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ESE-1 Is a Novel Transcriptional Mediator of Angiopoietin-1 Expression in the Setting of Inflammation*

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Angiogenesis is a critical component of the inflammatory response associated with a number of conditions. Angiopoietin-1 (Ang-1) is an angiogenic growth factor that promotes the chemotaxis of endothelial cells and facilitates the maturation of new blood vessels. Ang-1 expression is up-regulated in response to tumor necrosis factor-α (TNF-α). To begin to elucidate the underlying molecular mechanisms by which *Ang-1* gene expression is regulated during inflammation, we isolated 3.2 kb of the *Ang-1* promoter that contain regulatory elements sufficient to mediate induction of the promoter in response to TNF-α, interleukin-1β, and endotoxin. Surprisingly, sequence analysis of this promoter failed to reveal binding sites for transcription factors that are frequently associated with mediating inflammatory responses, such as NF-κB, STAT, NFAT, or C/EBP. However, putative binding sites for ETS and AP-1 transcription factor family members were identified. Interestingly, among a panel of ETS factors tested in a transient transfection assay, only the ETS factor ESE-1 was capable of transactivating the *Ang-1* promoter. ESE-1 binds to specific ETS sites within the *Ang-1* promoter that are functionally important for transactivation by ESE-1. ESE-1 and Ang-1 are induced in synovial fibroblasts in response to inflammatory cytokines, with ESE-1 induction slightly preceding that of Ang-1. Mutation of a high-affinity ESE-1 binding site leads to a marked reduction in Ang-1 transactivation by ESE-1, inducibility by inflammatory cytokines, and DNA binding to the ESE-1 protein. Transcriptional profiling of cells transiently transfected with an ESE-1 expression vector demonstrates that the endogenous *Ang-1* gene is directly inducible by ESE-1. Finally, Ang-1 and ESE-1 exhibit a similar and strong expression pattern in the synovium of patients with rheumatoid arthritis. Our results support a novel paradigm for the ETS factor ESE-1 as a transcriptional mediator of angiogenesis in the setting of inflammation.

Inflammation is an important component of several pathological conditions, including wound healing, atherosclerosis, and arthritis. Inflammation is often associated with the development of granulation tissue consisting of infiltrating mononuclear cells and blood vessels (1, 2). As this tissue proliferates there are zones of relative hypoxia where growth of the tissue has outstripped the blood vessel supply, triggering signals for further blood vessel development (3). The angiogenesis that results from these signals provides the necessary blood supply, oxygen, and nutrients to support the proliferating tissue, and plays an active role in the transport of inflammatory cells to the site of inflammation (4). The endothelial cells themselves also provide a source of proinflammatory cytokines.

One of the first steps in this process is the induction of angiogenic growth factors such as basic fibroblast growth factor (bFGF)[1] and vascular endothelial growth factor (VEGF) (5). These growth factors promote the proliferation and migration of endothelial cells to sites of inflammation, which is facilitated by the expression of matrix degrading enzymes and integrins on activated endothelial cells (6). Endothelial cells that have migrated to sites of inflammation then organize into small tubes. The formation of stable blood vessels requires the recruitment of surrounding mesenchymal cells and their differentiation into vascular smooth muscle cells. Vessel maturation is facilitated by the angiopoietins (7).

Ang-1 has the unique property of enhancing the stability of new blood vessels by recruiting surrounding mesenchymal cells and promoting their differentiation to vascular smooth muscle cells (7). In contrast to other angiogenic substances like VEGF or bFGF, Ang-1 is not a potent mitogen for endothelial growth. However, Ang-1 is a potent chemoattractant of endothelial cells and enhances endothelial cell migration. Other properties of Ang-1 include its ability to promote the adhesion of endothelial cells to fibronectin, as well as its ability to prevent endothelial cell death by inhibiting apoptosis (8, 9).

We and others (10–12) have recently demonstrated that Ang-1 mRNA and protein are expressed in the synovium of patients with rheumatoid arthritis (RA). Ang-1 is expressed at low levels in primary human synovial fibroblasts obtained from patients with RA, and can be markedly up-regulated in response to inflammatory cytokines such as TNF-α. However, the transcriptional mechanisms by which *Ang-1* gene expression is regulated are currently unknown.

The purpose of this study was to begin to identify the molecular mechanisms of *Ang-1* gene regulation in the setting of

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[1] The abbreviations used are: bFGF, basic fibroblast growth factor; FCS, fetal calf serum; DMEM, Dulbecco's modified Eagle's medium; VEGF, vascular endothelial growth factor; Ang-1, angiopoietin-1; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; RA, rheumatoid arthritis; TNF, tumor necrosis factor; RT, reverse transcriptase; TBS, Tris-buffered saline.

inflammation. Our findings support a central role for the ETS transcription factor ESE-1 during this process. ESE-1 was originally identified as a transcription factor that, under basal conditions, is highly restricted to cells of epithelial origin (13). However, in response to inflammatory stimuli, this factor can be induced in a variety of non-epithelial cells, including vascular smooth muscle cells, chondrocytes, synovial fibroblasts, and endothelial cells (14, 15). We recently demonstrated that ESE-1 is highly expressed in the synovium of patients with rheumatoid arthritis (15). In this study we present direct evidence indicating a role for ESE-1 in *Ang-1* gene regulation. ESE-1 can bind to specific ETS sites within the *Ang-1* promoter that are functionally important for the transactivation by ESE-1, expression of ESE-1 in cultured cells leads to induction of the endogenous *Ang-1* gene, and Ang-1 exhibits a similar and strong expression pattern in the synovium of patients with RA. In summary, our results support a role for the ETS factor ESE-1 as a novel transcriptional regulator of *Ang-1* gene regulation in the setting of inflammation.

EXPERIMENTAL PROCEDURES

Tissue Culture and Reagents—The cell lines HEK293 (human embryonic kidney), NIH3T3 (mouse fibroblast), and MCF-7 (human breast cancer) were grown in DMEM supplemented with 10% fetal calf serum (FCS; Hyclone, Logan, UT) and antibiotics (penicillin and streptomycin; Invitrogen). Synovial tissue and bone were obtained at the time of arthroplasty or joint replacement surgery from patients with the clinical diagnosis of RA. Tissue procurement was approved by the Institutional Review Board. Dispersed synovial tissues were prepared by a previously published method (16). Briefly, synovial tissues were minced on tissue culture plates and treated with Type I collagenase (4 mg/ml; Worthington Biochemical Corporation, Lakewood, NJ), in DMEM (Invitrogen), incubated for 1 h at 37 °C, treated with 0.25% trypsin for 30 min, harvested, and centrifuged at 1,000 rpm for 10 min. Pellets were suspended in 0.05% trypsin-0.02% EDTA, centrifuged, and resuspended in 50% phosphate-buffered saline (Ca^{2+}/Mg^{2+}-free), 50% DMEM containing 10% FCS (Sigma). Cells were then centrifuged and suspended in DMEM, 10% FCS, and plated at a density of 10×10^6 cells/10-cm plate. Cells were initially grown for 7–10 days and subsequently subjected to 2–4 passages. TNF-α and interleukin-1β (IL-1β) were purchased from R&D Systems (Minneapolis, MN).

Expression Vector and Luciferase Reporter Gene Constructs—3239-, 1998-, and 1020-bp fragments corresponding to nucleotides −3040 to +199, −1799 to +199, and −821 to +199 of the human *Ang-1* promoter were cloned from human genomic DNA (Clontech, Palo Alto, CA) by PCR and subcloned into the pGL2 luciferase reporter vector (Promega, Madison, WI). The 1998- and 1020-bp fragments were inserted into the XhoI-HindIII site and the 3239-bp fragment was inserted into the HindIII site upstream of the luciferase gene of the pGL2 vector.

DNA Transfection Assays—Cotransfections of 2×10^5 HEK293 or NIH3T3 cells were carried out with varying amounts of reporter gene construct DNA and expression vector DNA using 4 μl of LipofectAMINE (Invitrogen) as described (17). The cells were harvested 16 h after transfection and assayed for luciferase activity. Transfections for every construct were performed independently in duplicates. Cotransfection of a second plasmid for determination of transfection efficiency was omitted because potential artifacts with this technique have been reported and because many commonly used viral promoters contain potential binding sites for ETS factors (18).

