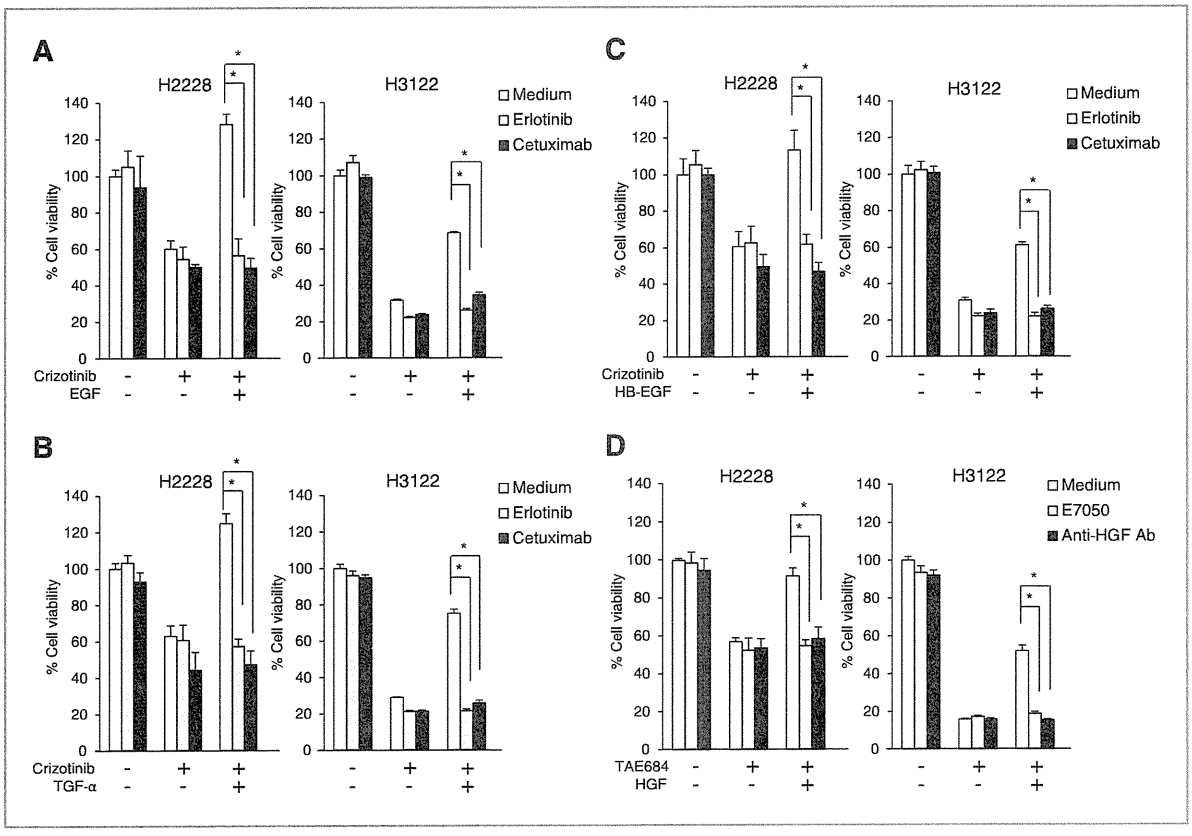

Figure 6. Ligand-triggered resistance to ALK inhibitors is abrogated by inhibitors of both HGF-Met and EGFR. A–C, the EGFR inhibitors erlotinib and cetuximab abrogated EGFR ligand-induced crizotinib resistance in EML4-ALK lung cancer cells. H2228 and H3122 cells were treated for 72 hours with or without crizotinib (100 nmol/L) and/or EGF (100 ng/mL), TGF-α (100 ng/mL), or HB-EGF (10 ng/mL) in the presence or absence of erlotinib (1 μmol/L) or cetuximab (2 μg/mL). Cell growth was determined by MTT assays. *, $P < 0.01$ (one-way ANOVA). Each experiment included triplicate determinations, and each experiment was repeated at least 3 times independently. D, Met-TKI E7050 or Anti-HGF antibody abrogated HGF-induced TAE684 resistance in EML4-ALK lung cancer cells. H2228 and H3122 cells were treated for 72 hours with or without TAE684 (100 nmol/L) and/or HGF (50 ng/mL) in the presence or absence of E7050 (1 μmol/L) or anti-HGF–neutralizing antibody (2 μg/mL). Cell growth was determined by MTT assays. *, $P < 0.01$ (one-way ANOVA). Each experiment included triplicate determinations, and each experiment was repeated at least 3 times independently.

Met (5). Selective ALK inhibitors are expected to be effective against *EML4-ALK* lung cancer cells, even after acquiring *ALK* amplification and *ALK* second mutations and becoming refractory to crizotinib (7, 35). Our findings, however, suggest that HGF-triggered resistance may be directed against selective ALK inhibitors, not crizotinib. Future clinical trials with selective ALK inhibitors may reveal the class of ALK inhibitors that is more beneficial for *EMK4-ALK* lung cancer patients.

EML4-ALK- and *EGFR*-mutant lung cancers show dramatic responses to ALK inhibitors and EGFR-TKIs, respectively (5, 36, 37). Complete responses, however, are rarely achieved, despite these cells express the target (EML4-ALK or mutant EGFR) of the drug. Low expression of BIM, a proapoptotic molecule, may explain, at least in part, the variations in sensitivity of *EGFR*-mutant lung cancer to EGFR-TKIs (38). This heterogeneous sensitivity may also be explained by HGF, as HGF is expressed more or less equally in *EGFR*-mutant lung tumors sensitive to EGFR-TKIs (32). Therefore, EGFR ligands in EML4-ALK lung tumors may be involved in their heterogeneous response to crizotinib. It is also curious whether ligand-triggered resistance is an independent mechanism or one that provided partial resistance when combined with another mechanism. Because crizotinib is expected to be approved in Japan to treat EML4-ALK lung cancer in 2012, we are planning a study to assess this possibility in clinical specimens.

In conclusion, we found that receptor ligands, such as EGFR ligands and HGF, could cause resistance to the ALK inhibitors crizotinib and/or TAE684 by activating bypass survival signals. These ligands and growth factors may be produced by host stromal cells, which constitute the cancer microenvironment. Paracrine HGF from stromal fibroblasts may also trigger resistance to EGFR-TKIs in EGFR-mutant lung cancer cells by activating bypass signals (22). Collectively, these observations suggest that paracrine receptor activation by the microenvironment

may be an important mechanism inducing resistance to molecular targeted drugs in oncogene-activated lung cancer cells. These findings suggest that targeting of receptor ligands may result in more successful therapy in lung cancer.

Disclosure of Potential Conflicts of Interest

S. Yano received honoraria from Chugai Pharma and AstraZeneca and research fundings from Chugai Pharma and Eisai co., ltd. H. Mano received honoraria from Pfizer Inc., and T. Nakagawa and T. Uenaka are employees of Eisai co., ltd.

Authors' Contributions

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Development of methodology: T. Yamada
Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): T. Yamada, H. Mano
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): K. Kita, T. Nakagawa, T. Uenaka
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Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): J. Nakade, S. Nanjo, T. Nakamura, K. Matsumoto, M. Soda, H. Mano, S. Yano
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TGF-β-induced mesenchymal transition of MS-1 endothelial cells requires Smad-dependent cooperative activation of Rho signals and MRTF-A

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Endothelial–mesenchymal transition (EndMT) plays important roles in various physiological and pathological processes. While signals mediated by transforming growth factor (TGF)-β have been implicated in EndMT, the molecular mechanisms underlying it remain to be fully elucidated. Here, we examined the effects of TGF-β signals on the EndMT of mouse pancreatic microvascular endothelial cells (MS-1). By addition of TGF-β2, MS-1 cells underwent mesenchymal transition characterized by re-organization of actin stress fibre and increased expression of various mesenchymal markers such as α-smooth muscle actin (α-SMA) through activation of Rho signals. Whereas activation of Rho signals via TGF-β-induced non-Smad signals has been implicated in epithelial–mesenchymal transition (EMT), we found that Arhgef5, a guanine nucleotide exchange factor, is induced by Smad signals and contributes to the TGF-β2-induced α-SMA expression in MS-1 cells. We also found that TGF-β2 induces the expression of myocardin-related transcription factor-A (MRTF-A) in a Smad-dependent fashion and its nuclear accumulation in MS-1 cells and that MRTF-A is required and sufficient for TGF-β2-induced α-SMA expression. These results indicate that activation of Smad signals by TGF-β2 have dual effects on the activation of Rho signals and MRTF-A leading to the mesenchymal transition of MS-1 endothelial cells.

Keywords: TGF-β2/Rho/MRTF-A/EndMT/α-SMA.

Abbreviations: ALK, activin receptor-like kinase; EMT, epithelial–mesenchymal transition; EndMT, endothelial–mesenchymal transition; FCS, fetal calf serum; GEF, guanine nucleotide exchange factor; MMP2, matrix metalloproteinase 2; PECAM1, platelet-endothelial cell adhesion molecule-1; R-Smad, receptor-regulated Smad; α-SMA, α-smooth muscle actin; TGF-β, transforming growth factor-β.

Epithelial–mesenchymal transition (EMT) converts polarized epithelial cells to motile mesenchymal cells (*1*), and plays important roles in gastrulation and cancer cell invasion (*2*). During EMT, epithelial markers including E-cadherin are down-regulated and the mesenchymal markers such as α-smooth muscle actin (α-SMA) and fibronectin are up-regulated. EMT is regulated by signalling pathways mediated by multiple cytokines such as Wnt, Notch and transforming growth factor (TGF)-β (*3*, *4*).

