast, thyroid and rectal colon cancers (15-19). The transgenic and knockout mouse models further support an oncogenic role of LPA₂ (14, 41). Expression of LPA₁, on the other hand, does not show consensus increases from normal to malignant phenotypes. Instead, several independent groups have reported a tendency of downregulation of LPA₁ in diverse cancers (15, 17-19, 42, 43) in sharp contrast to the upregulation of LPA₂ in malignant diseases. The findings of the current study offer a plausible explanation to this phenomenon. The enhanced TGF β signaling during cancer development and progression may serve as a repressor of expression of *LPA₁* but not other LPA receptors.

TGFβ controls a multitude of biological activities in mammalian cells. It inhibits proliferation of epithelial cells and thus plays a part in early tumor suppression. However, TGF β frequently fails to induce growth arrest in transformed epithelial cells. Instead, TGF β stimulates migration and invasion of cancer cells, thereby promoting the metastatic potential in advanced cancer (44). This presumed effect of TGF β on tumor cell invasion and metastasis is largely based on *in vitro* assays involving only TGF β as a motogen (45). The conclusion may not truly reflect the physiological role of TGF^β in *in vivo* conditions where tumor cells are exposed to a complex mix of multiple chemokines, cytokines, nutrients and growth factors. We found in the current study that the effects of TGF β on cell motility could be opposite under different conditions. In the cancer cell lines we tested, TGF β itself was a weak stimulus of tumor cell invasion. In the presence of LPA, however, the role of TGFB was reversed, counteracting the strong motogenic activity of LPA. Since both TGF β and LPA are present in the circulation and malignant effusions, TGF^β probably acts as a negative regulator of cell motility in physiological and pathophysiological conditions. By extension, the findings of the current work underscore the importance of crosstalk between LPA and other coexisting factors in coordination of the overall cellular responses.

MATERIALS AND METHODS

Materials

LPA (1-oleoly, 18:1) was obtained from Avanti Polar Lipids, Inc. (Alabaster, AL). Prior to use, LPA was dissolved in PBS containing 0.5% fatty acid-free bovine serum albumin (BSA) obtained from Roche (Indianapolis, IN). TGF β was obtained from PeproTech Inc. (Rocky Hill, NJ). Anti-Smad3 and Smad4 antibodies were from Abcam (Cambridge, MA). Tubulin α/β antibody was obtained from Cell Signaling (Danvers, MA). Anti-E2F4 antibody was from Santa Cruz Biotech (Santa Cruz, CA). FBS was obtained from Atlanta Biological (Atlanta, GA). All primers were synthesized by Operon Biotechnologies, Inc. (Huntsville, AL). Biotinylated dsDNA were synthesized by IDT (Coralville, IA). TRIzol and cell culture reagents were obtained from Invitrogen Inc. (Carlsbad, CA). The RT kit, TaqMan gene expression assays, SYBR Green PCR mix and QPCR master mix were obtained from

Applied Biosystems (Carlsbad, CA). The transfection reagent LT1 was obtained from Mirus (Madison, WI). Plasmid DNA was purified using the endo-free purification kit from Qiagen (Valencia, CA).

Cell Culture

MDA-MB-231 was provided by Dr. S. Spiegel (Virginia Commonwealth University) and was maintained in Dulbecco modified Eagle medium (DMEM) with 10% FBS and 100 U/ml penicillin and 100 μ g/ml streptomycin. IOSE-29 was originally obtained from Dr. N. Auersperg (University of British Columbia, Canada) and cultured as described previously (46). Primary Mammary epithelial cells (1001-8) and primary ovarian epithelial cells (NOE-71) were provided by Dr. Y. Yu (MD Anderson Cancer Center) and were cultured in HuMEC Ready Medium (Invitrogen) and 50:50 M199/F12 medium with 10% FBS, 20 ng/ml EGF and gentamicin (10 μ g/ml), respectively. MCF-10A was provided by Dr. D. Gewirtz (Virginia Commonwealth University) and cultured in DMEM/F12 medium with 5% horse serum, 10 μ g/ml insulin, 20 ng/ml EGF, 100 ng/ml cholera toxin and 0.5 μ g/ml hydrocortisone. Other cancer cell lines used in the study were cultured in RPMI 1640 supplemented with 10% FBS and antibiotics as we described previously (47).