Site-directed Mutagenesis—Site-directed mutagenesis of the *Ang-1* promoter was performed using the QuikChange site-directed mutagenesis kit (Stratagene) according to the manufacturer's recommendations. In brief, PCR primers encoding the *Ang-1* promoter ETS site, −1565 to −1562, and flanking sequences were used, with ATAT substituted for ATCC: 5′-TGTGAATTACATATTGTTAGCCTT-3′ and 3′-AAGGCTAACAATATGTAATTCACA-5′. PCR was performed with Turbo polymerase using the wild type *Ang-1* promoter fragment C luciferase reporter construct as a template. The PCR reaction was digested with DpnI, and the undigested plasmids were transformed into DH5α bacteria. Individual minipreps were sequenced to verify incorporation of the ETS site mutation.

Electrophoretic Mobility Shift Assay—These were performed as described previously (19). In brief, whole cell extracts were made from primary human synovial fibroblasts after incubation with TNF-α or IL-1β for 0, 2, 6, 18, 24, and 48 h, using as lysis buffer 10% glycerol, 0.5% Nonidet P-40, 150 mM NaCl, 10 mM Tris pH 7.4, 1 mM phenylmethanesulfonyl fluoride, and 1 mM dithiothreitol. Whole cell extracts were obtained instead of nuclear extracts because the number of cells were limited and the primary synovial fibroblasts do not maintain their phenotype after 4–5 passages. 10 μg of whole cell extract or 2 μl of *in vitro* translation product and 0.1–0.2 ng of [^{32}P]dATP-labeled double-stranded oligonucleotide probes (5,000–20,000 cpm) in the presence or absence of antibody were run on 4% polyacrylamide gels containing 0.5× TBE buffer. For supershift assays, 1 μl of rabbit polyclonal anti-ESE-1 antibody raised against a glutathione *S*-transferase fusion protein of the N terminus of human ESE-1 (East Acres Biologicals, Southbridge, MA) was used.

Oligonucleotides used as probes are as follows (ETS consensus binding sites underlined: 1) human *Ang-1* promoter site −2586 to −2567, 5′-TTTAATGCATCCTGAATTCT-3′ and 3′-AGAATTCAGGATGCATTAAA-5′; 2) human *Ang-1* promoter site −2207 to −2188, 5′-TTCCCTCAGGAAATTGTGCA-3′ and 3′-TGCACAATTTCCTGAGGGAA-5′; 3) human *Ang-1* promoter site −1573 to −1554, 5′-TGAATTACATCCTGTTAGCC-3′ and 3′-GGCTAACAGGATGTAATTCA-5′; 4) human *Ang-1* promoter mutated site −1573 to −1554, 5′-GCTCTGTTGAATTACATATTGTTAGCCTTTC-3′ and 3′-GAAAGGCTAACAATATGTAATTCACAGAGC-5′.

RT-PCR—Total RNA was isolated using the RNeasy Mini Kit (Qiagen, Valencia, CA). cDNAs were generated from 2 μg of mRNA isolated from human synovial fibroblasts using oligo(dT)$_{12–18}$ priming (Invitrogen) and Moloney murine leukemia virus-reverse transcriptase (Invitrogen). ESE-1, AML-1, and GAPDH RT-PCRs used equivalent amounts of 0.1 ng of cDNA, 4 ng/μl of each primer, 0.25 units of Taq polymerase (Promega), 150 μM of each dNTP, 3 mM of $MgCl_2$, reaction buffer, and water to a final volume of 25 μl. Ang-1 RT-PCRs used equivalent amounts of 0.1 ng of cDNA, 4 ng/μl of each primer, 0.25 units of Advantage cDNA polymerase mix (Clontech), 150 μM of each dNTP, reaction buffer, and water to a final volume of 25 μl.

The sequences of the primers used in this study are as follows: 1) Human ESE-1: sense, 5′-ACCTGGATCCCACTGATGGCAAGCTC-3′ and antisense, 5′-GGAGGAAGAGGTTCTCCAGAGTCGG-3′, with an expected amplification product of 457 bp. 2) Human Ang-1: sense, 5′-TTTCCTCGCTGCCATTCTGACTC-3′, and antisense, 5′-TATGGATGTCAATGGGGGAGGTT-3′, with an expected amplification product of 947bp. 3) Human AML-1: sense, 5′-AAGTCGCCACCTACCACAG-3′ and antisense, 5′-CTCAGCCTCAGAGTCAGATGC-3′, with an expected amplification product of 248 bp (21). 4) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH): sense, 5′-CAAAGTTGTCATGGATGACC-3′ and antisense, 5′-CCATGGAGAAGGCTGGGG-3′, with an expected amplification product of 200 bp.

RT-PCR amplifications were carried out using a MJ Research thermal cycler PTC-100 as follows: ESE-1, 32 cycles of 30 s at 94 °C and 1 min 30 s at 68 °C followed by 7 min at 68 °C; Ang-1, 35 cycles of 30 s at 94 °C, and 1 min 30 s at 64 °C followed by 7 min at 64 °C; AML-1, 32 cycles of 30 s at 94 °C, 1 min at 60 °C, and 1 min 30 s at 72 °C followed by 10 min at 72 °C; GAPDH, 32 cycles of 30 s at 94 °C, 1 min at 56 °C, and 1 min 30 s at 72 °C followed by 10 min at 72 °C. 5 μl of the amplification product was analyzed on a 2% agarose gel.

Western Blot Analysis—Whole cell lysates (50 μg) of MCF7 cells were boiled in Laemmli buffer and resolved on 10% SDS-PAGE acrylamide gel. Proteins were transferred on Hybond-polyvinylidene difluoride membranes and immunoblotted using the ECL Western blotting Detection reagents (Amersham Biosciences). Rabbit polyclonal anti-ESE-1 antibody raised against a glutathione *S*-transferase fusion protein of the N terminus of human ESE-1 (East Acres Biologicals, Southbridge, MA) was used at a dilution of 1:1,000, and revealed with an anti-rabbit horseradish peroxydase antibody (Cell Signaling Technology, Beverly, MA) at a dilution of 1:1,000.

cDNA Microarrays—Microarray experiments were performed as previously described (22). In brief, 1×10^6 human breast cancer MCF-7 cells were transiently transfected in duplicates with 8 μg of PCI-ESE-1 or PCI plasmid using the LipofectAMINE Plus system (Invitrogen). Total RNA was isolated separately from each plate 24 h after transfection using the RNeasy Kit (Qiagen) according to the manufacturer's instructions. Atlas Human Cancer 1.2 cDNA microarray nylon membranes (Clontech), each containing 1176 different genes, were hybridized with [^{32}P]dATP-labeled cDNAs derived from 4 μg of total RNA according to the manufacturer at 68 °C in ExpressHyb solution (Clontech) using a Model 2000 Micro Hybridization Incubator (Robbins Scientific, Sunnyvale, CA). The filters were washed according to the user's instruction and exposed to Bio-Max MS film (Fisher) for different exposure times. Hybridizations were performed with duplicate experiments. The spot intensities reflecting gene expression levels on the