Members of the TGF-β family bind to two different types of serine/threonine kinase receptors. Upon ligand binding, the constitutively active type II receptor kinase phosphorylates the type I receptor which, in turn, activates the downstream signal transduction cascades, including Smad pathways. TGF-βs signal through the type I receptor known as activin receptor-like kinase (ALK)-5. The activated type I receptor phosphorylate receptor-regulated Smad proteins (R-Smads). Smad2 and 3 transduce signals as R-Smads for TGF-βs (*5*). Once activated, R-Smads complex with the common mediator Smad4 (Co-Smad), and translocate to the nucleus, where Smad complexes regulate transcription of target genes. In addition, TGF-β has been shown to activate diverse non-Smad parallel downstream pathways, such as extracellular signal regulated kinase (ERK), c-Jun NH2-terminal kinase (JNK) and p38 MAP kinase (*6*, *7*).

Small Rho GTPases are activated by TGF-β and play important roles in TGF-β-induced actin cytoskeleton reorganization (*8*). Rho GTPases have been implicated in many cellular processes, including actin and microtubule cytoskeleton organization, cell adhesion, cell division and motility (*9*). Rho proteins cycle constantly between GTP-bound active forms and GDP-bound inactive forms, and this process is positively and negatively regulated by guanine nucleotide exchange factors (GEFs) and GTPase-activating proteins (GAPs), respectively. Activation of Rho GTPases leads to activation of downstream effectors including Rho-associated coiled-coil containing protein kinase (ROCK) and mDia. TGF-β rapidly activates various Rho GTPases including RhoA, RhoB, Rac and Cdc42 leading to short-term actin cytoskeleton remodelling via the ROCK1/LIMK/cofilin pathway in epithelial cells. This activation is mediated by non-Smad pathways including p38 MAP kinase (*10*) and phosphatidylinositol 3-kinase pathways (*11*). TGF-β also activates Rho GTPases via Smad-dependent induction of Rho GEFs such as Net1 (*12*) and GEF-H1 (*13*).

Several lines of evidence have shown that multiple transcription factors are involved in TGF-β-induced EMT. TGF-β signals induce the expression of Snail, SIP-1 and δEF-1 during EMT of mammary epithelial cells (*14*, *15*). Among them, Snail, a zinc finger-containing transcription factor, represses E-cadherin expression and induces EMT when over-expressed in epithelial cells (*16*, *17*). Knockout mice deficient for Snail gene die at gastrulation as they fail to undergo a complete EMT process, forming an abnormal mesodermal layer that retains E-cadherin expression (*18*).

Morita and colleagues (*19*) reported that myocardin-related transcription factors (MRTFs; also known as MAL and MKL) play critical roles in TGF-β-induced EMT. In epithelial cells, TGF-β triggers the nuclear translocation of MRTFs via activation of the Rho signalling pathway (*20–22*), leading to formation of a transcriptional complex of MRTFs and Smad3 which activates the Slug transcription. MRTFs also induce the expression of α-SMA in cooperation with serum response factor (SRF), leading to reorganization of the α-SMA containing actin cytoskeleton.

Differentiated endothelial cells have been shown to differentiate into mesenchymal cells *in vivo* (*23*). During heart development, cardiogenic mesodermal cells give rise to two types of heart cells, *i.e.* myocardial and endocardial cells. Endocardial cells acquire endothelial markers, such as VE cadherin and platelet-endothelial cell adhesion molecule-1 (PECAM1). A population of endocardial/endothelial cells in atrio-ventricular (AV) canal transit to the mesenchymal heart cushion cells, which resembles EMT. These cells further form the mesenchymal region of cardiac septa and valves (*24*, *25*). During endothelial–mesenchymal transition (EndMT) in heart development, expression of VE cadherin is down-regulated while that of α-SMA is up-regulated. This phenomenon was genetically documented by Zeisberg and colleagues (*26*) using the *Tie2-Cre*; *R26R-lox-STOP-lox-lacZ* transgenic mice, in which all cells of endothelial origin are irreversibly labelled with LacZ (β-galactosidase) expression. They found that the mesenchymal heart cushion cells express β-galactosidase, suggesting that these cells are formed through EndMT.

Roles of the TGF-β family in cardiovascular development have been implicated by the findings that knockout mice deficient in various TGF-β family signalling components exhibit defects in cardiovascular systems (*27–29*). Especially, TGF-β2-deficient mice have multiple defects in AV cushion formation, suggesting its roles in EndMT of endocardiac tissues (*30*, *31*). Furthermore, various *in vitro* studies have shown that TGF-βs induce differentiation of vascular endothelial cells into mesenchymal cells (*32–37*). However, molecular mechanisms that govern TGF-β-induced EndMT remain to be largely unknown.

Here, we found that TGF-β family members induce the EndMT of mouse pancreatic microvascular endothelial cells (MS-1). This mesenchymal transition of MS-1 cells by TGF-β requires cooperative activation of Rho signals and MRTF-A leading to the transcriptional activation of mesenchymal marker genes by MRTF-A. However, this TGF-β/Rho/MRTF signalling axis in EndMT of MS-1 cells is partly different from that observed in EMT.

Material and Methods

Cells and cell culture

MS-1 cells were obtained from American Type Culture Collection, and maintained in Minimum Essential Medium-α (MEM-α) medium (Invitrogen) supplemented with 10% fetal calf serum (FCS), 50 U/ml penicillin and 50 μg/ml streptomycin. TGF-β1, 2, 3 (R&D: 1 ng/ml), Y27632 (Sigma-Aldrich: 10 μM) and C3 exoenzyme (Cytoskeleton: 2 μg/ml) were used in each experiment.

RNA interference and oligonucleotides

siRNAs were introduced into cells as described previously (*38*, *39*). The target sequences of siRNAs for mouse Snail, Smad4, Arhgef5 and MRTF-A were:

5′-CGGAAGATCTTCAACTGCAAATATT-3′,
5′-GCAAAGGAGTGCAGTTGGAATGTAA-3′,
5′-CCCTATCATAGATCCTTCCTCTGAA-3′ and
5′-CCATCACCCATGGACACCTCTGAAT-3′,

respectively. Control siRNAs were obtained from Invitrogen.

Lentiviral production and infection

A lentiviral vector encoding constitutively active MRTF-A mutant (ca-MRTF-A) was generated by Gateway technology (Invitrogen) (*19*, *40*). Ca-MRTF-A cDNA was subcloned into the pENTR vector, and subsequently transferred into the pCSII-EF-RfA lentiviral expression vector by the LR recombination reaction (Invitrogen). Empty pENTR vector was used to prepare control lentiviral vector. 293FT cells were co-transfected with the expression plasmids and packaging plasmids (pCMV-VSV-G-RSV-Rev and pCAG-HIVgp) using Lipofectamine 2000 (Invitrogen). The viral supernatants were collected 72 h after transfection. For viral infection, 5.0×10^4 MS-1 cells/well in 6-well tissue culture plates were infected with lentiviral particles.

Immunohistochemistry and Western blot analysis

Immunohistochemistry of culture cells was performed as described previously (*41*, *42*) using monoclonal antibodies to VE cadherin (BV13: eBioscience) and α-SMA (1A4: Sigma-Aldrich). F-actin was stained by fixing the MS-1 cells that were treated with or without TGF-β2 for 24 h in 4% paraformaldehyde and 0.2% Triton X-100, followed by incubation with phalloidin–tetramethylrhodamine B isothio cyanate, from Amanita phalloides (Sigma-Aldrich). Stained cells were photographed using a confocal microscope (model LSM510 META; Carl Zeiss MicroImaging Inc.) with 40× (Plan-Neofluar 40×/1.3) objectives, and LSM Image Browser. All images were taken at room temperature. Western blot analyses were performed as described previously (*43*) using antibodies to α-SMA (Sigma-Aldrich), MRTF-A (abcam) and α-tubulin (Sigma-Aldrich).

Pull-down assay of GTP-bound Rho-GTPases

MS-1 cells (6.0×10^7) were used for each assay. Rho activation assay was performed as described previously (*44*) by using Rho activation assay kits (Millipore).

RNA isolation and RT-PCR

Total RNA was prepared with RNeasy reagent (QIAGEN) and reverse transcribed by random priming and a Superscript first strand synthesis kit (Invitrogen). Quantitative RT–PCR analysis was performed using the GeneAmp 5700 Sequence Detection System and Step One Plus Real-Time PCR System (Applied Biosystems). All expression data were normalized to those for GAPDH. The primer sequences are available online as indicated in Supplementary Table S1.

Collagen gel contraction assay

Type I collagen gel was prepared using an 8:1:1 ratio of cold collagen solution (Cellmatrix I-P; Nitta Gelatin, Osaka, Japan), 10 × concentrated MEM medium (Invitrogen) and collagen dilution buffer containing 0.05 N NaOH, 2.2% $NaHCO_3$ and 200 mM HEPES pH 7.4. MS-1 cell suspensions (1.0×10^6 cells/200 μl) were mixed in 800 μl of the collagen gel solution. A measure of 1 ml of the mixture was added to each well of 12-well culture plates and allowed to solidify at 37°C for 30 min. After solidification, 1 ml of MEM-α medium containing 10% FCS, 50 U/ml penicillin and 50 μg/ml streptomycin was overlaid to float the gel. The floating gels were incubated at 37°C in 5% CO_2 for 2 days. The gel surface area was quantified based on pixel number using ImageJ (US National Institutes of Health). The relative changes in the surface area are shown as the ratio of the original surface area.