Migration and invasion assays

Cell migration was measured using the Transwell chambers (Costar, Corning, NY). Transwells were coated with 10 µg/ml type I collagen and placed in the lower chamber containing serum-free medium supplemented with vehicle, TGF β , LPA or LPA+TGF β . Cells suspended in serum-free medium containing 0.01% fatty acid-free BSA were added to the upper chamber at 2 × 10⁴ cells/well. Cells were allowed to migrate for 6 hours at 37°C. Non-migrated cells were removed from the top filter surface with a cotton swab. Migrated cells attached to the underside of the Transwell were washed with PBS and stained with crystal violet and counted under a microscope. The invasion of tumor cell lines was measured using the growth factor–reduced Matrigel invasion chambers (BD Biosciences, San Jose, CA). The assays were performed as migration assays except that the cells were incubated for 20 hours. All migration and invasion assays were repeated three times with consistent results.

shRNA

short hairpin RNA (shRNA)-expressing lentivirus constructs were generated using pLV-RNAi vector (Biosettia, San Diego, CA). The Smad3 target sequences Smad3sh1 GTGACCACCAGATGAACCA (48), Smad3sh2 GGATTGAGCTGCACCTGAATG (49) and Smad4 target sequences Smad4sh1 GCAGGTGGCTGGTCGGAAA (50), Smad4sh2 GCCAGCTACTTACCATCATA (51) were inserted to the pLV-RNAi plasmid following the manufacturer's protocol. The LPA₁ shRNA lentiviral vectors were obtained from Dr. S. Huang (Medical College of Georgia) (11). The shRNA lentiviruses were propagated in 293FT cells. The culture supernatants were used to infect cancer cell lines. The GFPpositive cells were sorted out using flow cytometer 96 hours post virus infection.

qPCR

Total cellular RNA was isolated using Trizol (Invitrogen). Complementary DNA (cDNA) was synthesized from RNA (1 µg, random primers) using the High-Capacity cDNA Reverse Transcription Kit from Applied Biosystems. The mRNA levels of individual LPA receptors were determined using gene specific probes, the TaqMan Universal PCR Master Mix and the 7900HT Prism Real-Time PCR System.

Luciferase vectors, deletion, and site-directed mutagenesis

The luciferase reporter vector pGL2-LPA₁-Luc containing -1156 to +86 was generated by PCR amplification of the LPA₁ promoter sequence (forward 5'-GCACTCGAGTGCAAAGCTACACTGGGAAA-3', reverse 5'-GCAAAGCTTCACACTCTCACTGGCACTCG-3'). The PCR product was inserted into pGL2-Basic-Luc at XhoI and HindIII sites. The deletion mutant (-366 to +86) was made by PCR amplification of the fragment from pGL2-LPA₁-Luc (forward 5'-GCACTCGAGCTGACGCTCCCTGAGTGG-3', reverse 5'-GCAAAGCTTCACACTCTCACTGGCACTCG-3') and re-inserted into the pGL2-Basic-Luc at the XhoI and HindIII sites. The promoter sequences in these plasmids were verified by automatic sequencing. The -401 and -40 TIE consensus sites within pGL-LPA₁-Luc were converted into inactive sequences by site-directed mutagenesis. The wild type -401 TIE 5'-GGCTTTGGCGCG and wide type -40 TIE 5'-GGCTTCGCGC were converted into 5'-GGCTAATTCGCGC and 5'-GGCAATTCGCC, respectively. For luciferase assays, MDA-MB-231 and SKOV-3 were transfected with luciferase vectors along with β -gal plasmid using TransIT-LT1 (Mirus Bio). About 48 to 60 hours after transfection, the cells were treated with TGF β or vehicle for 16-20 hours. Cell extracts were prepared and assayed for luciferase activity using the luciferase assay kit from Promega.

DNA pull-down assay

Lysates of MDA-MB-231 and SKOV-3 cells were prepared by brief sonication in the HKMG buffer (10 mM, Tris-HCl, pH 7.9, 100 mM KCl, 5 mM MgCl₂, 10% glycerol, 1 mM DTT, 0.1% NP40 and protease inhibitors) using the Fisher Scientific Sonic Dismembrator Model 100, followed by 10 minutes of centrifugation at $12,000 \times g$ at 4 °C. Cellular proteins (400 µg) were incubated with 4 µg of biotinylated double-stranded oligonucleotides (5'-CCCTACTGCCCGGCTTTGGCGCGCTGGCAGGAGGAG–biotin) for 16 hours at 4 °C. The M-280 Streptavidin Dynabeads (Invitrogen) (30 µl) were added to each sample and incubated for another hour at 4 °C. The Dynabeads were washed three times with PBS before western analysis of Smad3 or E2F4.