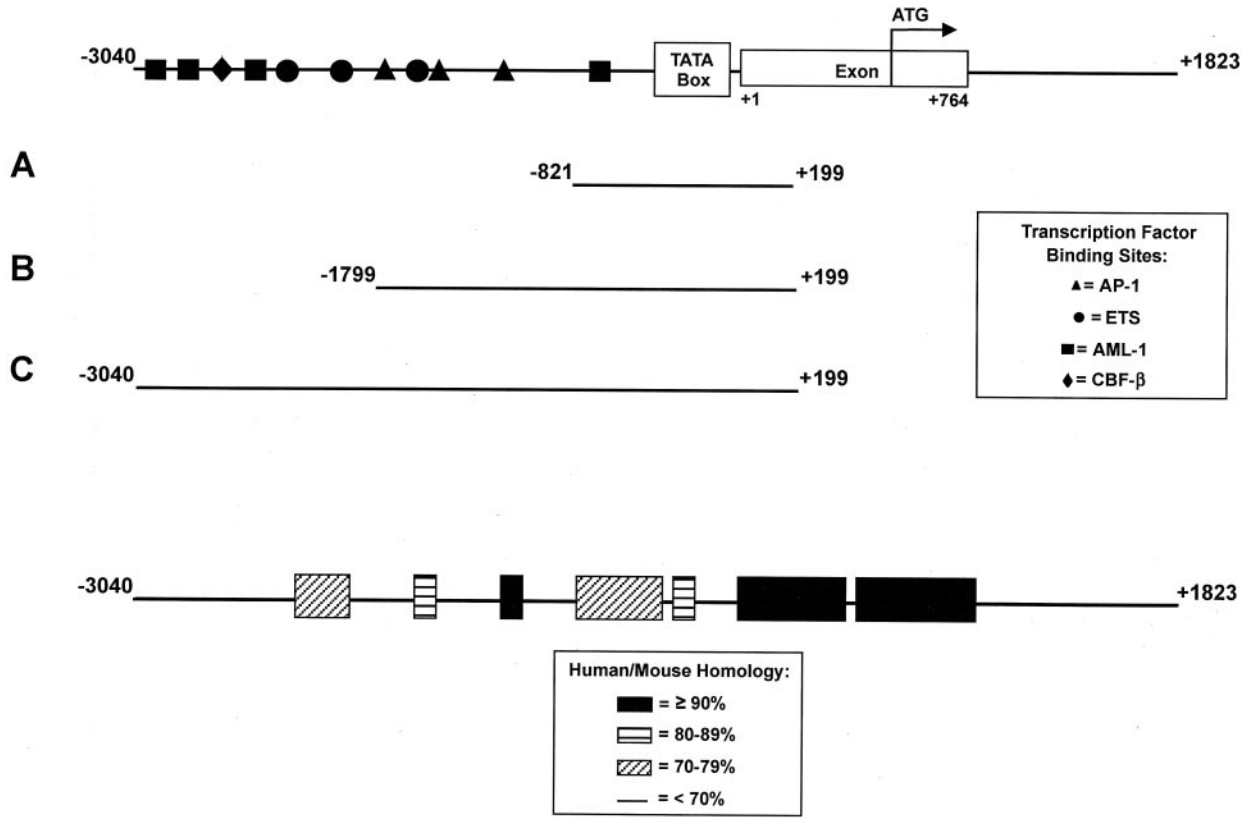

FIG. 1. **Schematic of the human *Ang-1* promoter.** *Ang-1* promoter, first exon, and intron, spanning from −3040 to +1823. Putative ETS (*filled circles*) and AP-1 (*filled triangles*) binding sites are shown, as well as AML-1 (*filled squares*) and CBF-β (*filled diamonds*) binding sites. Deletion constructs of the proximal promoter (*A–C*) and sequence homology between the human and mouse sequences are also depicted.

Atlas human cDNA array were quantified using the Atlas Image 2.0 Software (Clontech). The transcriptional profiles in the cells overexpressing ESE-1 were compared with those in the cells transfected with parental PCI vector, normalizing spot intensities based on the average of the intensities of all spots. Genes up-regulated or down-regulated by ESE-1 were validated by RT-PCR.

Immunohistochemistry—RA synovial soft tissue and bone were fixed for 48 h in 4% paraformaldehyde and specimens containing bone were subsequently decalcified for at least 2 weeks in 14% EDTA. Specimens were processed for paraffin embedding (Citadel 1000; Shandon, Pittsburgh, PA) and 4- or 5-μm serial sections were cut for immunohistochemical staining using an immunoperoxidase technique with diaminobenzidine (DAB; Dako, Carpinteria, CA) as the chromogen. Briefly, sections were deparaffinized followed by microwave antigen retrieval (GE Sensor convection microwave oven) in 10 mM EDTA pH 7.5 at 93 °C for 10 min and allowed to cool for at least 2 h. Sections were washed in Tris-buffered saline (TBS) and incubated for 60 min in serum block (10% fetal bovine serum and 10% normal rabbit serum diluted in TBS). Sections were then incubated with an affinity purified rabbit polyclonal anti-human Ang-1 antibody (L41309M, Regeneron Pharmaceuticals Inc., Tarrytown, NY), purified rabbit polyclonal anti-human ESE-1 antibody (AB3482, Chemicon International, Temecula, CA), or with an isotype matched control antibody (polyclonal Rabbit IgG, Santa Cruz Biotechnology Inc, Santa Cruz, CA) for 60 min. All incubations were carried out at room temperature. Sections were washed between every subsequent step with TBS. Endogenous peroxidase activity was blocked by incubating the sections in 3% H_2O_2 (diluted in TBS) for 30 min. Sections were subsequently incubated for 30 min with a biotinylated $F(ab')_2$ fragment of swine anti-rabbit immunoglobulin (Dako), followed by horseradish peroxidase-conjugated streptavidin (Dako), and developed with DAB (Dako) chromogen to the manufacturer's specifications. The sections were counterstained with hematoxylin (Sigma Diagnostics). Slides were examined and photographed using a transmitted light microscope and camera (Zeiss, Oberkochen, Germany).

RESULTS

Isolation and Characterization of the Human Ang-1 Promoter—The molecular mechanisms required for the induction of Ang-1 in response to inflammatory cytokines are currently unknown. To begin to identify potential mechanisms of *Ang-1* gene regulation we isolated a series of genomic fragments (Fig. 1, *A–C*) of the human *Ang-1* promoter, up to 3.2 kb in length, by long range PCR using human genomic DNA. The entire sequence of the *Ang-1* gene is published in the human genome data base (accession NT 008046). Verification of the sequence was performed by automated sequencing. Comparison of the mouse and human *Ang-1* promoter sequences revealed a relatively high overall degree of sequence homology. We examined the human *Ang-1* promoter sequence for potential binding sites for transcription factors known to be involved in inflammation, such as NF-κB, JAK/STAT, PPAR, NFAT, and C/EBP. Surprisingly, no obvious binding site for any of these transcription factor families was identified. However, putative binding sites for members of the AP-1 and ETS families were identified. In addition, putative AML-1 and CBF-β binding sites were identified in the *Ang-1* promoter.

Induction of the Ang-1 Promoter by Inflammatory Cytokines—To evaluate whether the *Ang-1* promoter contains regulatory elements capable of mediating induction in response to inflammatory cytokines the three genomic fragments encoding the *Ang-1* promoter (*A–C*) were incorporated into the pGL2 luciferase reporter construct. NIH3T3 fibroblasts were transiently transfected with each Ang-1 reporter construct, followed by stimulation with TNF-α (Fig. 2*A*). We have previously demonstrated that TNF-α consistently induces Ang-1 mRNA expression in cultured synovial fibroblasts (10). Stimulation of the 3.2-kb *Ang-1* promoter construct C (−3040/+199) with TNF-α resulted in a 4-fold induction of the promoter. Similarly, stimulation of the 2-kb construct B (−1799/+199) with TNF-α led to a 4-fold increase in transactivation. However, further deletion to a 1-kb construct (Ang-1 A, −821/+199) markedly reduced the inducibility of the promoter to TNF-α, suggesting that the main regulatory elements responsible for mediating