Luciferase assay

Construction of luciferase reporter plasmids was performed according to a previous report (*45*). Briefly, the −724/+51 sequence of the α-SMA gene, containing the promoter sequence, exon 1 and 7 bp of intron 1, was subcloned into the pGL4 basic vector containing the luciferase gene (Promega). By site-directed mutagenesis, wild-type CCTTGTTTGG (CArG A) and CCCTATATGG (CArG B) sequences were replaced by CCTTGAATTC and CCCGAATTC G sequences, respectively. MS-1 cells were seeded in 24-well plates and then transiently transfected with promoter–reporter constructs with or without expression plasmids encoding ca-MRTF-A. Cell lysates were then prepared, and luciferase activities in the lysates were measured with the Dual-Luciferase reporter system (Promega) using a luminometer (MicroLumat Plus, Berthold). Values were normalized to Renilla luciferase activity driven by thymidine kinase promoter.

Statistical analyses

Results were compared by Student's *t*-test. Differences were considered significant when $P < 0.05$. All statistical tests were two-sided.

Results

TGF-β2 induces differentiation of MS-1 endothelial cells into α-SMA-expressing cells

In order to examine the roles of TGF-β signals in the mesenchymal transition of endothelial cells, we treated mouse pancreatic microvascular endothelial cells (MS-1) with TGF-β2, which appears to be the physiologically most relevant TGF-β isoform for EndMT during heart cushion development (*46*). MS-1 cells contact with neighbouring cells, and exhibit cobblestone-like structures (Fig. 1A). However, when they were treated with 1 ng/ml TGF-β2, they lost the cell–cell contact and became spindle shaped (Fig. 1A).

Next, we investigated the effect of TGF-β2 on cytoskeletal structure of MS-1 cells. As shown in Fig. 1B, F-actin was stained on marginal region of control MS-1 cells, whereas TGF-β2-treated MS-1 cells have thicker stress fibres in central region which are parallel to long axis of cells.

Since expression of endothelial and mesenchymal markers decreases and increases, respectively, during the mesenchymal transition of endothelial cells, we examined the changes of these hallmark markers of EndMT. MS-1 cells were treated with 1 ng/ml TGF-β2 for 72 h, followed by staining for an endothelial marker VE cadherin and a mesenchymal marker α-SMA. As shown Fig. 1C, treatment of MS-1 cells with TGF-β2 decreased the expression of VE-cadherin protein and increased the expression of α-SMA. In order to further examine how TGF-β2 induces α-SMA expression, we studied the kinetics of the α-SMA expression in MS-1 cells treated with TGF-β2. As shown in Fig. 1D, the expression of α-SMA mRNA became significantly higher than control at 48 h and continued to increase until 96 h. This was confirmed at 48 and 72 h after the treatment by western blot analysis (Fig. 1E).

Mammalian TGF-β includes three isoforms, TGF-β1, 2 and 3. We examined the effects of other TGF-β isoforms on the α-SMA expression in MS-1 cells. As shown in Supplementary Fig. S1, when the equivalent levels of PAI-1 expression were induced by TGF-β1, 2 and 3 in MS-1 cells, the α-SMA expression was also induced at equivalent levels, suggesting that all three TGF-β isoforms are able to induce the α-SMA expression.

As one of the most characteristic features of mesenchymal cells is their ability to reorganize extracellular matrix, this property was determined by a collagen gel contraction assay (*47*). MS-1 cells pre-treated with TGF-β2 were suspended in a collagen type I gel. After the collagen had solidified, the gel was detached from the sides and bottoms of the dishes and floated in media containing the ligand for 48 h. There was no significant degradation of the collagen gel in the control cells, but the volume of the collagen gel was reduced by ~70% in cells treated with TGF-β2 (Fig. 1F). Taken together, we concluded that MS-1 endothelial cells undergo EndMT by the stimulation of TGF-β2.

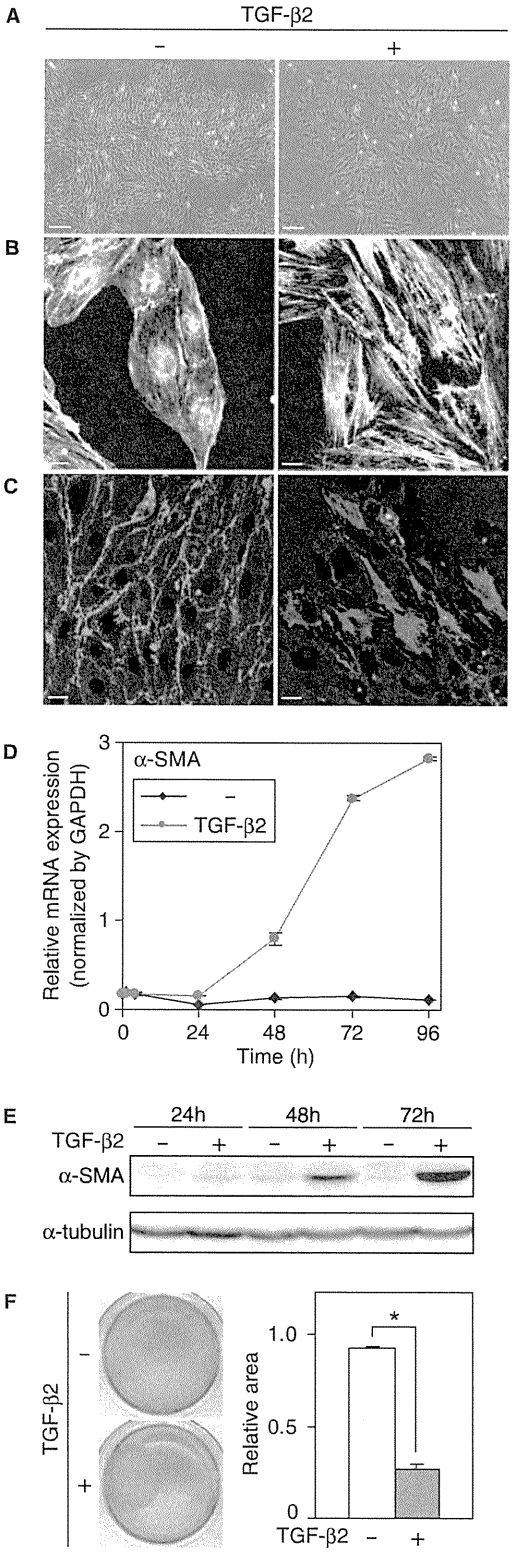

Fig. 1 Effects of TGF-β2 on MS-1 endothelial cells. (A–C) MS-1 cells were cultured in the absence (−) or presence (+) of 1 ng/ml of TGF-β2, followed by observation of morphology (A), fluorescence immunostaining for F-actin (white) and nuclei (blue) (B), and fluorescence immunostaining for VE cadherin (green), α-SMA (red) and nuclei (blue) (C). Scale bars: 200 μm (A) and 20 μm (B and C). (D and E) MS-1 cells were treated with TGF-β2 for various time periods, followed by quantitative RT–PCR analysis for α-SMA expression (D) and Western blot analysis for the expression of α-SMA (top) and α-tubulin (bottom) (E). Error bars represent standard deviations. (F) MS-1 cells were preincubated with or without TGF-β2 for 72 h, and then mixed in collagen matrices. After solidification, the mixtures were released from the culture dishes and incubated for additional 2 days. Experiments were performed in duplicate, and representative results are shown. $^*P<0.05$.

Activation of Rho signal by TGF-β2 is necessary for EndMT

Expressions of various EMT-related transcription factors including Snail, SIP-1 and δEF-1 have been shown to be induced by TGF-β during EMT. We previously reported that Snail is necessary for the TGF-β2-induced mesenchymal differentiation of mouse embryonic stem cell-derived endothelial cells (MESEC) (*48*). In order to examine the possibility that such EMT-related transcription factors are involved in TGF-β2-induced mesenchymal transition of MS-1 endothelial cells, we studied the effects of TGF-β2 on their expression. TGF-β2 induced the Snail expression while it did not induce the expression of Slug, SIP-1 and δEF-1 (Supplementary Fig. S2A–D). However, in contrast to MESEC, the knockdown of Snail expression in MS-1 cells did not suppress the TGF-β2-induced α-SMA expression (Supplementary Fig. S2E and F), suggesting that Snail is not involved in the TGF-β2-induced mesenchymal transition of MS-1 endothelial cells.

Since the activation of Rho signals by TGF-β has been implicated in EMT (*49*, *50*), we examined whether Rho signals are involved in the TGF-β2-induced EndMT. First, we examined whether TGF-β2 activates RhoA in MS-1 cells. When MS-1 cells were treated with TGF-β2, the amount of GTP-bound form of RhoA was increased (Fig. 2A). We next examined whether activation of Rho signals are necessary for TGF-β2-induced EndMT. The actions of the Rho GTPases are mediated by the multiple groups of downstream effectors including ROCK and mDia. Treatment of MS-1 cells with Y27632, an inhibitor of ROCK, inhibited the induction of actin reorganization, which was observed by phalloidin staining (Fig. 2B). Y27632 and C3 exoenzyme, an inhibitor of Rho GTPases, also abrogated the induction of α-SMA expression by TGF-β2 at both mRNA (Fig. 2C) and protein levels (Fig. 2D). These results suggest that activation of Rho signal is required for the TGF-β2-induced mesenchymal transition of MS-1 cells.

Expression of mesenchymal markers is induced by TGF-β2 in Rho-dependent and independent fashions

We next examined which mesenchymal markers are induced by TGF-β2 in MS-1 cells. TGF-β2 induced the expression of various other mesenchymal markers including SM22α (Fig. 3A), fibronectin 1 (Fig. 3B) and matrix metalloproteinase 2 (MMP2) (Fig. 3C) in MS-1 cells at 72 h after treatment. However, some of the fibroblast markers such as FSP-1 were not induced (data not shown).