ChIP assay

TGF β or vehicle-treated MDA-MB-231 and SKOV-3 cells were cross-linked with 1% formaldehyde for 10 minutes at room temperature. The cells were lysed for 10 minutes in ice-cold lysis buffer (5 mM HEPES, pH 8.0, 80 mM KCl, 1% NP40 and protease inhibitors). The nuclear fraction that was recovered by centrifugation (5 minutes at 5000×*g*) was resuspended in a ChIP assay buffer (50 mM HEPES, pH 8.0, 10 mM EDTA, 1% SDS, and protease inhibitors) and sonicated on ice to achieve an average chromatin length of

200-1000 bp. The sonicated samples were pre-cleared by incubation with Protein G Dynabeads (Invitrogen). The material recovered from the equivalent of 10^6 cells was incubated for 16 hours at 4 °C with 2 µg of either normal rabbit IgG (Santa Cruz) or anti-Smad or anti-E2F4 antibodies. Protein G Dynabeads were added and incubated for 2 hours. The DNA-protein-beads mixes were washed sequentially once with a low salt buffer (20 mM Tris, pH 8.0, 150 mM NaCl, 2 mM EDTA, 0.1% SDS, 1% Triton 100), once with a high salt buffer (20 mM Tris, pH 8.0, 500 mM NaCl, 2 mM EDTA, 0.1% SDS, 1% Triton 100), once with LiCl buffer (10 mM Tris-HCl, pH 8.0, 0,25 M LiCl, 1 mM EDTA, 1% deoxycholate, 1% NP-40), and finally twice with TE buffer (10 mM Tris-HCl, pH 8, 1 mM EDTA). The specifically bound complexes were eluted from the Protein G Dynabeads by incubation twice for 15 minutes at 65 °C with TE elution buffer (10 mM Tris-HCl, pH 8, 1 mM EDTA, 1% SDS). The immunoprecipitated complexes and the starting material (input) were incubated overnight at 65 °C to reverse cross linking, then treated with RNase A followed by proteinase K and purified using the QIAquick Spin Columns (Qiagen, Valencia, CA). The DNA samples were recovered in 100 µL H₂O, and analyzed by qPCR using SYBR Green. Details of the primer used for qPCR were listed in Table 1.

Statistics

All numerical data were presented as mean \pm SD of triplicate assays, representative of three independent experiments. The statistical significances were analyzed using Student's *t* test where *p*<0.05 was considered statistically significant. In all figures, the statistical significances were indicated with * if p<0.05 or ** if p<0.01.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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A. MDA-MB-231 and SKOV-3 cells were cultured with TGF β (2.5 ng/ml) or vehicle for 3 and 6 hours. LPA₁ mRNA levels were determined by RT and qPCR. The mRNA levels of LPA₁ in TGF β treated cells were presented as percentages relative to those in control cells (defined as 100%). *B*. Multiple cancer cell lines, immortalized breast (MCF-10A) and ovarian (IOSE-29) epithelial cell lines, primary mammary (1001-8) and ovarian (NOE71) epithelial cells were treated for 6 hours with TGF β (2.5 ng/ml) and analyzed for LPA₁ mRNA expression as in *A*. *C*. Cancer cell lines and primary cells were treated with TGF β (2.5 ng/ml) or vehicle for 1 hour before lysis with SDS sample buffer and immunoblotting analysis of Smad3 phosphorylated at Ser423/425. The intensity of phospho-Smad3 in each cell line was quantified by densitometry and presented as fold of that in control cells (arbitrary 1.0).