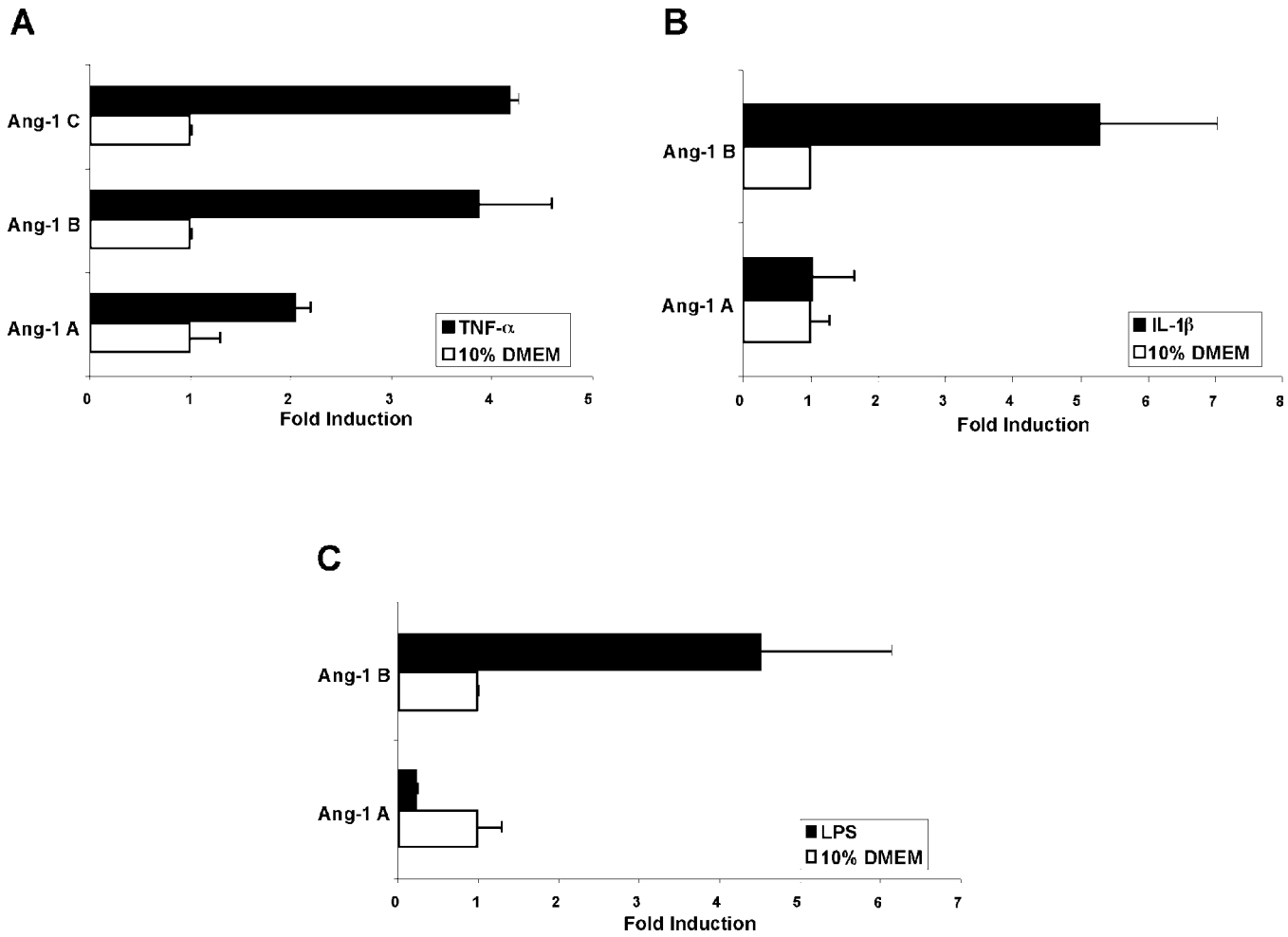

FIG. 2. **Transactivation of the *Ang-1* promoter in response to inflammatory stimuli.** Transactivation studies of Ang-1 luciferase reporter constructs A (−821/+199), B (−1799/+199), and C (−3040/+199) (300 ng each) in NIH3T3 fibroblasts after stimulation with TNF-α (50 ng/ml) (*A*), IL-1β (1 ng/ml) (*B*), or LPS (1 ng/ml) (*C*). The change in luciferase activity of the promoter construct after stimulation is expressed as fold induction compared with the activity of the promoter construct in unstimulated cells (DMEM supplemented with 10% FCS).

induction of the *Ang-1* gene reside in the nucleotide region between −1799 and −821. We also examined the inducibility of constructs A and B in NIH3T3 fibroblasts after stimulation with IL-1β and LPS (Fig. 2, *B* and *C*). A 4–5-fold level of induction of the activity of construct B was seen in response to IL-1β and LPS, but no induction was seen with construct A, suggesting the importance of regulatory elements between nucleotides −1799 and −821 in mediating this induction of *Ang-1* gene expression. This region contains putative AP-1 and ETS binding sites (Fig. 1).

Transactivation of the Ang-1 Promoter by ETS Factors—As shown in Fig. 1, there are several putative binding sites for members of the ETS transcription factor family in the *Ang-1* promoter. Selected members of the ETS transcription factor family have been shown previously to mediate the induction of other genes associated with inflammatory responses (23, 24). We therefore postulated that ETS factors might also be involved in the regulation of Ang-1 in response to inflammatory stimuli and tested the ability of a panel of ETS factors to transactivate the full-length *Ang-1* promoter. Cotransfection experiments using mammalian expression plasmids encoding a panel of ETS factors and the 3.2-kb *Ang-1* promoter luciferase construct were performed in HEK293 cells. We chose HEK293 cells because they do not express Ang-1 and can be transfected with high efficiency. As is shown in Fig. 3, only one of the ETS factors tested, ESE-1, was able to transactivate the *Ang-1* promoter by ~3-fold. These results suggest that ESE-1 is a potential transcriptional regulator of the *Ang-1* promoter.

Binding of ESE-1 to Putative ETS Binding Sites—To further define the potential role of ESE-1 in the regulation of Ang-1, we evaluated the ability of ESE-1 to bind to putative ETS binding sites identified in the *Ang-1* promoter by performing gel mobility shift assays. Three putative ETS binding sites were identified in the *Ang-1* promoter corresponding to regions beginning at −2578, −2199, and −1565 (Fig. 1). The binding of *in vitro* translated ESE-1 protein was compared with control extracts in a gel mobility shift assay using radiolabeled oligonucleotides encoding the three putative ETS binding sites (Fig. 4). Whereas weak binding of ESE-1 to the first two sites (*lanes 2* and *4*) compared with the control extract (*lanes 1* and *3*) was observed, ESE-1 bound with high affinity to the third site (*lane 6*). Interestingly, this high affinity ESE-1 binding site (−1565/−1562) is located within the region of the *Ang-1* promoter that is required for induction by inflammatory cytokines, whereas the low affinity sites are not.

Mutational Analysis of the Ang-1 Promoter ETS Binding Site—To assess the functional importance of the high affinity ESE-1 binding site, we mutated the ETS site corresponding to the region beginning at −1565 within the Ang-1 luciferase reporter construct C and evaluated the ability of ESE-1 to transactivate the mutant construct compared with the wild type *Ang-1* promoter construct C (Fig. 5). Whereas ESE-1 was able to increase transactivation of the wild type *Ang-1* pro-

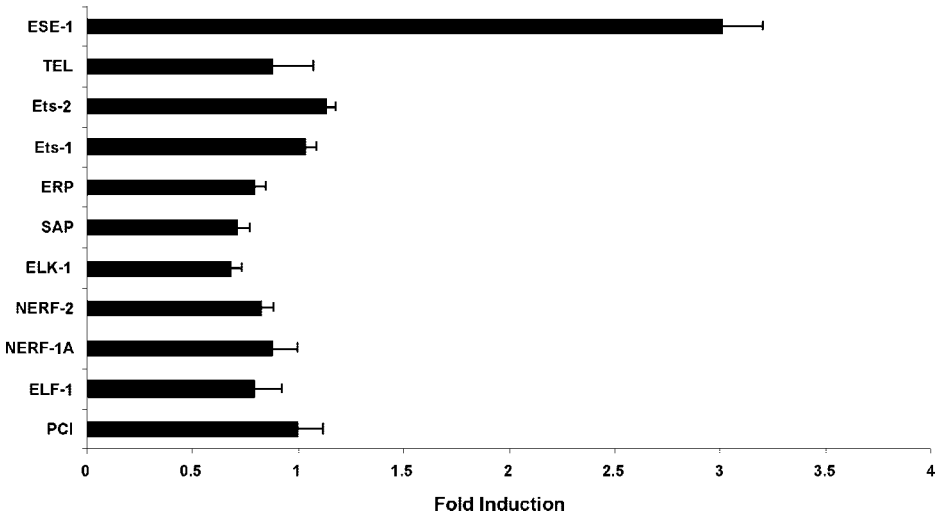

FIG. 3. **Transactivation of the *Ang-1* promoter by a panel of ETS factors.** Transactivation of the 3.2-kb Ang-1 luciferase reporter construct C (−3040/+199) (300 ng) by a panel of ETS transcription factors (150 ng each) compared with the empty mammalian expression plasmid (PCI, 150 ng) in HEK293 cells. The change in luciferase activity is expressed as fold induction compared with PCI.