Since TGF-β2-induced α-SMA expression was abrogated by Y27632, we next questioned whether expression of all of the mesenchymal markers requires

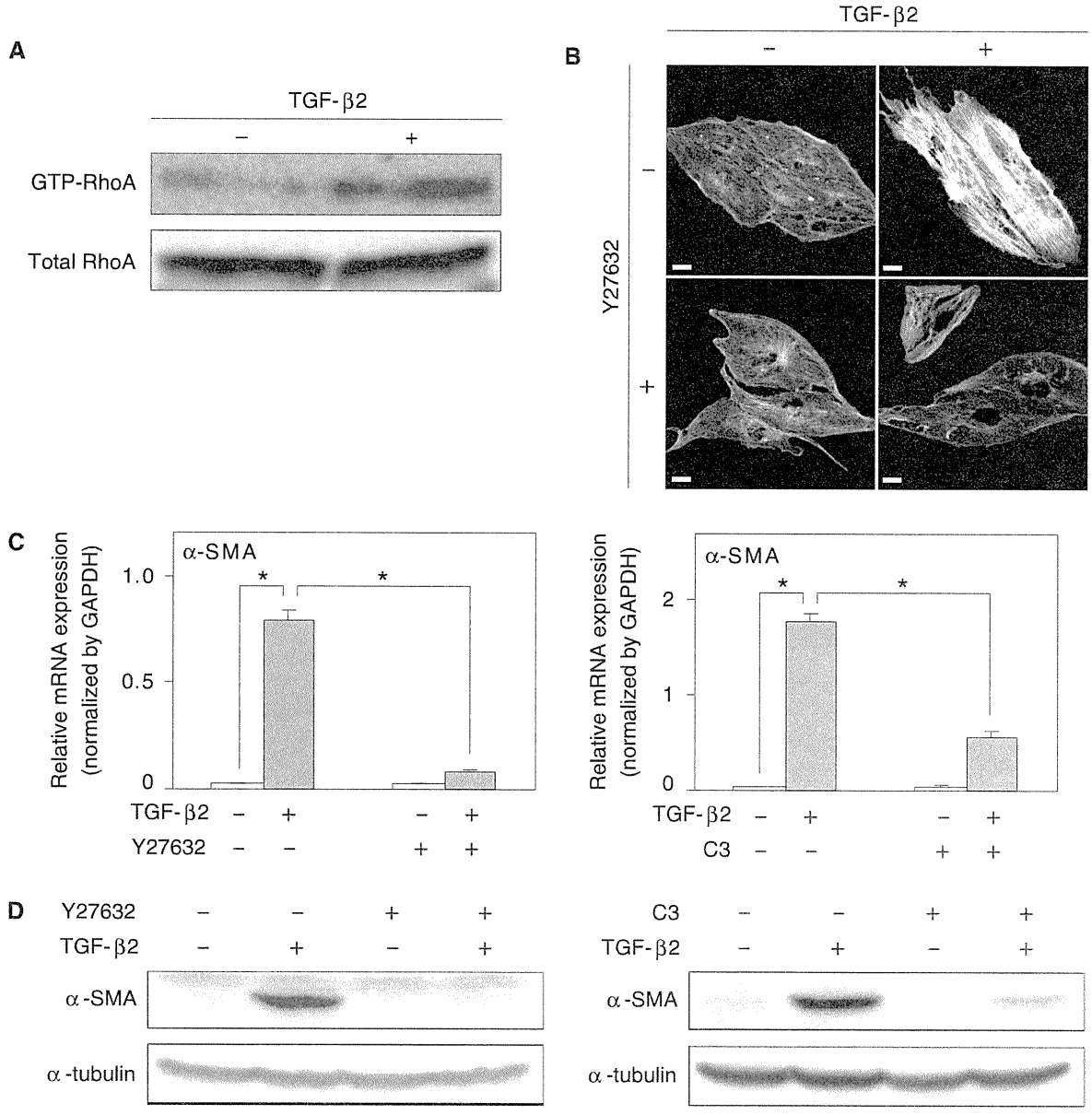

Fig. 2 Roles of Rho signals in the TGF-β2-induced mesenchymal transition of MS-1 cells. (A) MS-1 cells were cultured in the absence (–) or presence (+) of 1 ng/ml of TGF-β2 for 24 h, and were subjected to RhoA activation assays. The levels of GTP-bound RhoA (top) and total RhoA (bottom: internal control) are shown. (B) MS-1 cells were treated with TGF-β2 in the absence (–) or presence (+) of Y27632, a ROCK inhibitor, followed by fluorescence immunostaining for F-actin (white) and nuclei (blue). (C and D) MS-1 cells were treated with TGF-β2 in the absence (–) or presence (+) of Y27632 (left) and C3 exoenzyme (C3, right), an inhibitor of Rho GTPases for 72 h, followed by quantitative RT–PCR analysis for α-SMA expression (C) and Western blot analysis for the expression of α-SMA (top) and α-tubulin (bottom) (D). Scale bars: 20 μm. Error bars represent standard deviations. $^*P<0.05$.

the activation of Rho signals. When MS-1 cells were treated with Y27632, TGF-β2 failed to induce the expression of SM22α (Fig. 3A), while the induction of fibronectin 1 (Fig. 3B) and MMP2 (Fig. 3C) was not affected by Y27632. Treatment of MS-1 cells with C3 exoenzyme also elicited similar inhibitory effects to those of Y27632 on the expression of various mesenchymal markers (Supplementary Fig. S3). These results suggest that TGF-β2 induces the expression of a group of mesenchymal markers such as α-SMA and SM22α in a Rho-dependent fashion while Rho signals are not required for TGF-β2-induced expression of other mesenchymal markers including fibronectin 1 and MMP2.

Silencing of Smad4 abolishes the induction of mesenchymal markers by TGF-β2

Previous reports have shown that TGF-β-induced activation of non-Smad pathway is involved in the activation of Rho signals leading to EMT (*49*, *50*). We examined the involvement of Smad signals in the TGF-β2-induced expression of various mesenchymal markers in MS-1 cells. When Smad4 expression was decreased by siRNA (Fig. 4A), TGF-β2 failed to

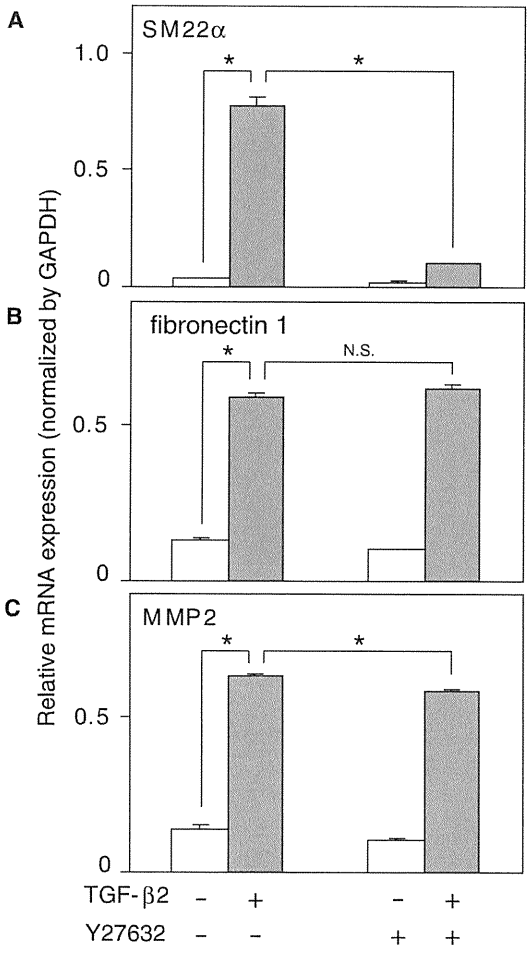

Fig. 3 Effects of Y27632 on the TGF-β2-induced expression of mesenchymal markers in MS-1 cells. MS-1 cells were treated with TGF-β2 in the absence (−) or presence (+) of Y27632, a ROCK inhibitor, for 72 h, followed by quantitative RT-PCR analysis for the expression of SM22α (A), fibronectin 1 (B) and MMP2 (C). Error bars represent standard deviations. $^*P<0.05$; N.S., not significant.

induce the expression of PAI-1 (Fig. 4B). To our interest, TGF-β2 was not capable of inducing the expression of α-SMA (Fig. 4C) and SM22α (Fig. 4D), whose expression was dependent on Rho signals, as well as fibronectin 1 (Fig. 4E) and MMP2 (Fig. 4F), when Smad4 expression was knocked down. These results suggest that Rho-dependent induction of mesenchymal markers by TGF-β2 is dependent on Smad pathways.

TGF-β2-induced expression of Arhgef5 is dependent on Smad pathways and is important for the α-SMA expression induced by TGF-β2

We next questioned whether TGF-β2-induced expression of mesenchymal markers is directly regulated by Smad signals. As shown in Fig. 1D, α-SMA expression started to be elevated at 48 h after treatment of TGF-β2. When we examined the kinetics of TGF-β2-induced expression of other mesenchymal markers, we found that SM22α also became induced at 72 h after treatment of TGF-β2 (Supplementary Fig. S4A), while the expression of fibronectin 1 (Supplementary