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Figure 2. TGF^β attenuates LPA₁-dependent cell migration and invasion

A. The chemotactic responses to TGF^β (2.5 ng/ml), LPA (5 µM), or LPA+TGF^β in the breast cancer cell line MDA-MB-231, and the ovarian cancer cell lines SKOV-3 and DOV-13 were measured by transwell chambers (*upper*). The cells $(2 \times 10^4 \text{ cells/well})$ were loaded to the upper wells and allowed to migrate for 6 hours. The migrated cells on the underside of the Transwell were stained with crystal violet, counted under a microscope and presented as numbers of cells/well. Cell invasion induced by TGF β (2.5 ng/ml), LPA (5 μ M), or LPA+TGF β in MDA-MB-231, SKOV-3 and DOV-13 cells was measured with the growth factor-reduced Matrigel invasion chambers (lower). The experiment was performed as the migration assay except that the cells were allowed to invade for 20 hours. B. MDA-MB-231 and SKOV-3 cells were pre-treated with TGFB (2.5 ng/ml) for 6 hours before analysis of LPA-induced migration (upper) and invasion (lower) as described in A. C. Expression of LPA1 in MDA-MB-231 and SKOV-3 cells was silenced with lentivirally transduced shRNA. The chemotactic migration of these knockdown and control cells induced by LPA was analyzed as described in A. D. LPA-induced migration of MDA-MB-231 and SKOV-3 cells was analyzed in the presence or absence of Ki16425 (Ki) (10 μM).



Figure 3. TGF β represses LPA₁ in a Smad-dependent manner

A. Expression of Smad3 in MDA-MB-231 and SKOV-3 cells was silenced with lentivirally transduced shRNA and confirmed by immunoblotting. *B*. Smad3 shRNA and control shRNA-transduced MDA-MB-231 and SKOV-3 cells were treated with TGF β (2.5 ng/ml) or vehicle for 6 hours followed by RT and qPCR analysis of LPA₁ mRNA. *C*. LPA-induced chemotactic migration (*upper*) and invasion (*lower*) of control and Smad3 knockdown cells were analyzed in the absence or presence of TGF β (2.5 ng/ml). *D*, *E* & *F*. The effects of TGF β on LPA₁ expression and LPA-induced migration were analyzed in Smad4 shRNA knockdown cells as detailed for the experiments in Smad3-silenced cells in *A*, *B* & *C*.



Figure 4. TGF β represses the transcriptional activity of the *LPA*₁ gene promoter containing TIEs *A*. DNA sequences of two potential TIEs of the human *LPA*₁ promoter were compared with that of the *c-myc* TIE (*upper*). The potential Smad, E2F4/5 and ATF3 binding sites were indicated. The *LPA*₁ promoter (-1156 to +86) was cloned into pGL2-Basic-Luc to constructed the pGL2-LPA₁-Luc luciferase reporter (WT) (*lower*). The deletion (del) and point mutations of each TIE (-401 Mut and -40 Mut) were made as described in Materials and Methods. *B*. MDA-MB-231 and SKOV-3 cells were transfected with the indicated plasmids and cultured with TGF β or vehicle for 16 hours before luciferase activities were determined. The results were presented as percentages relative to the values of the vehicle control cells (defined as 100%).



Figure 5. TGF β induces occupancy of the Smad complex to the *LPA*₁ gene promoter *A*. Cell extracts from MDA-MB-231 and SKOV-3 cells treated with TGF β (2.5 ng/ml) or vehicle for 1 h our were incubated with biotinylated DNA fragment containing the -401 TIE and strepatavidin beads. The DNA precipitates (DNAP) were subjected to western blot analysis for Smad3 and E2F4. Whole cell lysates were included as input. *B*. ChIP assays were performed to examine the binding of Smad3 and E2F4 to the -40 and -401 TIEs of the *LPA*₁ promoter and to the *c-myc* TIE (positive controls). The immunoprecipitation of Smad3 and E2F4 was verified by western blotting analysis of immunoprecipitates (IP) and whole cell lysates (WCL). The binding was quantitated by qPCR using SYBR Green and the specific primers listed in Table 1. The results were normalized to the Ct values of inputs and presented as percentages of inputs. ND: not detectable.

Table 1

Primers used in ChIP assays

-401 Forward	5'-GTGCTACGTGGAACAAGCAG-3'
-401 Reverse	5'-GGCGGGACAGTGTGAGC-3'
-40 Forward	5'-AGCGAGCGCAGGTAAGG-3'
-40 Reverse	5'-GCACCCACACTCTCACTGG-3'
c-myc TIE Forward	5'-TTATAATGCGAGGGTCTGGA-3'
c-myc TIE Reverse	5'-TGCCTCTCGCTGGAATTACT-3'