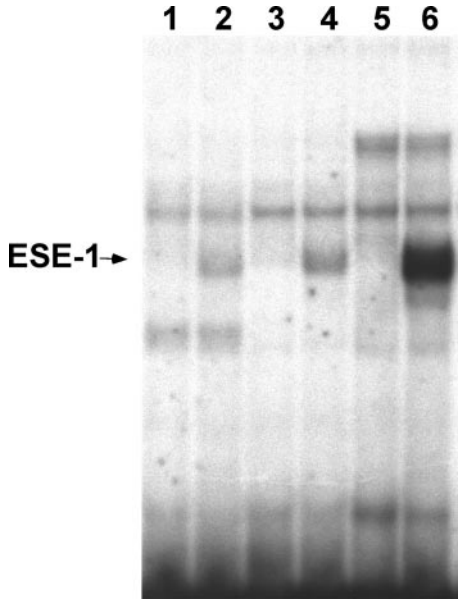

FIG. 4. **Gel mobility shift assays for ESE-1 binding to putative ETS sites in the *Ang-1* promoter.** *In vitro* translated ESE-1 protein (*lanes 2*, *4*, *6*) or control extract (*lanes 1*, *3*, *5*) was used with end-labeled oligonucleotide probes encoding putative ETS sites starting at positions −2578 (*lanes 1* and *2*), −2199 (*lanes 3* and *4*), and −1565 (*lanes 5* and *6*).

moter more than 8-fold and in a dose-dependent manner, only a minimal increase in transactivation of the mutated *Ang-1* promoter was observed, even at the highest doses of ESE-1. The effect of the ETS mutation on the inducibility of the promoter in response to inflammatory cytokines was also tested (Fig. 5*B*). This mutation led to a marked reduction in the inducibility of the promoter in response to the inflammatory cytokine TNF-α. We also tested the ability of ESE-1 to bind to a mutated ETS binding site through gel mobility shift assay analysis. As shown in Fig. 5*C*, the binding of *in vitro* translated ESE-1 protein compared with control extract was blocked by the mutated high-affinity ESE-1 binding site (−1565/−1562). An antibody to ESE-1 also blocked the binding of *in vitro* ESE-1 protein to the wild type high affinity ESE-1 binding site (−1565/−1562) compared with control extract, specifying that the protein binding to the high affinity site is indeed ESE-1. These results, together with Fig. 4, provide further support that the ETS binding site corresponding to the region beginning at −1565 is required for the transactivation of the *Ang-1* promoter by ESE-1.

Expression of ESE-1 and Ang-1 in Response to Inflammatory Cytokines—Having demonstrated the potential role for the ETS factor ESE-1 as a transcriptional regulator of the *Ang-1* promoter, we wished to examine the temporal relationship between Ang-1 and ESE-1 expression in primary cells after stimulation with inflammatory cytokines. Primary human synovial fibroblasts have been shown to express low levels of Ang-1 at base line (10). The levels of Ang-1 expression can be markedly increased in response to TNF-α. We therefore evaluated the temporal expression of ESE-1 and Ang-1 in primary synovial fibroblasts after stimulation with IL-1β and TNF-α. As is shown in Fig. 6*A*, Ang-1 was weakly expressed at base line. After stimulation with TNF-α, Ang-1 expression levels increased from base line to 2 h and peaked at about 6–24 h. ESE-1 expression was weakly expressed at base line, and was markedly induced at 2 h, peaking at 6 h with some expression persisting up to 24 and 48 h. Similar results were observed in synovial fibroblasts after stimulation with IL-1β (Fig. 6*B*). The temporal onset of ESE-1 expression in response to inflammatory cytokines followed by increases in Ang-1 levels further support a potential role for ESE-1 in the regulation of *Ang-1* gene expression.

Inflammatory Cytokine Stimulation Induces Binding of ESE-1 to a High Affinity Binding Site within the Ang-1 Promoter—To identify the specific protein binding to the ETS Ang-1 site, gel mobility shift assays were performed using whole cell extracts derived from human primary synovial fibroblasts stimulated with TNF-α. As shown in Fig. 7 (*lanes 3–8*), TNF-α stimulation is associated with an inducible change in binding pattern to the ETS Ang-1-binding site starting at position −1565. To identify the protein specifically binding to this site, EMSAs were performed in the presence or absence of antiserum to ESE-1. As shown in Fig. 7 (*lanes 9–14*), the ESE-1 antibody is able to block binding of the protein to the high affinity ETS Ang-1 site. Similar results were seen with IL-1β (data not shown). This suggests that the induction of Ang-1 is mediated by inducible binding of the ESE-1 protein to the *Ang-1* promoter.

Microarray Analysis of Ang-1 Expression in ESE-1-transfected Cells—To further evaluate the role of Ang-1 as a potential target of ESE-1, the MCF-7 breast cancer cell line was transiently transfected with a mammalian CMV expression plasmid encoding ESE-1 (PCI-ESE-1). Several cell lines were screened for high transfection efficiency and for expression of ESE-1. The MCF-7 cell line was chosen because the transfection efficiency is routinely over 50% and ESE-1 is only weakly expressed in these cells prior to transfection. Microarray anal-