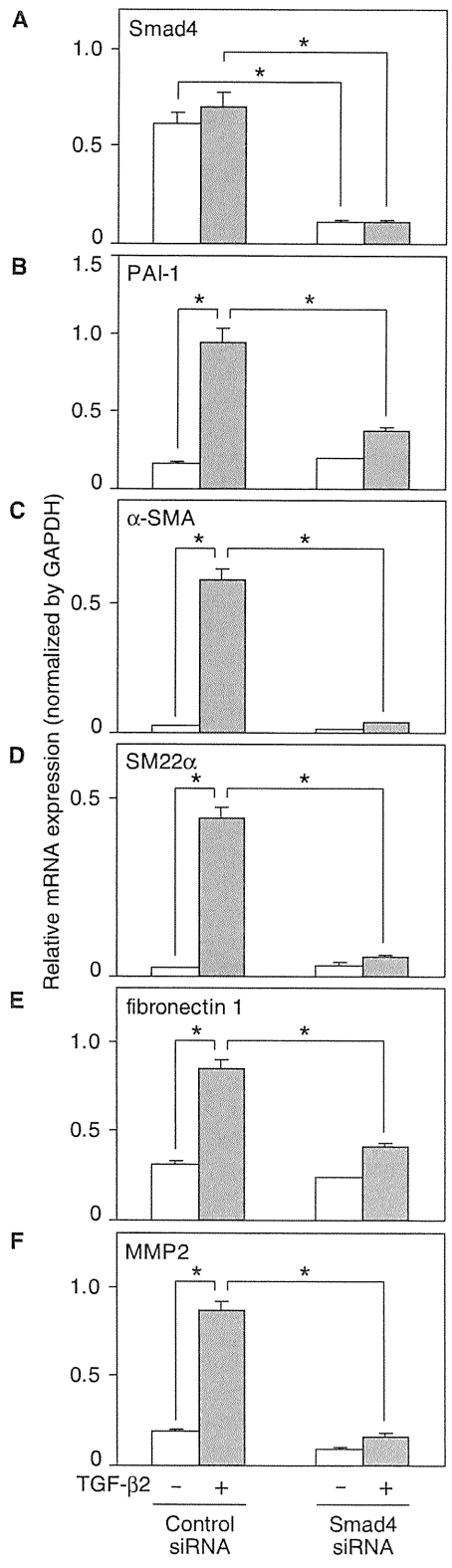

Fig. 4 Roles of Smad4 in the TGF-β2-induced expression of mesenchymal markers in MS-1 cells. MS-1 cells transfected with control siRNA or siRNA for Smad4 were cultured in the absence (−) or presence (+) of 1 ng/ml of TGF-β2 for 72 h, followed by quantitative RT–PCR analysis for the expression of Smad4 (A), PAI-1 (B), α-SMA (C), SM22α (D), fibronectin 1 (E) and MMP2 (F). Error bars represent standard deviations. $^*P<0.05$.

Fig. S4B) and MMP2 (Supplementary Fig. S4C) was significantly induced at 24 h after treatment, suggesting that α-SMA and SM22α, whose expression is dependent on TGF-β2-activated Rho signals, are indirectly regulated by Smad signals.

Previous reports have shown that TGF-β activates Rho signals not only by non-Smad pathways but by Smad pathways, which induce the expression of GEFs including Net1 (*12*) and GEF-H1 (*13*). Based on Smad dependency of mesenchymal marker induction by Rho signals, we examined the effects of TGF-β2 on the expression of various GEFs and the involvement of Smad signals by knocking down Smad4 expression (Fig. 5A and Supplementary Fig. S5). We found that TGF-β2 increased the expression of Arhgef5 (also known as Tim1), a member of the Dbl family of GEFs (*51*), in MS-1 cells (Fig. 5B) to a higher extent than those of Net1 (Supplementary Fig. S5A) and GEF-H1 (Supplementary Fig. S5B). Furthermore, we confirmed that the TGF-β2-induced expression of Arhgef5 is dependent on Smad4 by knocking down the Smad4 expression (Fig. 5B).

We next examined the causal relationship between TGF-β2-induced Arhgef5 expression and TGF-β2-induced α-SMA expression in MS-1. When Arhgef5 expression was knocked down by siRNA in MS-1 cells (Fig. 5C), the effect of TGF-β2 on the α-SMA expression in MS-1 cells was partially but decreased (Fig. 5D). These results suggest that Arhgef5 expression induced by Smad4-dependent TGF-β2 signals is involved in α-SMA induction in TGF-β2-treated MS-1 cells.

TGF-β2 induces the expression and nuclear accumulation of MRTF-A protein

Rho signals activate multiple cellular events to induce EMT. A previous report showed that Rho activity induces the nuclear translocation of MRTFs, myocardin family proteins, leading to the complex formation with SRF on the CArG box in the actin cytoskeletal genes including α-SMA and with Smad3 on the GCCG box in Slug promoter in MDCK epithelial cells (*19*). These dual functions of Rho-MRTF pathways are important for the TGF-β-induced EMT.

We first examined whether TGF-β2 changes the level of nuclear accumulation of MRTF-A protein in MS-1 cells. As shown in Fig. 6A, to our surprise, TGF-β2 increased the level not only of nuclear accumulated MRTF-A protein but also of total MRTF-A protein, suggesting that TGF-β2 regulates the expression of MRTF-A protein in addition to its nuclear transport. Furthermore, we found that Y27632 suppressed the effects of TGF-β2 on the nuclear accumulation of MRTF-A protein but not on its expression (Fig. 6A), suggesting that Rho signals play important roles not in the MRTF-A expression but in its nuclear transport. In order to examine whether the TGF-β2-induced increase in MRTF-A expression is regulated transcriptionally, we carried out RT-PCR analysis, and found that TGF-β2 increases the level of MRTF-A mRNA (Fig. 6B). It is noteworthy that this increase in MRTF-A

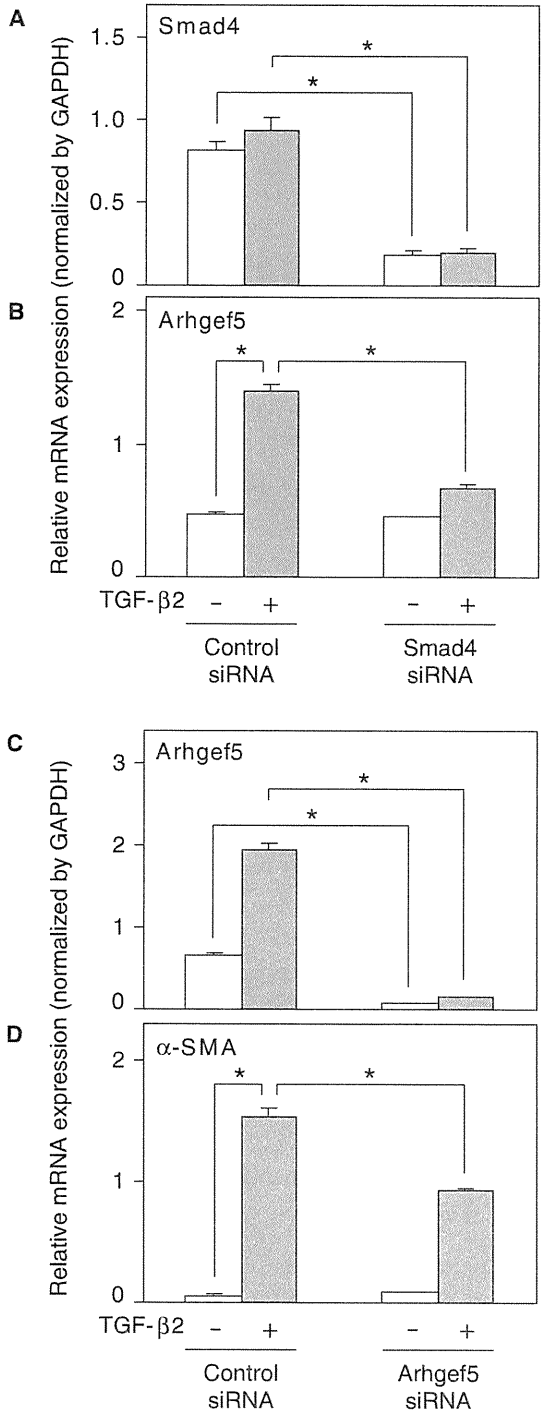

Fig. 5 Induction of Arhgef5 by TGF-β2 and its contribution to the TGF-β2-induced α-SMA expression in MS-1 endothelial cells. (A and B) MS-1 cells transfected with control siRNA or siRNA for Smad4 were cultured in the absence (−) or presence (+) of 1 ng/ml of TGF-β2 for 72 h, followed by quantitative RT–PCR analysis for the expression of Smad4 (A) and Arhgef5 (B). (C and D) MS-1 cells transfected with control siRNA or siRNA for Arhgef5 were cultured in the absence (−) or presence (+) of 1 ng/ml of TGF-β2 for 72 h, followed by quantitative RT–PCR analysis for the expression of Arhgef5 (C) and α-SMA (D). Error bars represent standard deviations. $^*P<0.05$.

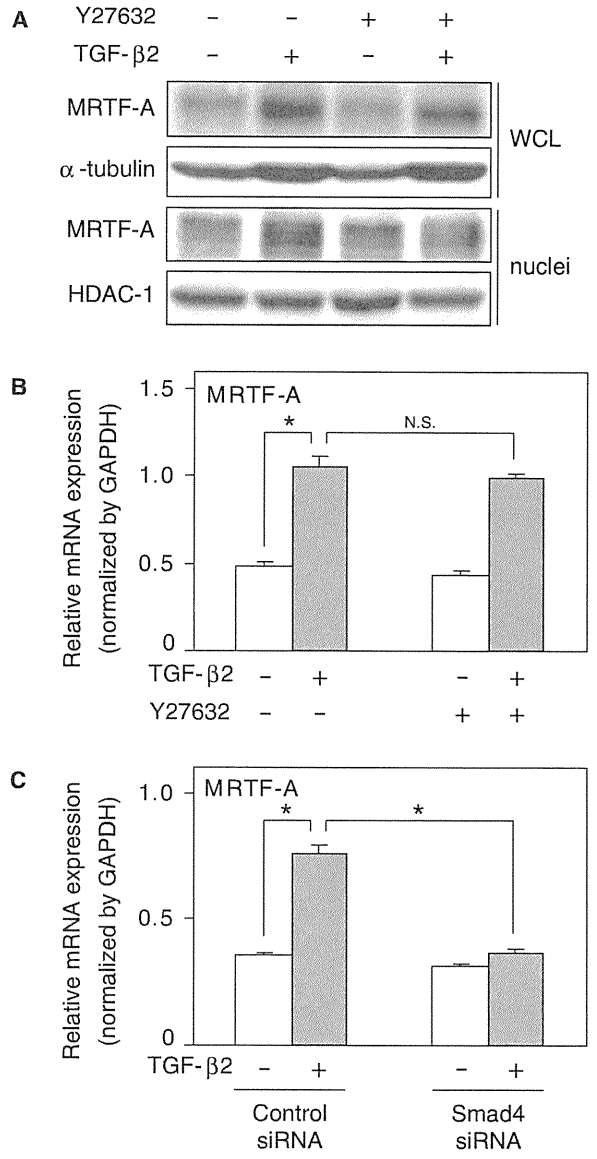

Fig. 6 Effects of TGF-β2 and Rho signals in the expression and nuclear localization of MRTF-A in MS-1 endothelial cells. (A and B) MS-1 cells were treated with TGF-β2 in the absence (−) or presence (+) of Y27632 for 72 h, followed by Western blot analysis for the expression of MRTF-A in whole-cell lysates (WCL) (top panel) and in the nuclei (third panel) and α-tubulin (second panel) and HDAC-1 (bottom panel) (A), and quantitative RT-PCR analysis for the expression of MRTF-A transcripts (B). (C) MS-1 cells transfected with control siRNA or siRNA for Smad4 were cultured in the absence (−) or presence (+) of 1 ng/ml of TGF-β2 for 72 h, followed by quantitative RT–PCR analysis for the expression of MRTF-A. Error bars represent standard deviations. $^*P<0.05$; N.S., not significant.

mRNA by TGF-β2 was not inhibited by Y27632 (Fig. 6B) or C3 exoenzyme (Supplementary Fig. S3D) but was inhibited by knocking down Smad4 expression (Fig. 6C). These results suggest that TGF-β2 induces MRTF-A expression through Smad signals rather than Rho signal, which is involved in the nuclear translocation of MRTF-A in MS-1 cells.

MRTF-A is necessary and sufficient for TGF-β2-induced α-SMA expression in MS-1 endothelial cells

We next examined whether the TGF-β2-induced MRTF-A activation is involved in the α-SMA upregulation in MS-1 cells. When the endogenous level of MRTF-A expression was decreased by siRNA (Fig. 7A), TGF-β2 failed to induce the α-SMA expression in MS-1 cells (Fig. 7B), suggesting that MRTF-A is necessary for the TGF-β2-induced mesenchymal transition of MS-1 cells.

We next studied the effect of gain-of-function of MRTF-A on the expression of α-SMA. When constitutively active (ca) MRTF-A was introduced to MS-1 cells by lentivirus, the expression of α-SMA in MS-1 cells increased in the absence of TGF-β2 (Fig. 7C), suggesting that activation of MRTF-A can mimic the effect of TGF-β2 on the α-SMA expression (*19*).

In order to further dissect the molecular mechanisms underlying the transcriptional regulation of α-SMA gene by MRTF-A, we used the promoter region of α-SMA gene. As previously reported (*45*), the 724 bp fragment of 5′-flanking region of α-SMA gene consists of two CArG boxes that contribute to the MRTF-A-mediated transcription of α-SMA gene (Fig. 7D). When MS-1 cells were transfected with a luciferase reporter construct containing the 724 bp promoter fragment in the absence or presence of ca-MRTF-A, the reporter activity was enhanced by ca-MRTF-A (Fig. 7E). α-SMA transcription is regulated via interaction of multiple transcription factors with distinct *cis*-elements in the promoter. When point mutations were introduced to the two CArG elements, the effects of ca-MRTF-A on the α-SMA promoter were abolished (Fig. 7D and E). These results suggest that TGF-β2 induces the α-SMA expression in MS-1 cells by inducing the expression of MRTF-A which binds to the CArG elements in the α-SMA promoter.

Discussion

In the present study, we illustrated a novel mechanism by which TGF-β2 induces the mesenchymal transition of MS-1 endothelial cells (Fig. 8). TGF-β2 induces the expression of Arhgef5, a GEF, in a Smad-dependent fashion, and activates Rho signals. TGF-β2 also enhances the expression of MRTF-A by Smad signals, and its translocation to nucleus, which is required and sufficient for TGF-β2-induced expression of α-SMA. These results highlighted novel molecular mechanisms by which TGF-β2 activates Rho signals and MRTF-A in order to induce the mesenchymal transition of MS-1 endothelial cells.

In epithelial cells, TGF-β-induced activation of Rho signals is involved in mesenchymal transition (*8*). While many reports have shown that TGF-β activates Rho signals via non-Smad signalling pathways, recent studies including the present study have shown that Smad signalling pathways induce the expression of Rho GEFs, which in turn activates Rho GTPases (*12*, *13*). While Arhgef5 has been implicated in many biological events including changes in cell shape and cytoskeletal organization (*52*), immature dendritic cell migration (*53*) and podosome formation (*54*), the

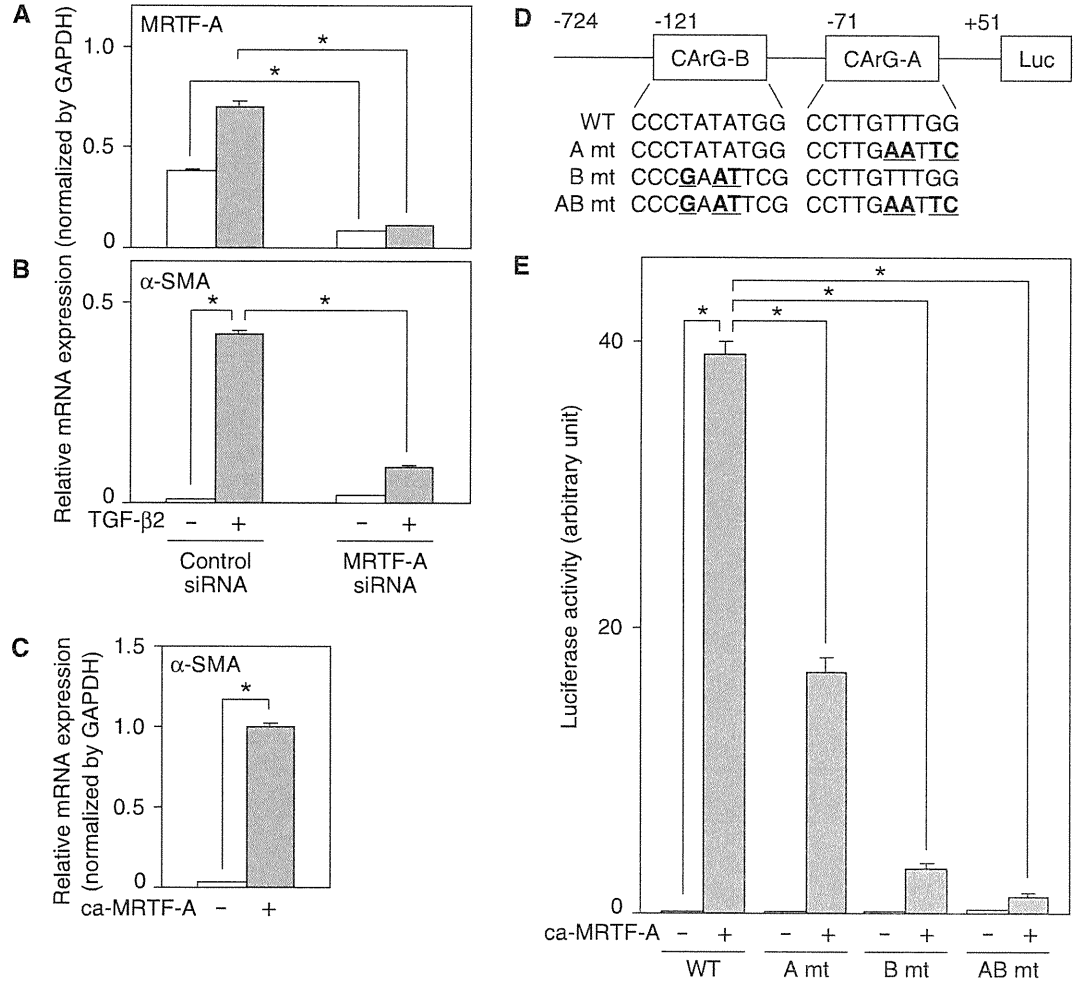

Fig. 7 Roles of MRTF-A in the TGF-β2-induced α-SMA expression in MS-1 endothelial cells. (A and B) MS-1 cells transfected with control siRNA or siRNA for MRTF-A were cultured in the absence (−) or presence (+) of 1 ng/ml of TGF-β2 for 72 h, followed by quantitative RT–PCR analysis for the expression of MRTF-A (A) and α-SMA (B). (C) MS-1 cells were infected with lentivirus encoding control (−) or constitutively active MRTF-A (+) and were subjected to quantitative RT–PCR analysis for the expression of α-SMA. (D and E) Effect of MRTF-A on the α-SMA promoter activity. (D) Schematic representation of mouse α-SMA promoter construct (WT) and its site-mutated series (mt). The indicated numbers present nucleic acid positions from the transcription initiation site. The mutated nucleotides are underlined. (E) MS-1 cells were transfected with the site-mutated reporter constructs along with expression construct encoding ca-MRTF-A (+) or control (−), followed by measurement of luciferase activity. Error bars represent standard deviations. $^{*}P<0.05$.