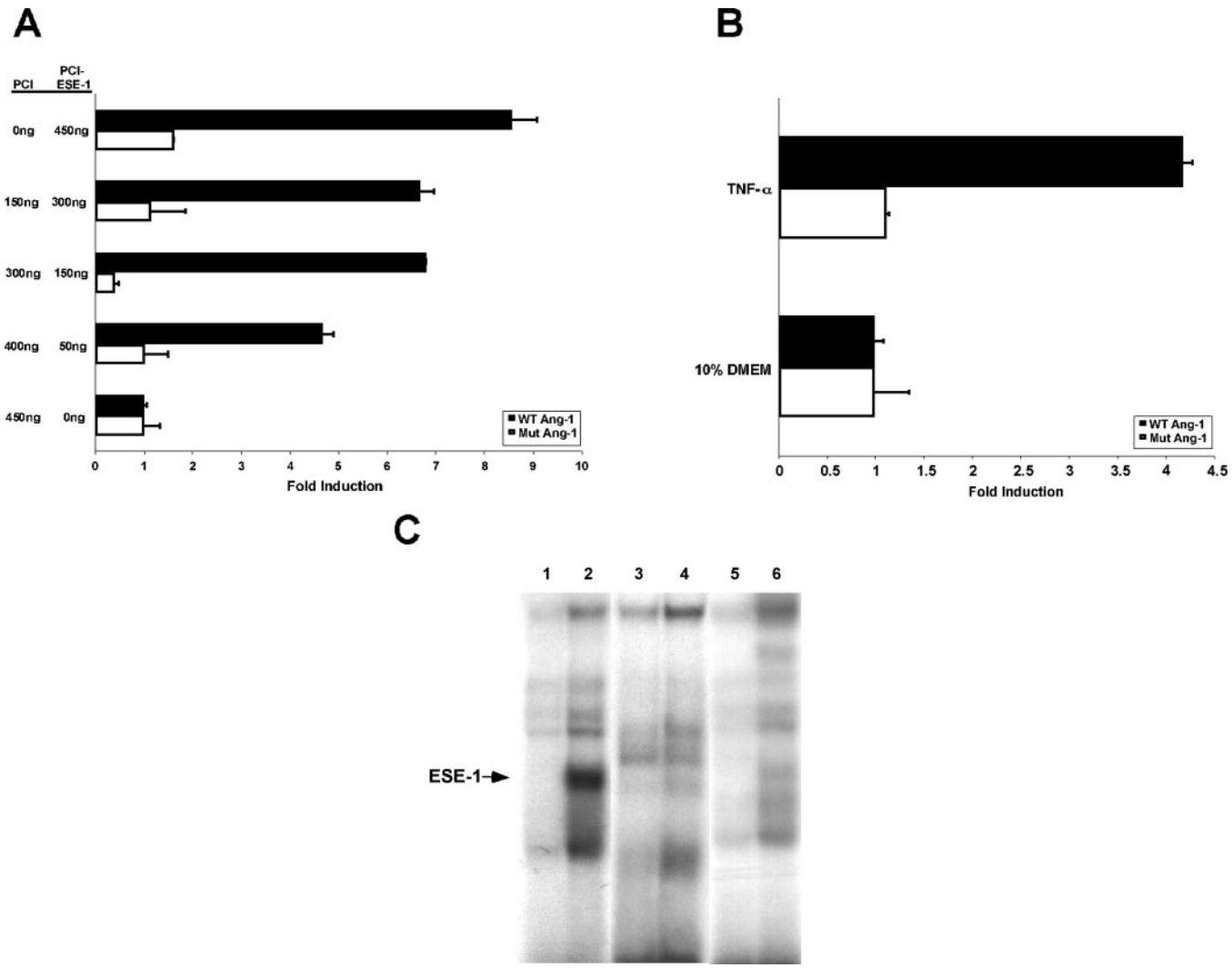

FIG. 5. **Mutational analysis of the *Ang-1* promoter.** Transactivation studies of wild type (*filled bars*) and mutant ETS binding site −1565/−1562 (*open bars*) Ang-1 luciferase reporter construct C (−3040/+199) (300 ng each) in HEK293 cells with increasing doses of ESE-1 (*A*). The change in luciferase activity is expressed as fold induction compared with PCI. Transactivation studies of wild type (*filled bars*) and mutant ETS binding site −1565/−1562 (*open bars*) Ang-1 luciferase reporter construct C (−3040/+199) (300 ng each) in NIH3T3 fibroblasts after stimulation with TNF-α (50 ng/ml) (*B*). The change in luciferase activity is expressed as fold induction compared with the promoter construct in unstimulated cells (DMEM supplemented with 10% FCS). *In vitro* translated ESE-1 protein (*lanes 2*, *4*, and *6*) or control extract (*lanes 1*, *3*, and *5*) in the presence (*lanes 5* and *6*) or absence (*lanes 1–4*) of ESE-1 antibody was used with end-labeled oligonucleotide probes encoding either the wild-type ETS binding site starting at position −1565 on the *Ang-1* promoter (*lanes 1*, *2*, *5*, and *6*) or the mutated ETS binding site starting at position −1565 (*lanes 3* and *4*) (*C*).

ysis was performed with total RNA extracted from the transiently transfected cells after 24 h. Following ESE-1 transfection, a 2.4-fold induction of Ang-1 mRNA expression was observed (Fig. 8*A*). Semi-quantitative RT-PCR was also performed to confirm the changes observed by microarray (Fig. 8*B*). These results demonstrate low levels of Ang-1 and ESE-1 in control-transfected cells, and a similar increase in Ang-1 expression in ESE-1-transfected cells. Western blot analysis of ESE-1-transfected cells confirmed increased expression of the ESE-1 protein in these cells compared with control cells transfected with empty vector (Fig. 8*C*). The results of these experiments further support a direct role for ESE-1 in the regulation of *Ang-1* gene expression.

AML-1 Is Constitutively Expressed in Human Synovial Fibroblasts and Interacts Synergistically with ESE-1 and CBF-β to Regulate the Ang-1 Gene—AML-1 (CBF-α/CBFA2) is a member of the runt transcription factor family that was recently shown to be one of the main factors regulating constitutive expression of Ang-1 in hematopoietic cells (25). Targeted disruption of AML-1 leads to a marked reduction in Ang-1 expression in hematopoietic cells, resulting in defective angiogenesis that can be rescued by administration of Ang-1. Because synovial fibroblasts constitutively express low levels of Ang-1, we postulated that AML-1 could also regulate the expression of Ang-1 in these cells. Evaluation of AML-1 expression by RT-PCR demonstrated constitutively high levels of AML-1 in the synovial fibroblasts that did not change in response to TNF-α (Fig. 9*A*). Similar results were observed with IL-1β stimulation (data not shown). Another transcription factor, core binding factor β (CBF-β), enhances the DNA binding activity of AML-1 (26, 27). This factor was also constitutively expressed at base line in the synovial fibroblasts (data not shown).

We were also interested in determining whether AML-1 is capable of transactivating the *Ang-1* promoter. Cotransfection experiments with the *Ang-1* promoter luciferase construct C and increasing amounts of AML-1 resulted in a maximal 3-fold increase in the activity of the *Ang-1* promoter (Fig. 9*B*). AML-1 has also been shown to interact synergistically with other ETS family members, including ETS-1, ETS-2, and PU.1, to promote the transactivation of several

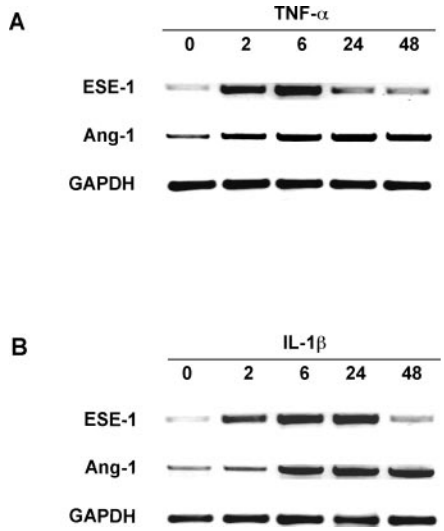

FIG. 6. **Assessment of ESE-1 and Ang-1 mRNA expression after inflammatory stimulation.** Semi-quantitative RT-PCR of ESE-1 and Ang-1 mRNA expression in primary human synovial fibroblasts stimulated with TNF-α (5 ng/ml) (*A*) or IL-1β (100 pg/ml) (*B*) and harvested at different time points (0, 2, 6, 24, and 48 h) after stimulation. GAPDH is used as an internal control.

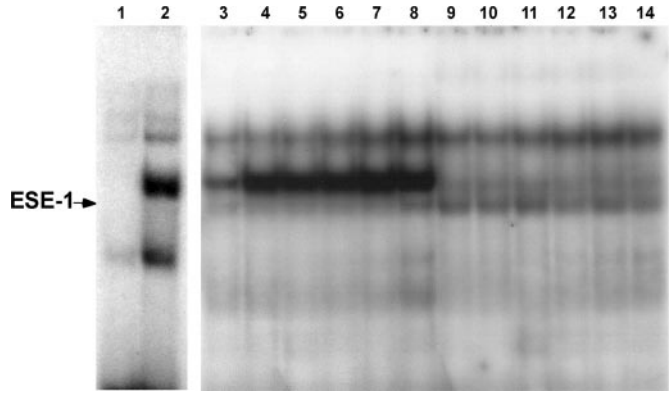

FIG. 7. **Gel mobility shift assays with *Ang-1* promoter high affinity ETS binding site.** *In vitro* translated ESE-1 protein (*lane 2*), control extract (*lane 1*), or whole cell extracts (10 μg) (*lanes 3–14*) from human primary synovial fibroblasts stimulated with TNF-α (5 ng/ml) and harvested at different time points (0 h, *lanes 3* and *9*; 2 h, *lanes 4* and *10*; 6 h, *lanes 5* and *11*; 18 h, *lanes 6* and *12*; 24 h, *lanes 7* and *13*; 48 h, *lanes 8* and *14*) after stimulation in the presence (*lanes 9–14*) or absence (*lanes 3–8*) of ESE-1 antibody used with end-labeled oligonucleotide probe encoding the high affinity ETS binding site on the *Ang-1* promoter starting at position −1565.

other genes (28–30). Therefore, we tested the ability of AML-1 to cooperate with the ETS factor ESE-1 to transactivate the *Ang-1* promoter. Cotransfection of AML-1 and ESE-1 resulted in a marked synergistic transactivation of the *Ang-1* promoter (Fig. 9*C*). Whereas cotransfection with AML-1 or ESE-1 alone only led to a 2–3-fold increase in *Ang-1* promoter activity, cotransfection of both factors resulted in a synergistic 11-fold increase in *Ang-1* promoter activity.

AML-1 also associates with CBF-β to enhance the DNA binding activity of AML-1. Similar synergistic transactivation of the *Ang-1* promoter was observed in cotransfection experiments using all three transcription factors, ESE-1, AML-1, and CBF-β (Fig. 9*D*). Little to no induction of the *Ang-1* promoter was seen with low doses (75–100 ng) of CBF-β (data not shown). These results are consistent with the fact that CBF-β does not bind DNA directly, but rather enhances the binding of AML-1 (CBF-α). Weaker induction of the *Ang-1* promoter by AML-1 alone was observed in Fig. 9*D* than in 9*C* (3.5-fold *versus* 11-fold) because lower amounts of the AML-1 plasmid DNA (75 *versus* 100 ng) were used in these transfection experiments while maintaining the same total amounts of DNA. The combination of ESE-1, AML-1, and CBF-β resulted in a 9-fold induction of the *Ang-1* promoter (Fig. 9*D*). Site-directed mutagenesis of the ETS binding site −1565 to −1562 in the *Ang-1* promoter resulted in a marked reduction in the synergistic transactivation by the combination of ESE-1, AML-1, and CBF-β compared with the wild-type construct (Fig. 9*D*), further supporting the requirement of this high affinity ESE-1 binding site in activation of the *Ang-1* promoter. The results of these transactivation studies demonstrate that the interactions between AML-1, CBF-β, and ESE-1 are more than additive and result in synergistic regulation of *Ang-1* gene expression.