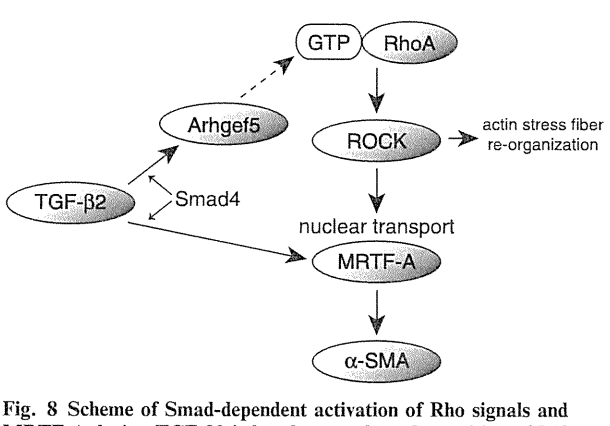

Fig. 8 Scheme of Smad-dependent activation of Rho signals and MRTF-A during TGF-β2-induced mesenchymal transition of MS-1 endothelial cells. TGF-β2 induces the expression of Arhgef5, a GEF, and activates Rho signals. TGF-β2 also enhances the expression of MRTF-A, and its translocation to nucleus. Induction of both Arhgef5 and MRTF-A by TGF-β2 is dependent on Smad4, and is required for TGF-β2-induced expression of α-SMA.

present study, for the first time, showed that Arhgef5 plays critical roles in TGF-β-induced EndMT. However, decreased expression of Arhgef5 did not completely abrogate the TGF-β-induced α-SMA expression while inhibition of Rho signals by Y27632 completely suppressed it, suggesting that Arhgef5 is not a sole component of TGF-β-induced activation of Rho GTPases.

MRTFs have been implicated in the TGF-β-induced α-SMA expression (*19*). This induction is mediated by stimulation of the nuclear transport of MRTF proteins by TGF-β-induced activation of Rho signals. In the present study, we, for the first time, found that TGF-β additionally enhanced the transcription of MRTF-A via Smad signals. Therefore, TGF-β-induced accumulation of MRTF-A proteins in the nuclei of MS-1 might be caused by both the elevated expression of MRTF-A and the induction of its nuclear transport by Rho signals.

We previously reported that TGF-β2 increased the expression of Snail, but not of other EMT-related transcription factors including Slug, δEF-1, SIP-1 and Twist in MESEC (*48*). Furthermore, Snail is necessary and sufficient for TGF-β2-induced EndMT of MESEC. Medici and colleagues recently reported that Snail is required for TGF-β2-induced α-SMA expression in human cutaneous microvascular endothelial cells (HCMEC) (*37*). However, over-expression of Snail was not sufficient to induce EndMT of HCMEC, suggesting that MESEC and HCMEC have differential responses to Snail expression. While we also found that Snail expression was induced by TGF-β2 in MS-1 cells, decreased expression of Snail in MS-1 cells did not suppress the TGF-β2-induced α-SMA expression, suggesting that MS-1 cells have less requirement of Snail for the induction of EndMT. Molecular mechanisms underlying these differential necessity and sufficiency of Snail for mesenchymal transition of various types of endothelial cells remain to be elucidated in the future.

TGF-β2 induces the expression of various mesenchymal markers during mesenchymal transition of epithelial and endothelial cells. In the present study, we found that TGF-β2 increased the expression of α-SMA, SM22α, fibronectin 1 and MMP2 in MS-1 cells. To our interest, while Smad4 is dispensable for the expression of all four mesenchymal markers above, inhibition of Rho signals by Y27632 and C3 exoenzyme suppressed the TGF-β2-induced expression of α-SMA and SM22α, but not of fibronectin 1 and MMP2. These results suggest that TGF-β2 triggers multiple signalling cascades that induce multiple groups of the target genes in different manners.

During EMT and EndMT, TGF-β2 not only induces the mesenchymal markers, but also decreases the expression of E-cadherin and VE cadherin, respectively. In the present study, TGF-β2 decreased the VE-cadherin expression in MS-1 cells. However, this decrease in VE-cadherin expression was not observed in all MS-1 cells treated with TGF-β2. In consistent with this finding, Hashimoto *et al.* (*36*) showed that the extent of TGF-β2-induced decrease in VE-cadherin expression was not as potent as that of TGF-β2-induced increase in α-SMA expression in MS-1 cells. TGF-β decreased the VE-cadherin expression in concert with Notch signals by inducing the expression of Slug, which directly binds to the VE-cadherin promoter in human microvascular endothelial cells (*55*).

EndMT has also been implicated in several pathological situations. During cardiac fibrosis, accumulated fibroblasts cause deposition of extracellular matrix, which can cause heart failure. Furthermore, activated fibroblasts promote the progression of cancers. Zeisberg and colleagues reported that the TGF-β-induced EndMT plays important roles in the formation of fibroblasts from endothelial cells during cardiac and renal fibrosis (*26*, *56–58*) and cancer progression (*59*). Since fibroblasts are culprits in various pathological situations, EndMT is expected to be a target for the therapies of cardiac dysfunction and cancer. Therefore, the present findings may lead to greater understanding of not only normal cardiovascular development but also such pathological situations, and eventually to development of the strategies to manipulate these signals for therapeutic benefit.

Supplementary Data

Supplementary Data are available at *JB* online.

Acknowledgements

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Conflict of interest
None declared.

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Cancer Research

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Molecular and Cellular Pathobiology

Cancer Research

Angiopoietin-like Protein 2 Is an Important Facilitator of Inflammatory Carcinogenesis and Metastasis

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Abstract

Chronic inflammation plays important roles at different stages of cancer development, including carcinogenesis, tumor invasion, and metastasis, but molecular mechanisms linking inflammation to cancer development have not been fully clarified. Here, we report that expression of angiopoietin-like protein 2 (Angptl2), recently identified as a chronic inflammation mediator, is highly correlated with the frequency of carcinogenesis in a chemically induced skin squamous cell carcinoma (SCC) mouse model. Furthermore, Angptl2 expression in SCC is highly correlated with the frequency of tumor cell metastasis to distant secondary organs and lymph nodes. When SCC was induced in transgenic mice expressing Angptl2 in skin epithelial cells, epithelial-to-mesenchymal transitions in SCC as well as tumor angiogenesis and lymphangiogenesis were significantly increased, resulting in increased tumor cell metastasis and shortened survival compared with wild-type mice. Conversely, in a chemically induced SCC mouse model, carcinogenesis and metastasis were markedly attenuated in *Angptl2* knockout mice, resulting in extended survival compared with wild-type mice. Overall, we propose that Angptl2 contributes to increased carcinogenesis and metastasis and represents a novel target to antagonize these pathologies. *Cancer Res; 71(24); 7502–12. ©2011 AACR.*

Introduction

Cancer is an increasingly prevalent medical and social problem and remains a major cause of mortality (1). Therefore, the identification of mechanisms underlying its development is essential to develop new therapeutic approaches. Recently, the concept that chronic inflammation plays an important role at different stages of cancer development, including carcinogenesis, invasion, and metastasis, has emerged (2); it is well established that inflammation induced by bacterial and viral infections increases cancer risk, as does chronic inflammation induced by environmental exposure, including tobacco smoking and inhaled pollutants, such as silica and asbestos (3–5). It has also been recently reported that chronic and often subclinical levels of inflammation—for example, obesity-induced inflammation—may increase cancer risk (6). In fact, obesity, which increases cancer risk by 1.6-fold (7), can cause chronic inflammation, which can then promote carcinogenesis of the liver and pancreas (8). Recently, we found that angiopoietin-like protein 2 (Angptl2) is a causative mediator of chronic inflammation in obesity, and its related metabolic abnormalities (9). In obesity, Angptl2 is secreted by adipose tissue, and its expression is increased by obesity-related pathologic conditions, including hypoxia and endoplasmic reticulum (ER) stress (9). Both hypoxic stress and ER stress are commonly induced in cancer tissues, particularly in cancer progression and metastasis (10), suggesting a role of Angptl2 in these processes. Along these lines, it has been reported that increased levels of Angptl2 derived from tumor- or cancer-associated fibroblasts (CAF), respectively, in cancer tissues refractory to anti-VEGF therapy, which when combined with chemotherapy, is efficacious in treating several human cancers (11). Integrins, which act as functional receptors for Angptl2 in endothelial cells and monocytes/macrophages (9, 12), are also expressed on several cancer cells, in which they regulate tumor cell growth, survival, and invasion (13, 14). Angptl2 is expressed in some tumor cell types (15). Thus, cancer cell- and/or CAF-derived Angptl2 may be a critical factor in cancer development.

Carcinogenesis consists of 2 different processes: "preneoplastic change" and "malignant conversion" (16). The protocol used to chemically induce carcinogenesis in mouse skin consists of 2-stage application of chemicals to the skin, resulting in cutaneous tumors (17, 18). A single application of the initiator mutagen 7,12-dimethylbenzanthracene (DMBA) is followed by repeated applications of phorbol 12-myristate 13-acetate

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(PMA) (17). In this model (19, 20), papilloma formation as epidermal dysplasia, which represents a "preneoplastic change" in skin epidermal cells, is caused by DMBA-induced mutations in the *H-ras* gene, and the degree of "preneoplastic change" can be estimated by the number and size of papillomas, whose growth is stimulated by subsequent, repeated PMA applications. Finally, "malignant conversion" is accelerated by mutations in the *p53* gene brought on by subsequent serial PMA treatment (16) and is reflected in the rate of conversion from large papillomas to squamous cell carcinoma (SCC).

In this study, we found that Angptl2 expression was induced during chemically induced skin SCC development, whereas Angptl2 expression was faintly detected in normal skin tissues, suggesting a possible role for Angptl2 in chemically induced skin SCC. Therefore, we examined skin carcinogenesis and cancer progression by comparing chemically induced skin SCC in 3 mouse genotypes: K14-*Angptl2* transgenic mice (K14-*Angptl2* Tg), *Angptl2* knockout mice (*Angptl2* KO), and respective wild-type littermates. Our finding in this study shows the first evidence that Angptl2 contributes to both increased susceptibility to "preneoplastic change" and "malignant conversion" in carcinogenesis and enhanced cancer cell metastasis, suggesting that Angptl2 represents a new target to block cancer development.

Materials and Methods

Mice

Only male mice were used for the experiments. For chemical carcinogenesis assays, K14-*Angptl2* Tg (9) and *Angptl2* KO (9) were backcrossed to the FVB/N strain for more than 10 generations. All experiments were conducted according to guidelines of the Institutional Animal Committee of Kumamoto University.

Immunoblot analysis

Cells were homogenized in lysis buffer (10 mmol/L NaF, 1 mmol/L Na_3VO_4, 1 mmol/L EDTA, 300 mmol/L NaCl, 50 mmol/L Tris-HCl, 1% Triton X-100, pH 7.5). Extracts derived from supernatants were subjected to SDS-PAGE, and proteins were electrotransferred to nitrocellulose membranes. Immunodetection was carried out using an ECL Kit (Amersham) according to the manufacturer's protocol. Polyclonal antibodies against Smad2/3 and phospho-Smad2 (138D4) and monoclonal antibodies (mAb) against Hsc70 (B-6) were obtained from Cell Signaling and Santa Cruz, respectively.

Immunohistochemical staining

Tumors were fixed by perfusion with 4% paraformaldehyde in PBS (pH 7.4), washed in PBS for 15 minutes, dehydrated through a graded series of ethanol and xylene, and embedded in a single paraffin block. Sections (5 μm) were cut, air-dried, deparaffinized, and pretreated with 5 mmol/L periodic acid for 10 minutes at room temperature to inhibit endogenous peroxidase. Specimens were incubated for 1 hour with 50- to 100-fold diluted polyclonal antibody against Angptl2 (9), Keratin 5 (Covance), Keratin 14 (Covance), Snail (Cell Signaling), or Slug (Cell Signaling), or mAb against E-cadherin (BD Biosciences) or N-cadherin (BD Biosciences) and then washed 3 times with PBS for 5 minutes. Sections were incubated with biotinylated anti-mouse IgG or anti-rabbit IgG (1:200 dilution; Vector Laboratories). Immunostaining was done using the peroxidase-labeled avidin–biotin complex method (1:100 dilution; Dako). Sections were counterstained with hematoxylin.

Calculation of survival data

The Kaplan–Meier log-rank test was applied to analyze mouse survival data using JMP7 software (SAS Institute). A P value of less than 0.05 was considered significant.

Quantification of extent of metastasis

Tumor cells within lung, liver, spleen tissues, and lymph nodes were visualized in tissue slices stained with hematoxylin and eosin (H&E) and histologically identified by 2 independent investigators. The number and area of the metastatic region in lung tissue were quantified by evaluating 10 slices from K14-*Angptl2* Tg, *Angptl2* KO, and respective wild-type littermates. The area was quantified as pixels using the BZ-H1M system (Keyence).

Results

Expression of Angptl2 is induced in chemically promoted squamous cell carcinoma

Increased *Angptl2* mRNA expression was detected in skin tissues of chemically induced papilloma and SCC compared with that seen in normal skin tissues before treatment (Supplementary Fig. S1). Abundant Angptl2 protein was also observed in induced mouse skin SCC, whereas Angptl2 was weakly expressed in normal skin tissues before treatment (Supplementary Fig. S2A). We next asked which cell types express Angptl2. As shown in Supplementary Fig. S2B and Fig. S3, Angptl2 expressed faintly in keratinocytes of the interfollicular epidermis, basal keratinocytes, suprabasal keratinocytes, and hair follicles. In contrast, Angptl2 was abundantly expressed not only in tumor cells at the primary site but at metastatic regions, including distant secondary lung organ and lymph nodes (Supplementary Fig. S2C–E). Normal lymph node and lung tissues showed little Angptl2 expression (Supplementary Fig. S4).

Accelerated carcinogenesis in skin tissues constitutively expressing Angptl2

As shown in Fig. 1A, the ears of K14-*Angptl2* Tg were redder in color than ears of wild-type mice, indicative of constitutive inflammation. We found that expression levels of the inflammatory markers *IL-6* and *IL-1β* were significantly increased in skin tissues of K14-*Angptl2* Tg compared with wild-type mice (Supplementary Fig. S5A). K14-*Angptl2* Tg did not show papillomas or SCC during their lifespan, indicating that Angptl2 overexpression is not sufficient to cause carcinogenesis. To investigate whether Angptl2 overexpression affects chemically induced carcinogenesis, K14-*Angptl2* Tg were subjected to the skin carcinogenesis regimen. This model requires application of both DMBA and PMA (16–18). PMA treatment alone induced Angptl2 expression in wild-type mice (Supplementary

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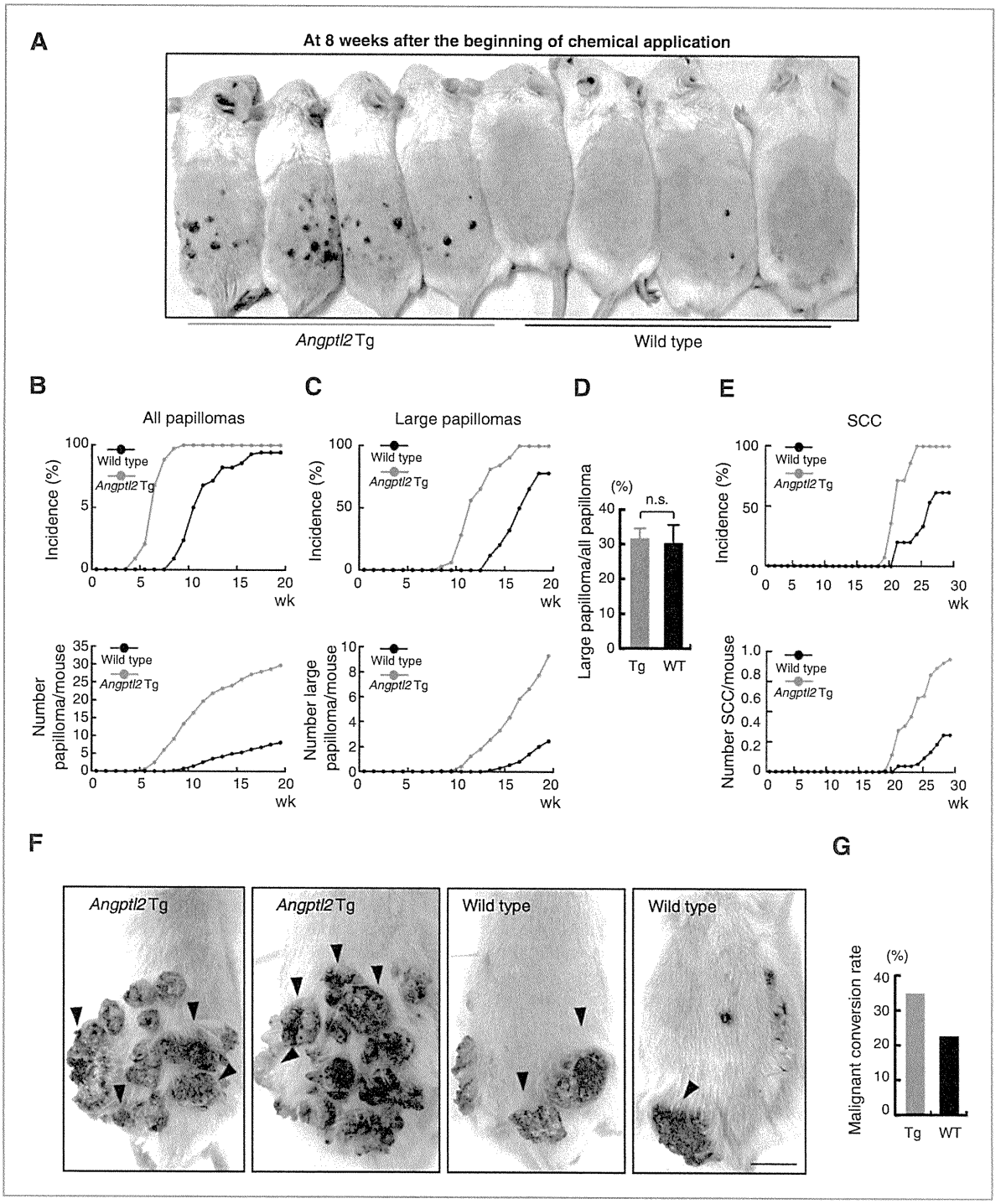

Figure 1. K14-*Angptl2* transgenic mice exhibit accelerated and increased skin carcinogenesis. A, photograph of skin of K14-*Angptl2* Tg (left) and wild-type mice (right) 8 weeks after the first chemical application. B and C, top graphs, the percentage of mice with papillomas as the incidence. Bottom graphs, number of all detectable (>1 mm; B) and large (>3 mm; C) papillomas from K14-*Angptl2* Tg ($n = 34$; red circles) and wild-type mice ($n = 34$; black circles). $P < 0.001$ from weeks 14 to 20 (bottom graph in B), $P < 0.001$ from weeks 9 to 20 (bottom graph in C). D, proportion of large relative to all detectable papillomas in K14-*Angptl2* Tg and wild-type mice. n.s., not significant. Data represent means ± SEM. E, increased incidence of SCC (top graph) and number of SCC per mouse (bottom graph, $P < 0.001$ after week 21) in K14-*Angptl2* Tg ($n = 33$; red circles) compared with wild-type mice ($n = 34$; black circles). F, photograph of SCC on K14-*Angptl2* Tg (left) and wild-type mice (right) 8 weeks after first diagnosis of SCC. Arrowheads indicate SCC. Scale bars, 10 mm. G, comparison of ratio of malignant conversion of large papillomas to SCC in K14-*Angptl2* Tg and wild-type mice. WT, wild type.