Evaluation of ESE-1 and Ang-1 in Patients with Rheumatoid Arthritis—We have previously shown that Ang-1 is expressed in the synovium of patients with rheumatoid arthritis (10), and that ESE-1 is expressed in rheumatoid synovium (15). Because our results support a role for ESE-1 in regulating Ang-1, we were interested in determining whether ESE-1 and Ang-1 are expressed in similar regions of the rheumatoid synovium. Their expression was evaluated by immunohistochemistry in serial sections of tissue samples obtained from patients with RA. Representative examples of the immunohistochemistry are shown in Fig. 10. Ang-1 and ESE-1 exhibit very similar staining patterns, with strong expression in the synovial lining layer as well as in individual cells within the subsynovium and with a complete absence of staining in the isotype-matched control sample. These results further support a role for ESE-1 in the regulation of *Ang-1* gene expression and angiogenesis in the setting of inflammation.

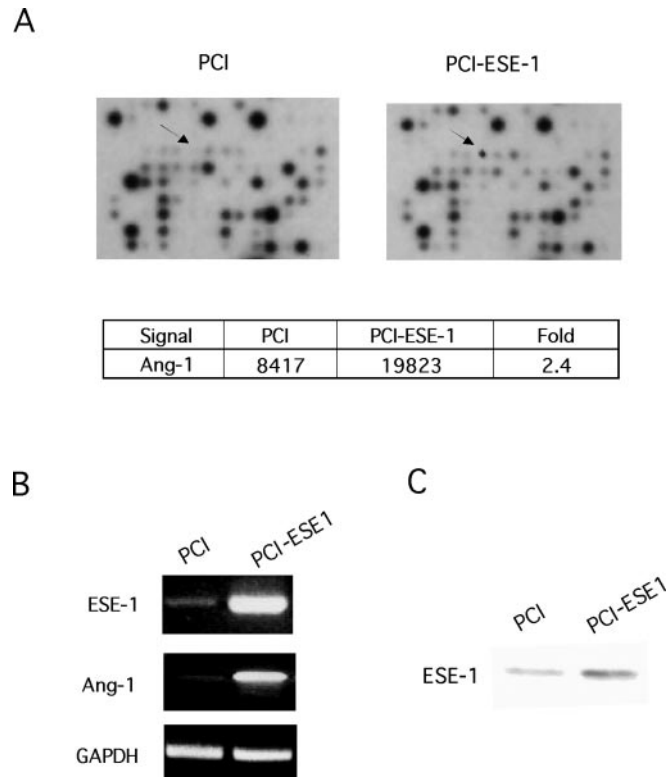

FIG. 8. **Analysis of Ang-1 expression in ESE-1-transfected cells.** Microarray analysis in MCF-7 cells transfected with control (PCI) expression plasmid *versus* ESE-1-transfected cells. *Arrow* points to location of Ang-1 on microarray grid. Total counts and fold induction of Ang-1 are shown below grid (*A*). Assessment of ESE-1 and Ang-1 mRNA expression in PCI and PCI-ESE-1-transfected cells by semi-quantitative RT-PCR. GAPDH is used as internal control (*B*). Western blot analysis of ESE-1 in PCI and PCI-ESE-1-transfected cells (*C*).

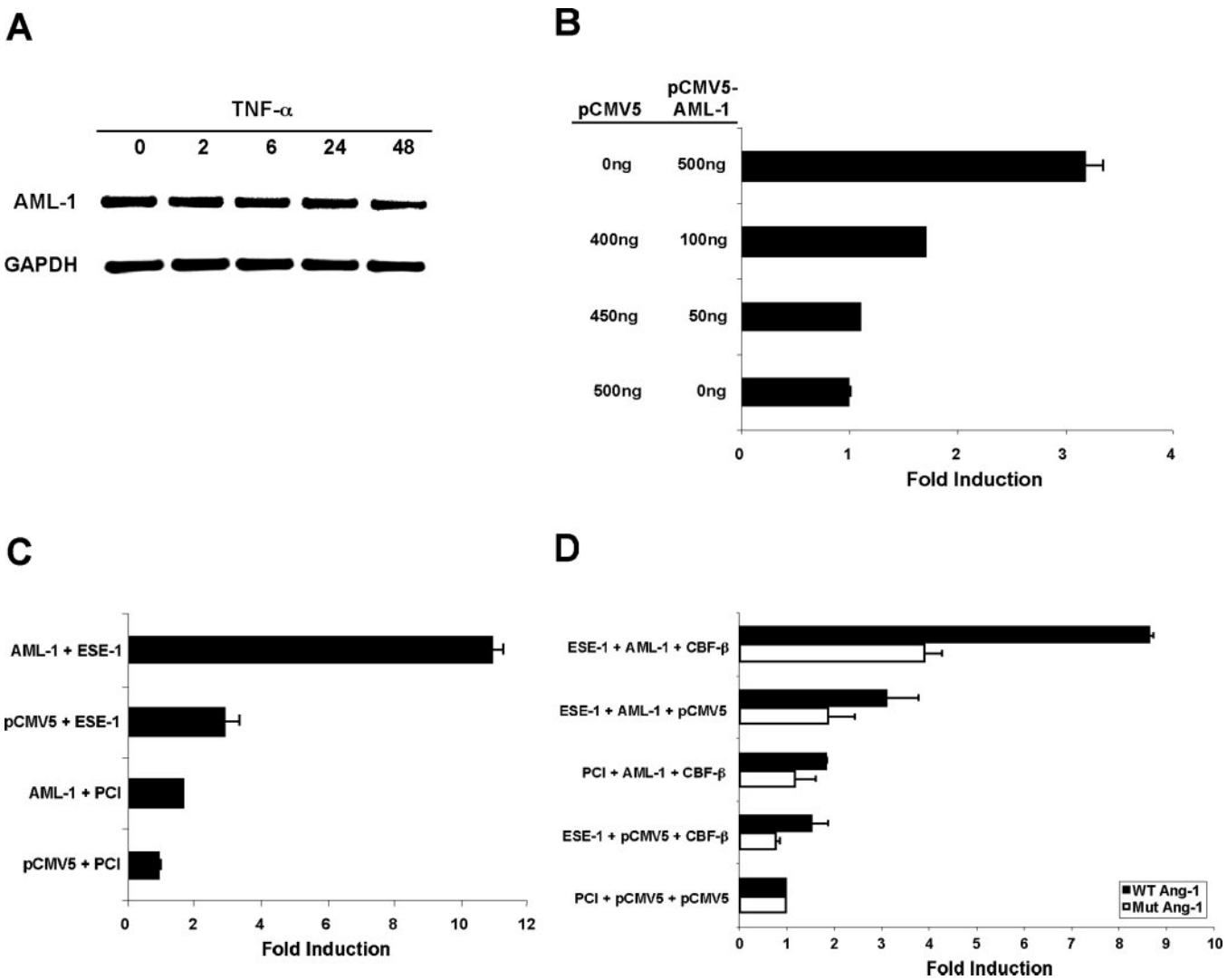

FIG. 9. **Evaluation of AML-1 in primary human synovial fibroblasts and on transactivation of the *Ang-1* promoter.** Semi-quantitative RT-PCR of AML-1 mRNA expression in primary human synovial fibroblasts stimulated with TNF-α (5 ng/ml) at different time points (0, 2, 6, 24, and 48 h) after stimulation. GAPDH is used as an internal control (*A*). Transactivation studies of wild type Ang-1 luciferase reporter construct C ($-3040/+199$) (300 ng) with increasing doses of AML-1 (*B*) and with cotransfections of AML-1 and ESE-1 (100 ng of each transcription factor) (*C*) in HEK293 cells. Transactivation studies of wild type Ang-1 luciferase reporter construct C (*filled bars*) or mutant ETS binding site $-1565/-1562$ Ang-1 luciferase reporter construct C (*open bars*) (150 ng of each) with AML-1, CBF-β, and ESE-1 (75 ng of each) in HEK293 cells (*D*). The change in luciferase activity is expressed as fold induction compared with the empty vectors (PCI + pCMV5).

DISCUSSION

Angiogenesis is required for the growth and proliferation of inflammatory tissue in a number of diseases. Angiogenic growth factors such as VEGF, bFGF, and Ang-1 are critical mediators of angiogenesis. These angiogenic growth factors act upon endothelial cells, enhancing their proliferation and migration to sites of inflammation. The release of inflammatory cytokines and hypoxia promotes the local expression of these growth factors. Inflammatory cytokines such as IL-1β and TNF-α have been shown to induce the expression of both VEGF and bFGF (31–33). The results of our studies as well as others have recently shown that Ang-1 expression is also stimulated by TNF-α (10, 11). The primary goal of our study was to identify the transcriptional mechanisms responsible for mediating the induction of the *Ang-1* gene in the setting of inflammation.

The regulation of other angiogenic growth factors in the setting of inflammation is dependent on several transcription factors. Members of the Rel/NF-κB family represent prototype transcription factors that mediate inflammatory responses. Activation of these factors does not require protein synthesis, as they are sequestered in the cytoplasm, where they are bound noncovalently to the endogenous inhibitors, the Iκ-B proteins. Upon stimulation by inflammatory cytokines or endotoxin, these inhibitors are phosphorylated and proteolytically degraded, allowing NF-κB to be translocated to the nucleus, where it binds to the regulatory regions of target genes as a homo- or heterodimer (34, 35). The induction of both bFGF and VEGF by TNF-α has been shown to be mediated at least in part by NF-κB (31). The promoters of both of these angiogenic growth factors contain binding sites for NF-κB. In contrast, we were unable to identify obvious binding sites for NF-κB within the proximal 3 kb of the *Ang-1* promoter.

The absence of putative NF-κB binding sites in the *Ang-1* promoter led us to look for alternative regulatory mechanisms. Several other transcription factors have been identified to play a role in mediating inflammatory responses, including ETS, Egr-1, C/EBP, STAT, and AP-1 (36, 37). Among these, only binding sites for AP-1 and ETS family members were identified within the *Ang-1* promoter. The AP-1 family member c-Jun has been shown to be a critical transcriptional regulator of *VEGF*

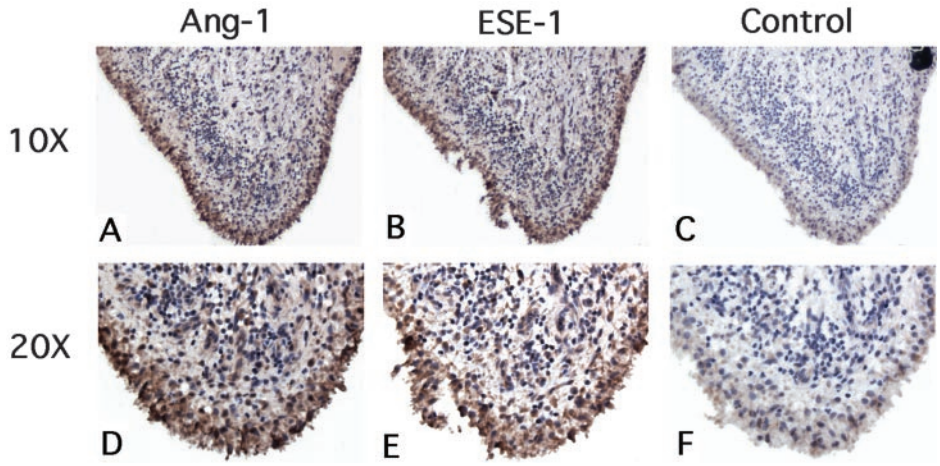

FIG. 10. **Ang-1 and ESE-1 expression in RA synovial soft tissue and bone.** Evaluation of Ang-1 (*A* and *D*) and ESE-1 (*B* and *E*) expression in RA synovial soft tissue and bone by immunohistochemistry compared with isotype-matched control (*C* and *F*) at low magnification (10×) and high magnification (20×).

gene expression during inflammation and cooperate with the transcription factor HIF-1α to regulate the *VEGF* gene in the setting of hypoxia (38, 39).

The *ETS* genes are a family of at least thirty members that function as transcription factors (23). All ETS factors share a highly conserved DNA binding domain of 80–90 amino acids, known as the ETS domain. ETS factors play a central role in regulating genes involved in development, cellular differentiation, and proliferation. Several studies have demonstrated a role for members of the ETS factor family in inflammation and angiogenesis. For example, the *TNF-α* gene is regulated by ETS-1 (24). TNF-α can also induce the expression of ETS-1 and is up-regulated in animal models of vascular inflammation (40). ETS-1 has also been shown to be enriched in angiogenic blood vessels and can cooperate with another transcription factor, HIF-1α, to regulate the expression of the VEGF receptor Flk-1 (41, 42). We have recently demonstrated a role for the ETS factor ESE-1 as a transcriptional mediator of inflammation (14). ESE-1 is inducible in several cell types in response to inflammatory cytokines and endotoxin. In the current study we demonstrate that, among a panel of ETS factors tested, only ESE-1 was able to transactivate the *Ang-1* promoter, and was co-expressed with Ang-1 in primary synovial fibroblasts after stimulation with inflammatory cytokines. That Ang-1 is indeed a target for ESE-1 was further validated in transcriptional profiling studies. We demonstrate that the endogenous *Ang-1* gene is induced after overexpression of ESE-1 by transient transfection, strongly suggesting that the endogenous *Ang-1* gene is regulated by ESE-1.

The transcription factor AML-1 (CBF-α/CBFA2) is a critical regulator of constitutive *Ang-1* gene expression in hematopoietic cells (25). AML-1 belongs to the runt transcription factor family, members of which share a 128-amino acid domain known as the runt domain that mediates DNA binding as well as dimerization to CBF-β (CBFB) (43, 44). CBF-β has no direct DNA binding capability, but enhances binding of AML-1 to DNA (45). AML-1 has been shown to be involved in the regulation of a wide variety of genes in cells of hematopoietic origin, including several B- and T cell-specific genes, cytokines, and their receptors, and several enzymes including neutrophil elastase, granzyme B, and myeloperoxidase (46–48). Other members of the runt transcription factor family are also expressed in several other cell types. For example, AML-3 (CBFA1) is involved in the regulation of the osteopontin gene in skeletal tissues. Overlapping expression of osteopontin and AML-3 was observed in osteoblasts, chondrocytes, and periosteal fibroblasts (49). We observed constitutive expression of AML-1 in synovial fibroblasts that remained unchanged after stimulation with inflammatory cytokines. This is the first example that we are aware of demonstrating AML-1 expression in nonhematopoietic cells. Because Ang-1 is a known target of AML-1 under normal conditions in hematopoietic cells, this would also support a role for AML-1 in the regulation of Ang-1 in synovial cells (25). AML-1 forms a ternary complex together with CBF-β and ETS-1 to regulate the expression of the osteopontin gene, and AML-1 and ETS-1 have been shown to synergistically transactivate the osteopontin promoter (49). We similarly observed a synergistic response in transactivation of the *Ang-1* promoter with the combination of ESE-1 and AML-1, suggesting that AML-1 may also act to promote the induction of the *Ang-1* gene under inflammatory conditions through cooperativity with ESE-1, even though AML-1 expression levels remain unchanged.

Several studies have demonstrated that there is marked neovascularization within the rheumatoid synovium (50, 51). In addition to its role in supplying blood to the inflamed synovium, the endothelial cells derived from these new blood vessels actively participate in the inflammatory response by recruiting lymphocytes and releasing cytokines and angiogenic factors (4). We recently showed that ESE-1 is also highly expressed in the synovium of patients with RA (15). We and others (10) have also shown that Ang-1 is expressed in synovial tissues from patients with RA. Ang-1 and ESE-1 were detected not only around developing blood vessels but also within the synovial lining layer and other less vascular regions within the subsynovium. The similar expression pattern of ESE-1 and Ang-1 in patients with RA further supports a role for ESE-1 as a transcriptional regulator of Ang-1 expression in the setting of inflammation. In addition to its role in promoting vessel maturation, Ang-1 may also act to promote the migration of endothelial cells to sites of active inflammation.

In summary, the results of our studies demonstrate that Ang-1 is one of several critical regulators of angiogenesis that is up-regulated in the setting of inflammatory conditions such as rheumatoid arthritis. In contrast to other angiogenic factors, the induction of the *Ang-1* gene does not appear to be directly dependent upon NF-κB, but instead is mediated in part by the ETS factor ESE-1 acting cooperatively with the runt transcription factors AML-1 and CBF-β.

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